

Protein IDs	Majority pr	Peptide coi	Peptide coi	Peptide coi	Protein names	Gene name
P61604;B8ZZL8;B8ZZ54	P61604;B8	8;6;4;3	8;6;4;3	8;6;4;3	10 kDa heat shock protein,	HSPE1
Q15029-2;Q15029;Q15029	Q15029-2;(	10;10;9;4;3	9;9;8;3;2;1	9;9;8;3;2;1	116 kDa U5 small nuclear ribonucleoprotein	EFTUD2
Q9NRX4-2;Q9NRX4	Q9NRX4-2; 1;1	1;1	1;1	1;1	14 kDa phosphohistidine phosphatase	PHPT1
P31946-2;P31946;Q4VY	P31946-2;F8	8;3;3;3;2	4;4;1;1;1;1	4;4;1;1;1;1	14-3-3 protein beta/alpha;1	YWHAH
P62258;P62258-2;B4DJI	P62258;P6	15;12;5;5;5	12;10;3;3;4	12;10;3;3;4	14-3-3 protein epsilon	YWHAH
Q04917;A2IDB2;F8WEB	Q04917	12;5;3;3	9;4;2;2	9;4;2;2	14-3-3 protein eta	YWHAH
P61981	P61981	10	7	7	14-3-3 protein gamma;14-3	YWHAH
P31947-2;P31947	P31947-2;F	17;17	17;17	14;14	14-3-3 protein sigma	SFN
P27348;E9PG15	P27348;E9	12;8	8;6	8;6	14-3-3 protein theta	YWHAH
P63104;E7EX29;E7ESK7	P63104;E7	14;11;8;8;7	11;8;6;7;6;1	10;7;6;6;5;1	14-3-3 protein zeta/delta	YWHAH
Q9C0C2;Q9C0C2-2	Q9C0C2;Q	3;2	3;2	3;2	182 kDa tankyrase-1-binding protein	TNKS1BP1
Q9NUQ2	Q9NUQ2	2	2	2	1-acyl-sn-glycerol-3-phosphatase	AGPAT5
P09543-2;P09543	P09543-2;F	1;1	1;1	1;1	2,3-cyclic-nucleotide 3-phosphodiesterase	CNP
Q16698-2;Q16698;E5RJ	Q16698-2;(	7;7;3;3;3;1	7;7;3;3;3;1	7;7;3;3;3;1	2,4-dienoyl-CoA reductase,	DECR1
Q9Y6K5;F8VWK9;F8VS3	Q9Y6K5;F8	4;2;2	4;2;2	4;2;2	2-5-oligoadenylate synthetase	OAS3
A0A087X211;P62333;H0A0A087X21	A0A087X21	7;7;5;4;1;1	7;7;5;4;1;1	7;7;5;4;1;1	26S protease regulatory subunit	PSMC6
P62191-2;P62191;G3V4	P62191-2;F	5;5;1	5;5;1	5;5;1	26S protease regulatory subunit	PSMC1
E9PM69;R4GNH3;P179E	E9PM69;R4	5;5;5;3;3;3	5;5;5;3;3;3	5;5;5;3;3;3	26S protease regulatory subunit	PSMC3
P43686-2;P43686	P43686-2;F	4;4	4;4	4;4	26S protease regulatory subunit	PSMC4
P35998;A0A1W2PQS1;F	P35998;A0	10;9;5;4	10;9;5;4	10;9;5;4	26S protease regulatory subunit	PSMC2
J3QQM1;P62195-2;P62195	J3QQM1;P	5;5;5;4;4;4	5;5;5;4;4;4	4;4;4;3;3;3	26S protease regulatory subunit	PSMC5
A0A087WW66;Q99460	A0A087WW	6;6;6;2;1;1	6;6;6;2;1;1	6;6;6;2;1;1	26S proteasome non-ATPase	PSMD1
B1AJY5;B1AJY7;O75832	B1AJY5;B1	2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	26S proteasome non-ATPase	PSMD10
O00231;O00231-2;J3QF	O00231;O	10;10;6;1	10;10;6;1	10;10;6;1	26S proteasome non-ATPase	PSMD11
O00232-2;O00232;J3KT	O00232-2;(	6;6;1;1	6;6;1;1	6;6;1;1	26S proteasome non-ATPase	PSMD12
J3KNQ3;Q9UNM6;Q9UI	J3KNQ3;Q	6;6;6;5;4;4	6;6;6;5;4;4	6;6;6;5;4;4	26S proteasome non-ATPase	PSMD13
O00487	O00487	1	1	1	26S proteasome non-ATPase	PSMD14
Q13200;Q13200-3;Q13200	Q13200;Q	12;10;8;3;2	12;10;8;3;2	12;10;8;3;2	26S proteasome non-ATPase	PSMD2
O43242-2;O43242	O43242-2;(	5;5	5;5	5;5	26S proteasome non-ATPase	PSMD3
Q5VWC4;P55036;H0Y3	Q5VWC4;P	2;2;1;1;1	2;2;1;1;1	2;2;1;1;1	26S proteasome non-ATPase	PSMD4
Q15008-3;Q15008-2;Q15008	Q15008-3;(	4;4;4;4;3;2	4;4;4;4;3;2	4;4;4;4;3;2	26S proteasome non-ATPase	PSMD6
H3BNT7;H3BTM8;P516H	H3BNT7;H	3;3;3;1	3;3;3;1	3;3;3;1	26S proteasome non-ATPase	PSMD7
F5H5V4;F5GX23;J3KN2	F5H5V4;F	5;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	26S proteasome non-ATPase	PSMD9
Q13442	Q13442	5	5	5	28 kDa heat- and acid-stable protein	PDAP1
P82912-2;P82912	P82912-2;F	1;1	1;1	1;1	28S ribosomal protein S11,	MRPS11
A6ND22;Q9Y3D3-2;Q9YA	A6ND22;Q	1;1;1	1;1;1	1;1;1	28S ribosomal protein S16,	MRPS16
E9PE17;I3L0E3;Q9Y2R5	E9PE17;I3	2;2;2	2;2;2	2;2;2	28S ribosomal protein S17,	MRPS17;hC
Q9Y676;A0A0G2JIC6	Q9Y676;A	4;3	4;3	4;3	28S ribosomal protein S18b	MRPS18B
Q9Y399;Q5T8A0	Q9Y399;Q	5;3;2	3;2	3;2	28S ribosomal protein S2, r	MRPS2
P82921	P82921	1	1	1	28S ribosomal protein S21,	MRPS21
G5E9W7;G5E9V5;P8265	G5E9W7;G	4;4;4;3;3;3	4;4;4;3;3;3	4;4;4;3;3;3	28S ribosomal protein S22,	MRPS22
J3QLR8;Q9Y3D9	J3QLR8;Q	9;2;2	2;2	2;2	28S ribosomal protein S23,	MRPS23
P82663;E7EPW2;P8266	P82663	3;1;1;1	3;1;1;1	3;1;1;1	28S ribosomal protein S25,	MRPS25
D6RH20;G5EA06;Q9255	D6RH20;G	5;2;2;2;2;1	2;2;2;2;1	2;2;2;2;1	28S ribosomal protein S27,	MRPS27
Q9Y2Q9;E5RFT8;E5RGC	Q9Y2Q9;E	5;2;1;1;1;1	2;1;1;1;1;1	2;1;1;1;1;1	28S ribosomal protein S28,	MRPS28
P82909;D6R941	P82909;D	6;2;1	2;1	2;1	28S ribosomal protein S36,	MRPS36
P82675	P82675	1	1	1	28S ribosomal protein S5, r	MRPS5
P82932	P82932	1	1	1	28S ribosomal protein S6, r	MRPS6

J3QQS1;J3QLS3;Q9Y2R9	J3QQS1;J3(3;3;3;2;2	3;3;3;2;2	3;3;3;2;2	28S ribosomal protein S7, r	MRPS7	
P82933	P82933	2	2	2	28S ribosomal protein S9, r	MRPS9
E9PDF2;E9PCR7;Q0221	E9PDF2;E9(18;18;18;1	18;18;18;1	18;18;18;1	2-oxoglutarate dehydrogen	OGDH	
H0Y8N7;Q9BYD6	H0Y8N7;Q(1;1	1;1	1;1	39S ribosomal protein L1, r	MRPL1	
Q9Y3B7-2;Q9Y3B7;Q9Y	Q9Y3B7-2;(3;3;2;1;1	3;3;2;1;1	3;3;2;1;1	39S ribosomal protein L11, r	MRPL11	
B4DLN1;P52815	B4DLN1;P5 6;3	6;3	3;3	39S ribosomal protein L12, r	MRPL12	
H0YAX3;E5RJI7;Q9BYD1	H0YAX3;E5 2;2;2	2;2;2	2;2;2	39S ribosomal protein L13, r	MRPL13	
Q9H0U6	Q9H0U6	3	3	3	39S ribosomal protein L18, r	MRPL18
C9IY40;Q5T653	C9IY40;Q5(1;1	1;1	1;1	39S ribosomal protein L2, r	MRPL2	
E7ESL0;J3KQY1;Q9NWL	E7ESL0;J3K 2;2;2;2;2	2;2;2;2;2	2;2;2;2;2	39S ribosomal protein L22, r	MRPL22	
Q96A35	Q96A35	2	2	2	39S ribosomal protein L24, r	MRPL24
H0Y4J2;A6NHR2;S4R36	H0Y4J2;A6(1;1;1;1	1;1;1;1	1;1;1;1	39S ribosomal protein L37, r	MRPL37	
Q96DV4;Q96DV4-2	Q96DV4;Q(2;1	2;1	2;1	39S ribosomal protein L38, r	MRPL38	
C9JG87;Q9NYK5;Q9NYK	C9JG87;Q9 1;1;1	1;1;1	1;1;1	39S ribosomal protein L39, r	MRPL39	
K7EKI4;K7ELF1;K7ELQ0	K7EKI4;K7E 1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	39S ribosomal protein L4, r	MRPL4	
H0YBU8;H0Y6Y8;B1AL0	H0YBU8;H(2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	39S ribosomal protein L43, r	MRPL43	
Q9H9J2	Q9H9J2	1	1	1	39S ribosomal protein L44, r	MRPL44
E9PI78;E9PNF1;Q13405	E9PI78;E9P 1;1;1	1;1;1	1;1;1	39S ribosomal protein L49, r	MRPL49	
Q8N5N7-2;Q8N5N7	Q8N5N7-2; 2;2	2;2	2;2	39S ribosomal protein L50, r	MRPL50	
Q96EL3	Q96EL3	2	2	2	39S ribosomal protein L53, r	MRPL53
Q9BYD2	Q9BYD2	1	1	1	39S ribosomal protein L9, r	MRPL9
Q15125;C9J719;C9JJ78	Q15125;C9 3;2;2	3;2;2	3;2;2	3-beta-hydroxysteroid-Delta	EBP	
Q99714;Q99714-2;Q5H	Q99714;Q(9;8;5	9;8;5	9;8;5	3-hydroxyacyl-CoA dehydro	HSD17B10	
P31937;H7BZL2	P31937;H7 2;1	2;1	2;1	3-hydroxyisobutyrate dehy	HIBADH	
K7ERC8;Q06136	K7ERC8;Q0 1;1	1;1	1;1	3-ketodihydrosphingosine r	KDSR	
P51857-2;P51857	P51857-2;F 1;1	1;1	1;1	3-oxo-5-beta-steroid 4-dehy	AKR1D1	
P46783;Q9NQ39;F6U21	P46783;Q9 5;4;3;3;3	5;4;3;3;3	5;4;3;3;3	40S ribosomal protein S10;f	RPS10;RPS:	
P62280;M0QZC5;M0R1	P62280;M(10;8;4;2	10;8;4;2	10;8;4;2	40S ribosomal protein S11	RPS11	
P25398	P25398	7	7	7	40S ribosomal protein S12	RPS12
P62277;J3KMX5;E9PS5	P62277;J3(6;5;3	6;5;3	6;5;3	40S ribosomal protein S13	RPS13	
P62263;H0YB22;E5RH7	P62263;H0 7;5;5	7;5;5	7;5;5	40S ribosomal protein S14	RPS14	
I3L3P7;P62244;H3BVC7	I3L3P7;P62 7;7;1	7;7;1	2;2;1	40S ribosomal protein S15a	RPS15A	
P62249;M0R3H0;M0R2	P62249;M(6;5;5;4;3;3	6;5;5;4;3;3	6;5;5;4;3;3	40S ribosomal protein S16	RPS16	
P08708;H0YN88;A0A07	P08708;H0 7;6;6;3;1	7;6;6;3;1	7;6;6;3;1	40S ribosomal protein S17	RPS17	
P62269;J3JS69;A0A0G2	P62269 6;2;1;1	6;2;1;1	6;2;1;1	40S ribosomal protein S18	RPS18	
P39019;M0R2L9;M0QX	P39019;M(8;4;4;4;4;3	8;4;4;4;4;3	8;4;4;4;4;3	40S ribosomal protein S19	RPS19	
P15880;H0YEN5;E9PQD	P15880;H0 9;8;8;4;4;4	9;8;8;4;4;4	9;8;8;4;4;4	40S ribosomal protein S2	RPS2	
P60866;P60866-2;E5RIF	P60866;P(3;3;2;2;1	3;3;2;2;1	3;3;2;2;1	40S ribosomal protein S20	RPS20	
Q8WVC2;P63220;Q9BY	Q8WVC2;P 5;5;3	5;5;3	5;5;3	40S ribosomal protein S21	RPS21	
P62266;D6RD47;D6RDJ	P62266;D6 4;3;2;2;2	4;3;2;2;2	4;3;2;2;2	40S ribosomal protein S23	RPS23	
E7ETK0;A0A087WUS0;F	E7ETK0;A0(3;3;3;3;3	3;3;3;3;3	3;3;3;3;3	40S ribosomal protein S24	RPS24	
P62851	P62851	3	3	3	40S ribosomal protein S25	RPS25
P62854;Q5JNZ5	P62854;Q5 3;2	3;2	3;2	40S ribosomal protein S26;f	RPS26;RPS:	
P42677;Q5T4L4;H0YMV	P42677;Q5 4;3;2;2;1;1	4;3;2;2;1;1	4;3;2;2;1;1	40S ribosomal protein S27;f	RPS27;RPS:	
P62857	P62857	2	2	2	40S ribosomal protein S28	RPS28
P62273;P62273-2;A0A0	P62273;P6(2;2;1	2;2;1	2;2;1	40S ribosomal protein S29	RPS29	
P23396;P23396-2;E9PL	P23396;P2(13;12;11;9	13;12;11;9	13;12;11;9	40S ribosomal protein S3	RPS3	
E9PR30;P62861	E9PR30;P6(1;1	1;1	1;1	40S ribosomal protein S30	FAU	
P61247;D6RG13;D6RAT	P61247;D6 12;11;10;9	12;11;10;9	12;11;10;9	40S ribosomal protein S3a	RPS3A	
P62701;C9JEH7;Q8TD4	P62701;C9(12;6;6;6	12;6;6;6	12;6;6;6	40S ribosomal protein S4, X	RPS4X;RPS:	

MOR0F0;P46782;MOR0I	MOR0F0;P47;7;6;3	7;7;6;3	7;7;6;3	40S ribosomal protein S5;40	RPS5	
P62753;A2A3R5;A2A3R	P62753;A2.6;4;3	6;4;3	6;4;3	40S ribosomal protein S6	RPS6	
P62081;B5MCP9	P62081;B5 4;3	4;3	4;3	40S ribosomal protein S7	RPS7	
P62241;Q5JR95	P62241;Q5 10;9	10;9	10;9	40S ribosomal protein S8	RPS8	
A0A024R4M0;P46781;E	A0A024R4 9;9;6;6;1;1	9;9;6;6;1;1	9;9;6;6;1;1	40S ribosomal protein S9	RPS9	
C9J9K3;A0A0C4DG17;P	C9J9K3;A0 8;8;8;4	8;8;8;4	8;8;8;4	40S ribosomal protein SA	RPSA	
P08195-2;F5GZS6;J3KPF	P08195-2;F 25;24;24;2	25;24;24;2	25;24;24;2	4F2 cell-surface antigen hez	SLC3A2	
Q9H0D6-2;Q9H0D6	Q9H0D6-2; 2;2	2;2	2;2	5-3 exoribonuclease 2	XRN2	
P21589-2;P21589;HOY3	P21589-2;F 2;2;1;1;1	2;2;1;1;1	2;2;1;1;1	5-nucleotidase	NT5E	
P10809;E7ESH4;E7EXB4	P10809 28;7;6;3;2	28;7;6;3;2	28;7;6;3;2	60 kDa heat shock protein,	HSPD1	
F8VU65;P05388;F8VPE	F8VU65;P0 9;9;8;8;8;8	9;9;8;8;8;8	9;9;8;8;8;8	60S acidic ribosomal protein	RPLP0;RPLI	
P05386	P05386	2	1	1	60S acidic ribosomal protein	RPLP1
P05387;HOYDD8;P0538	P05387 7;3;1	7;3;1	6;2;0	60S acidic ribosomal protein	RPLP2	
X1WI28;P27635;B8A6G	X1WI28;P2 8;8;3;3	8;8;3;3	2;2;2;2	60S ribosomal protein L10	RPL10	
P62906	P62906	8	8	8	60S ribosomal protein L10a	RPL10A
P62913;Q5VVC8;Q5VVC	P62913;Q5 4;3;2	4;3;2	1;0;0	60S ribosomal protein L11	RPL11	
P62913-2	P62913-2	4	1	1	60S ribosomal protein L11	RPL11
P30050;P30050-2	P30050;P3 6;4	6;4	6;4	60S ribosomal protein L12	RPL12	
P26373;P26373-2;J3QSI	P26373;P2 7;6;4;1;1	7;6;4;1;1	7;6;4;1;1	60S ribosomal protein L13	RPL13	
P40429;M0QYS1;Q8J01	P40429;MC 8;7;6;3;1;1	8;7;6;3;1;1	8;7;6;3;1;1	60S ribosomal protein L13a	RPL13A;RP	
E7EPB3;P50914	E7EPB3;P5 4;4	4;4	4;4	60S ribosomal protein L14	RPL14	
P61313;E7EX53;E7EQV	P61313;E7 6;5;5;4;2	6;5;5;4;2	6;5;5;4;2	60S ribosomal protein L15;F	RPL15	
A0A087WXM6;J3QQT2;A0A087WX	7;7;7;7;7;7 7;7;7;7;7;7	7;7;7;7;7;7	7;7;7;7;7;7	60S ribosomal protein L17	RPL17;RPL1	
G3V203;HOYHA7;J3QQ	G3V203;HC 4;4;4;4;4;3	4;4;4;4;4;3	4;4;4;4;4;3	60S ribosomal protein L18	RPL18	
MOR3D6;MOR1A7;MOR	MOR3D6;M 5;5;5;5;4	5;5;5;5;4	5;5;5;5;4	60S ribosomal protein L18a	RPL18A	
G3V1B3;MOR181;P4677	G3V1B3;M 2;2;2	2;2;2	2;2;2	60S ribosomal protein L21	RPL21	
K7EJT5;K7EP65;K7EKS7;K7EJT5;K7E	2;2;2;2;2;2 2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	60S ribosomal protein L22	RPL22	
P62829;J3KTJ3;C9JD32;P62829;J3k	4;2;2;2;2 4;2;2;2;2	4;2;2;2;2	4;2;2;2;2	60S ribosomal protein L23	RPL23	
H7BY10;K7EJV9;K7ERT8	H7BY10;K7 4;4;4;4;4;3	4;4;4;4;4;3	4;4;4;4;4;3	60S ribosomal protein L23a	RPL23A	
C9JXB8;C9JNW5;P8373;C9JXB8;C9J	6;6;6 6;6;6 6;6;6	6;6;6	6;6;6	60S ribosomal protein L24	RPL24	
P61254;J3KTJ8;J3QRI7;J	P61254;J3k 6;5;5;5;5;5	6;5;5;5;5;5	6;5;5;5;5;5	60S ribosomal protein L26;	RPL26;RPL2	
P61353;K7ELC7;K7EQQ	P61353;K7 4;3;2;1	4;3;2;1	4;3;2;1	60S ribosomal protein L27	RPL27	
E9PLL6;P46776;E9PJD9;E9PLL6;P4	4;4;3;1 4;4;3;1	4;4;3;1	4;4;3;1	60S ribosomal protein L27a	RPL27A	
HOYMF4;HOYKD8;P4677	HOYMF4;H 5;5;5;5;5;5	5;5;5;5;5;5	5;5;5;5;5;5	60S ribosomal protein L28	RPL28	
P47914	P47914	2	2	2	60S ribosomal protein L29	RPL29
P39023;G5E9G0;H7C42	P39023;G5 16;13;9;8;7	16;13;9;8;7	16;13;9;8;7	60S ribosomal protein L3	RPL3	
P62888;E5RI99;A0A0B4	P62888;E5 5;4;3;2;1	5;4;3;2;1	5;4;3;2;1	60S ribosomal protein L30	RPL30	
H7C2W9;C9JU56;B7Z4E	H7C2W9;C 4;4;4;4;4;4	4;4;4;4;4;4	4;4;4;4;4;4	60S ribosomal protein L31	RPL31	
D3YTB1;F8W727;P6291	D3YTB1;F8 5;5;5	5;5;5	5;5;5	60S ribosomal protein L32	RPL32	
P49207	P49207	6	6	6	60S ribosomal protein L34	RPL34
F2Z388;P42766	F2Z388;P4 2;2	2;2	2;2	60S ribosomal protein L35	RPL35	
C9K025;P18077;F8WBS	C9K025;P1 5;5;3;3	5;5;3;3	5;5;3;3	60S ribosomal protein L35a	RPL35A	
Q9Y3U8;J3QSB5;J3KTD	Q9Y3U8;J3 3;2;1	3;2;1	3;2;1	60S ribosomal protein L36	RPL36	
HOY5B4;H7BZ11;J3KQN	HOY5B4;H7 2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	60S ribosomal protein L36a	RPL36A;RP	
C9J4Z3;P61513;MOR0A	C9J4Z3;P6 4;4;3;3;3;3	4;4;3;3;3;3	4;4;3;3;3;3	60S ribosomal protein L37a	RPL37A	
J3KT73;J3QL01;P63173	J3KT73;J3Q 1;1;1	1;1;1	1;1;1	60S ribosomal protein L38	RPL38	
P36578;H3BM89;H3BTF	P36578;H3 15;9;7;7	15;9;7;7	15;9;7;7	60S ribosomal protein L4	RPL4	
P46777;Q5T7N0	P46777	9;4	9;4	9;4	60S ribosomal protein L5	RPL5
Q02878;F8VZ45;U3KQR	Q02878 13;3;3;2;1; 13;3;3;2;1;	13;3;3;2;1;	13;3;3;2;1;	60S ribosomal protein L6	RPL6	
A8MUD9;P18124;C9JZ8	A8MUD9;P 6;6;2;2	6;6;2;2	6;6;2;2	60S ribosomal protein L7	RPL7	

P62424;Q5T8U2;Q5T8U	P62424;Q5 14;8;8	14;8;8	14;8;8	60S ribosomal protein L7a	RPL7A	
R4GMU7;Q6DKI1-2;Q6L	R4GMU7;C 1;1;1	1;1;1	1;1;1	60S ribosomal protein L7-like	RPL7L1	
P62917;E9PKZ0;E9PKU4	P62917;E9I 5;4;4;3;2	5;4;4;3;2	5;4;4;3;2	60S ribosomal protein L8	RPL8	
P32969;E7ESE0;D6RAN	P32969;E7I 5;4;4;4;2	5;4;4;4;2	5;4;4;4;2	60S ribosomal protein L9	RPL9	
J3QLW7;Q9Y221-2;Q9Y	J3QLW7;Q 2;2;2	2;2;2	2;2;2	60S ribosome subunit biog	NIP7	
P52209-2;P52209;K7EN	P52209-2;F 10;10;7;6;6	10;10;7;6;6	10;10;7;6;6	6-phosphogluconate dehyd	PGD	
MOROU3;MOR261;O953	MOROU3;N 2;2;2;1	2;2;2;1	2;2;2;1	6-phosphogluconolactonase	PGLS	
P36639-4;P36639-3;P36	P36639-4;F 2;2;2;2	2;2;2;2	2;2;2;2	7,8-dihydro-8-oxoguanine t	NUDT1	
P11021	P11021	30	30	29	78 kDa glucose-regulated p	HSPA5
Q9UBM7;E9PJ54;E9PM	Q9UBM7;E 6;4;4;3;3;3	6;4;4;3;3;3	6;4;4;3;3;3	7-dehydrocholesterol reduc	DHCR7	
Q7L2J0	Q7L2J0	1	1	1	7SK snRNA methylphosphat	MEPCE
A0A0J9YWL0;Q9Y4K1;C	A0A0J9YW 3;3;1;1	3;3;1;1	3;3;1;1	Absent in melanoma 1 prot	AIM1	
MOR026;A1L0T0	MOR026;A 1;1	1;1	1;1	Acetolactate synthase-like	ILVBL	
Q9BWD1;Q9BWD1-2	Q9BWD1;C 2;2	2;2	2;2	Acetyl-CoA acetyltransferas	ACAT2	
P24752;H0YEL7;P24752	P24752;H0 6;3;3;2;1	6;3;3;2;1	6;3;3;2;1	Acetyl-CoA acetyltransferas	ACAT1	
O00763-3;Q13085-3;Q1	O00763-3;( 1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Acetyl-CoA carboxylase 2;Bi	ACACB;ACA	
H0YN26;P39687;O4342	H0YN26;P3 4;4;2;1	4;4;2;1	3;3;2;1	Acidic leucine-rich nuclear	ANP32A;AN	
Q92688-2;Q92688	Q92688-2;( 2;2	1;1	1;1	Acidic leucine-rich nuclear	ANP32B	
A2A274;Q99798	A2A274;Q 9;9	9;9	9;9	Aconitate hydratase, mitoc	ACO2	
P60709;G5E9R0;E7EVS	P60709 19;8;8;7;6; 1;1;1;1;1;0	1;1;1;1;1;0	1;1;1;1;1;0	Actin, cytoplasmic 1;Actin, c	ACTB	
P63261;I3L3I0;I3L1U9;I	P63261;I3L 19;11;11;9	19;11;11;9	1;1;1;1;1;1	Actin, cytoplasmic 2;Actin, c	ACTG1	
P63267;P68133;P68032	P63267;P6 10;10;10;1	1;1;1;1;1;1	1;1;1;1;1;1	Actin, gamma-enteric smoo	ACTG2;ACT	
O96019;O96019-2;H7C	O96019;O 6;5;3;1;1	6;5;3;1;1	6;5;3;1;1	Actin-like protein 6A	ACTL6A	
P61160;P61160-2;F5H6	P61160;P6 5;4;3;1;1	5;4;3;1;1	5;4;3;1;1	Actin-related protein 2	ACTR2	
O15143;C9J4Z7;F8VXW	O15143;C9 4;2;2;2;2;2	4;2;2;2;2;2	4;2;2;2;2;2	Actin-related protein 2/3 cc	ARPC1B	
O15144;G5E9S7;C9JTV5	O15144 4;1;1;1	4;1;1;1	4;1;1;1	Actin-related protein 2/3 cc	ARPC2	
F8VR50;C9JZD1;O15145	F8VR50;C9 1;1;1	1;1;1	1;1;1	Actin-related protein 2/3 cc	ARPC3	
F8WDD7;F8WCF6;A0A0	F8WDD7;F 4;4;4;4;4;3	4;4;4;4;4;3	4;4;4;4;4;3	Actin-related protein 2/3 cc	ARPC4;ARP	
B1ALC0;O15511;O1551	B1ALC0;O1 1;1;1	1;1;1	1;1;1	Actin-related protein 2/3 cc	ARPC5	
Q9BPX5	Q9BPX5	1	1	1	Actin-related protein 2/3 cc	ARPC5L
P61158;B4DXW1;F8WD	P61158;B4 7;6;3;1;1;1	7;6;3;1;1;1	7;6;3;1;1;1	Actin-related protein 3	ACTR3	
P53999	P53999	3	3	3	Activated RNA polymerase I	SUB1
O95433-2;O95433;H0YJ	O95433-2;( 8;8;6;4;3;3	8;8;6;4;3;3	8;8;6;4;3;3	Activator of 90 kDa heat sh	AHSA1	
Q86WX3	Q86WX3	1	1	1	Active regulator of SIRT1	RPS19BP1
O14561;I3L505;H3BNK	O14561;I3L 2;1;1	2;1;1	2;1;1	Acyl carrier protein, mitoch	NDUFAB1	
C9JIF9;P13798	C9JIF9;P13 2;2	2;2	2;2	Acylamino-acid-releasing er	APEH	
Q9H845;H0Y8Z9	Q9H845 5;2	5;2	5;2	Acyl-CoA dehydrogenase fa	ACAD9	
O00767	O00767	2	2	2	Acyl-CoA desaturase	SCD
B8ZWD1;A0A0A0MTI5;I	B8ZWD1;A 3;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	Acyl-CoA-binding protein	DBI	
Q9NPJ3-2;Q9NPJ3	Q9NPJ3-2;( 1;1	1;1	1;1	Acyl-coenzyme A thioestera	ACOT13	
H7C5A7;O14734;E9PRD	H7C5A7;O12;2;1;1	2;2;1;1	2;2;1;1	Acyl-coenzyme A thioestera	ACOT8	
Q9Y305-3;Q9Y305-2;Q9	Q9Y305-3;( 5;5;5;5;3	5;5;5;5;3	5;5;5;5;3	Acyl-coenzyme A thioestera	ACOT9	
A0A087X1K9;E5RGR0;O	A0A087X1 3;3;3;3;2;1	3;3;3;3;2;1	3;3;3;3;2;1	Acyl-protein thioesterase 1	LYPLA1	
Q5QPQ0;O95372	Q5QPQ0;O 2;2	2;2	2;2	Acyl-protein thioesterase 2	LYPLA2	
Q6P587;Q6P587-2;Q6P	Q6P587;Q 1;1;1	1;1;1	1;1;1	Acylpyruvase FAHD1, mitoc	FAHD1	
H3BSW3;H3BQF1;H3BC	H3BSW3;H 3;3;3;3;3;2	3;3;3;3;3;2	3;3;3;3;3;2	Adenine phosphoribosyltra	APRT	
Q8TB61-5;Q8TB61-4;Q8	Q8TB61-5;( 2;2;2;2;2	2;2;2;2;2	2;2;2;2;2	Adenosine 3-phospho 5-ph	SLC35B2	
P55263-3;P55263-4;P55	P55263-3;F 1;1;1;1	1;1;1;1	1;1;1;1	Adenosine kinase	ADK	
P23526;P23526-2	P23526;P2 15;13	15;13	15;13	Adenosylhomocysteinase	AHCY	
F8W1A4;P54819-5;P548	F8W1A4;P 6;6;6;6;5;5	6;6;6;6;5;5	6;6;6;6;5;5	Adenylate kinase 2, mitoch	AK2	



P27144;D3DQ64	P27144;D3 2;1	2;1	2;1	Adenylate kinase 4, mitochondria	AK4
Q5T9B7;P00568;H0Y4J6	Q5T9B7;P0 5;5;3;1	5;5;3;1	5;5;3;1	Adenylate kinase isoenzyme 1	AK1
A0A096LNY6;A0A1B0G1	A0A096LN\ 2;2;2;2;1	2;2;2;2;1	2;2;2;2;1	Adenylosuccinate lyase	ADSL
P30520	P30520	5	5	5 Adenylosuccinate synthetase	ADSS
Q01518-2;Q01518;Q5T9B7	Q01518-2;( 11;11;4;4;4	11;11;4;4;4	11;11;4;4;4	Adenylyl cyclase-associated	CAP1
Q9HDC9-2;Q9HDC9;H0Y4J6	Q9HDC9-2; 6;6;5	6;6;5	6;6;5	Adipocyte plasma membrane	APMAP
Q15847	Q15847	1	1	1 Adipogenesis regulatory factor	ADIRF
P05141;Q9H0C2	P05141 15;3	15;3	6;0	ADP/ATP translocase 2;ADP	SLC25A5
P12236	P12236	13	4	2 ADP/ATP translocase 3;ADP	SLC25A6
Q9BRR6-2;Q9BRR6;Q9BRR6	Q9BRR6-2; 3;3;2;2;1;1	3;3;2;2;1;1	3;3;2;2;1;1	ADP-dependent glucokinase	ADPGK
P84077;P61204;F5H423	P84077;P6 6;6;5;4;3;1	6;6;5;4;3;1	3;3;2;2;1;1	ADP-ribosylation factor 1;ARF1;ARF3	ARF1;ARF3
C9JPM4;P18085;C9JAK5	C9JPM4;P1 3;3;1	1;1;1	1;1;1	ADP-ribosylation factor 4	ARF4
C9J1Z8;P84085;F5H1V1	C9J1Z8;P8 4;5;5;1;1;1	2;2;0;0;0	2;2;0;0;0	ADP-ribosylation factor 5	ARF5
P62330	P62330	3	3	3 ADP-ribosylation factor 6	ARF6
Q9NVJ2	Q9NVJ2	2	2	1 ADP-ribosylation factor-like	ARL8B
A6NCQ0;A6NJU6;A6NF0	A6NCQ0;A( 3;3;3;3;2;1	3;3;3;3;2;1	3;3;3;3;2;1	ADP-sugar pyrophosphatase	NUDT5
Q9Y4W6	Q9Y4W6	2	2	2 AFG3-like protein 2	AFG3L2
A0A087X208;O00468-2	A0A087X2( 5;5;5;5;5;5	5;5;5;5;5;5	5;5;5;5;5;5	Agrin;Agrin N-terminal 110	AGRN
O00170	O00170	1	1	1 AH receptor-interacting protein	AIP
H0YK84;H0YMW2;Q128	H0YK84;H0 1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	A-kinase anchor protein 13	AKAP13
H3BU82;F8VZ44;Q9NRC	H3BU82;F8 2;2;2;2;1	2;2;2;2;1	2;2;2;2;1	Aladin	AAAS
P49588;P49588-2;H3BP	P49588;P4 7;6;1	7;6;1	7;6;1	Alanine--tRNA ligase, cytoplasmic	AARS
P14550;V9GYG2;V9GYP	P14550;V9 4;2;2;2	4;2;2;2	4;2;2;2	Alcohol dehydrogenase [NADP+]	AKR1A1
P11766;D6RFE4;H0YAG	P11766 4;1;1	4;1;1	4;1;1	Alcohol dehydrogenase class I	ADH5
P47895;H0Y2X5;H0YKF5	P47895;H0 18;16;7;6;2	18;16;7;6;2	16;15;6;6;1	Aldehyde dehydrogenase family 1 class 1 member 1	ALDH1A3
P30837	P30837	4	2	2 Aldehyde dehydrogenase X, class 1 member 1	ALDH1B1
Q04828;H0Y804	Q04828;H0 11;6	11;6	0;0	Aldo-keto reductase family 10 subfamily 1 member 1	AKR1C1
B4DK69;P52895;S4R3P	B4DK69;P5 10;10;5;2	2;2;2;0	2;2;2;0	Aldo-keto reductase family 10 subfamily 1 member 2	AKR1C2
A0A0A0MSS8;P42330;S	A0A0A0MS 8;8;7;4;4;4	2;2;1;0;1;0	2;2;1;0;1;0	Aldo-keto reductase family 10 subfamily 1 member 3	AKR1C3;AKR1C3
P15121;E9PEF9;E9PCX2	P15121;E9 5;3;3;1;1	5;3;3;1;1	5;3;3;1;1	Aldose reductase	AKR1B1
O00116;A0A1B0GWA2; O00116;A0	10;7;4	10;7;4	10;7;4	Alkyl dihydroxyacetone phosphate	AGPS
Q9H553-2;Q9H553	Q9H553-2; 1;1	1;1	1;1	Alpha-1,3/1,6-mannosyltransferase	ALG2
E9PK47;P11217-2;P067	E9PK47;P1 1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Alpha-1,4 glucan phosphorylase	PYGL;PYGN
P30533	P30533	2	2	2 Alpha-2-macroglobulin receptor	LRPAP1
P12814;P12814-3;P128	P12814;P1 36;35;34;3	36;35;34;3	23;22;21;1	Alpha-actinin-1	ACTN1
O43707;O43707-2;F5G	O43707;O4 35;24;19;1	22;15;13;1	22;15;13;1	Alpha-actinin-4	ACTN4
A0A1B0GTY9;A0A1B0G1	A0A1B0GT 5;5;5;5;5;5	5;5;5;5;5;5	5;5;5;5;5;5	Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1
R4GMT0;P61163	R4GMT0;P( 1;1	1;1	1;1	Alpha-centractin	ACTR1A
A0A1W2PRU0;A6NMQ5	A0A1W2PR 1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Alpha-endosulfine	ENSA
P06733;P06733-2;K7E	P06733;P0 23;14;11;2	23;14;11;2	23;14;11;2	Alpha-enolase	ENO1
Q16706	Q16706	2	2	2 Alpha-mannosidase 2	MAN2A1
H0YKM7;H0YLB9;A0A0	H0YKM7;H( 1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Alpha-mannosidase;Alpha-mannosidase	MAN2A2
M0R0Y2;P54920;M0R2	M0R0Y2;P( 6;6;5;2;1;1	6;6;5;2;1;1	6;6;5;2;1;1	Alpha-soluble NSF attachment protein	NAPA
P40222	P40222	1	1	1 Alpha-taxilin	TXLNA
P21397;P21397-2;P273	P21397;P2 4;3;1;1	4;3;1;1	4;3;1;1	Amine oxidase [flavin-containing]	MAOA
Q12904;Q12904-2;D6R	Q12904;Q1 4;4;1	4;4;1	4;4;1	Aminoacyl tRNA synthetase class 1	AIMP1
Q13155;A8MU58;F8W9	Q13155;A8 3;2;2	3;2;2	3;2;2	Aminoacyl tRNA synthetase class 2	AIMP2
A6NKB8;Q9H4A4;A0A0	A6NKB8;Q( 6;6;4;3;1	6;6;4;3;1	6;6;4;3;1	Aminopeptidase B	RNPEP
Q86SJ2	Q86SJ2	2	2	2 Amphotericin-induced protein	AMIGO2
E9PG40;P05067-7;P050	E9PG40;P0 8;8;8;8;8;8	8;8;8;8;8;8	8;7;7;7;7;7	Amyloid beta A4 protein;N-amyloid	APP

Q06481-3;Q06481-6;QC Q06481-3;(7;7;7;5;5;5 6;6;6;4;4;4 6;6;6;4;4;4;	Amyloid-like protein 2	APLP2
Q9Y679-3;Q9Y679-2;Q9 Q9Y679-3;(1;1;1 1;1;1 1;1;1	Ancient ubiquitous protein	AUP1
A0A1W2PQ15;E9PDP5;A A0A1W2PC 1;1;1;1;1 1;1;1;1;1 1;1;1;1;1;1;	Ankyrin repeat and KH dom	ANKHD1;AI
P04083;Q5T3N1;Q5T3N P04083 23;9;6 23;9;6 23;9;6	Annexin A1	ANXA1
Q9UJ72 Q9UJ72 1 1 1	Annexin A10	ANXA10
P50995-2;P50995;H0Y6 P50995-2;F 7;7;2;1;1;1 7;7;2;1;1;1 7;7;2;1;1;1	Annexin A11	ANXA11
P07355;P07355-2;H0YN P07355;P0 25;24;23;2 25;24;23;2 25;24;23;2;	Annexin A2;Annexin;Putativ	ANXA2;AN
P12429;D6RA82;D6RFG P12429;D6 12;10;5;2;2 12;10;5;2;2 12;10;5;2;2	Annexin A3;Annexin	ANXA3
P09525;Q6P452;P09525 P09525;Q6 11;10;9;4 11;10;9;4 11;10;9;4	Annexin A4;Annexin	ANXA4
P08758;D6RBL5;D6RBE P08758;D6 11;8;7;5;1 11;8;7;5;1 11;8;7;5;1	Annexin A5;Annexin	ANXA5
P20073-2;P20073 P20073-2;F 11;11 11;11 11;11	Annexin A7	ANXA7
P13928;A0A087WTN9;( P13928;A0 10;9;8;7;7; 10;9;8;7;7; 10;9;8;7;7;	Annexin A8;Annexin;Annexi	ANXA8;AN
P46013-2;P46013 P46013-2;F 15;15 15;15 15;15	Antigen KI-67	MKI67
A0A140T9T7;Q03518 A0A140T9T2;2 2;2 2;2	Antigen peptide transport	TAP1
Q10567-4;Q10567-3;Q1 Q10567-4;(7;7;7;7;5 7;7;7;7;5 3;3;3;3;1	AP-1 complex subunit beta-	AP1B1
H7C1E4;P61966;P61966 H7C1E4;P6 2;2;1 2;2;1 2;2;1	AP-1 complex subunit sigma	AP1S1
O95782-2;O95782;A0A( O95782-2;(4;4;2;2;2;2 4;4;2;2;2;2 4;4;2;2;2;2;	AP-2 complex subunit alpha	AP2A1;AP2
A0A087WU93;A0A087V A0A087WL 6;6;6;6;4 2;2;2;2;2;2 2;2;2;2;2;2;	AP-2 complex subunit beta	AP2B1
A0A087WY71;E9PFW3;A A0A087WY 3;3;3;2;1 3;3;3;2;1 3;3;3;2;1;	AP-2 complex subunit mu	AP2M1
O14617-3;O14617-4;O1 O14617-3;(1;1;1;1;1 1;1;1;1;1 1;1;1;1;1	AP-3 complex subunit delta	AP3D1
Q9Y2T2 Q9Y2T2 1 1 1	AP-3 complex subunit mu-1	AP3M1
Q92572;F5H459 Q92572;F5 2;1 2;1 2;1	AP-3 complex subunit sigma	AP3S1
P04114 P04114 7 5 5	Apolipoprotein B-100;Apoli	APOB
B0YIW2;P02656 B0YIW2;P0 1;1 1;1 1;1	Apolipoprotein C-III	APOC3
J3KQL8;Q9BQE5;E9PM9 J3KQL8;Q9 2;2;1 2;2;1 2;2;1	Apolipoprotein L2	APOL2
G3V1B6;H7C1U8;Q9BU G3V1B6;H7 2;2;2;2 2;2;2;2 2;2;2;2	Apolipoprotein O	APOO
Q9BZZ5-2;G3V1C3;Q9B Q9BZZ5-2;(4;3;3;3;3;2 4;3;3;3;3;2 4;3;3;3;3;2;	Apoptosis inhibitor 5	API5
Q07812-5;Q07812-7;QC Q07812-5;(3;3;3;3;3;2 3;3;3;3;3;2 3;3;3;3;3;2;	Apoptosis regulator BAX	BAX
O95831-3;O95831;E9PM O95831-3;(9;9;5;5;5;4 9;9;5;5;5;4 9;9;5;5;5;4;	Apoptosis-inducing factor 1	AIFM1
S4R3H4;E7EQT4;Q9UKV S4R3H4;E7 8;7;7;7;5;5 8;7;7;7;5;5 8;7;7;7;5;5;	Apoptotic chromatin conde	ACIN1
A0A087X1E4;P53365-2; A0A087X1E 1;1;1;1 1;1;1;1 1;1;1;1	Arfaptin-2	ARFIP2
P54136;P54136-2;E5RH P54136;P5 8;7;1;1 8;7;1;1 8;7;1;1	Arginine--tRNA ligase, cyto	RARS
P08243-2;P08243;P082 P08243-2;F 5;5;4;3;2;2 5;5;4;3;2;2 5;5;4;3;2;2;	Asparagine synthetase [glut	ASNS
O43776;K7EIU7;K7EPK2 O43776 6;2;2;2;2;1 6;2;2;2;2;1 6;2;2;2;2;1;	Asparagine--tRNA ligase, cy	NARS
P17174;P17174-2 P17174;P1 4;3 4;3 4;3	Aspartate aminotransferase	GOT1
P00505;P00505-2 P00505;P0 13;10 13;10 13;10	Aspartate aminotransferase	GOT2
P14868;P14868-2;C9J75 P14868;P1 20;17;9;9;9 20;17;9;9;9 20;17;9;9;9;	Aspartate--tRNA ligase, cytc	DARS
Q6PI48 Q6PI48 2 2 2	Aspartate--tRNA ligase, mit	DARS2
Q12797;Q12797-10;E5F Q12797;Q1 4;3;2;2;2;2 4;3;2;2;2;2 4;3;2;2;2;2;	Aspartyl/asparaginy beta-h	ASPH
B1AKZ5;Q15121;Q1512 B1AKZ5;Q1 1;1;1 1;1;1 1;1;1	Astrocytic phosphoprotein I	PEA15
Q8WWM7-6;Q8WWM7 Q8WWM7- 2;2;2;2;2;2 2;2;2;2;2;2 2;2;2;2;2;2;	Ataxin-2-like protein	ATXN2L
B5MCN0;Q8NHH9-3;Q8 B5MCN0;Q 3;3;3;3;3;3 3;3;3;3;3;3 3;3;3;3;3;3;	Atlastin-2	ATL2
F5H6I7;Q6DD88;F5GWF F5H6I7;Q6 2;2;1 2;2;1 2;2;1	Atlastin-3	ATL3
Q5QNZ2;P24539 Q5QNZ2;P 7;7 7;7 7;7	ATP synthase F(0) complex	ATP5F1
P00846 P00846 1 1 1	ATP synthase subunit a	MT-ATP6
P25705;P25705-2;P257 P25705;P2 24;23;22;1 24;23;22;1 24;23;22;1;	ATP synthase subunit alpha	ATP5A1
P06576;H0YH81;F8W07 P06576;H0 22;18;11;6 22;18;11;6 22;18;11;6;	ATP synthase subunit beta,	ATP5B
O75947;O75947-2;F5H O75947;O7 8;6;3 8;6;3 8;6;3	ATP synthase subunit d, mit	ATP5H
P30049 P30049 2 2 2	ATP synthase subunit delta,	ATP5D
P56385 P56385 2 2 2	ATP synthase subunit e, mit	ATP5I

P56134-3;P56134;C9JJT	P56134-3;F 2;2;1;1;1;1	2;2;1;1;1;1	2;2;1;1;1;1	2;2;1;1;1;1	ATP synthase subunit f, mitochondrial	ATP5J2;ATF
E9PN17;O75964	E9PN17;O7 3;3	3;3	3;3	3;3	ATP synthase subunit g, mitochondrial	ATP5L
P36542-2;P36542	P36542-2;F 10;10	10;10	10;10	10;10	ATP synthase subunit gamma	ATP5C1
P48047;H7C0C1;H7C06	P48047;H7 7;4;3;2	7;4;3;2	7;4;3;2	7;4;3;2	ATP synthase subunit O, mitochondrial	ATP5O
P18859;P18859-2;A8MI	P18859;P1 4;4;3	4;4;3	4;4;3	4;4;3	ATP synthase-coupling factor	ATP5J
Q9NVI7-2;Q9NVI7;H0Y2	Q9NVI7-2;( 6;6;5;4;4;3	6;6;5;4;4;3	6;6;5;4;4;3	6;6;5;4;4;3	ATPase family AAA domain-	ATAD3A;AT
E9PJR8;B4DGL8;A0A087	E9PJR8;B4 1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	ATP-binding cassette sub-family 1	ABCB7
P28288;P28288-3;P282	P28288;P2 2;1;1	2;1;1	2;1;1	2;1;1	ATP-binding cassette sub-family 1	ABCD3
P61221;D6R9I9;H0Y990	P61221;D6 4;2;1;1	4;2;1;1	4;2;1;1	4;2;1;1	ATP-binding cassette sub-family 1	ABCE1
H0YGW7;Q8NE71-2;Q8	H0YGW7;Q 2;2;2	2;2;2	2;2;2	2;2;2	ATP-binding cassette sub-family 1	ABCF1
Q9UG63;Q9UG63-2	Q9UG63;Q 1;1	1;1	1;1	1;1	ATP-binding cassette sub-family 1	ABCF2
Q9NUQ8-2;Q9NUQ8	Q9NUQ8-2 1;1	1;1	1;1	1;1	ATP-binding cassette sub-family 1	ABCF3
P53396-2;P53396;P533	P53396-2;F 22;22;15;5	22;22;15;5	22;22;15;5	22;22;15;5	ATP-citrate synthase	ACLY
P17858;P17858-2	P17858;P1 4;3	2;2	2;2	2;2	ATP-dependent 6-phosphofruct	PFKL
P08237-2;P08237;P082	P08237-2;F 4;4;4;1	3;3;3;1	3;3;3;1	3;3;3;1	ATP-dependent 6-phosphofruct	PFKM
Q01813;Q01813-2;B1AI	Q01813;QC 13;12;4;3;3	13;12;4;3;3	11;11;4;3;2	11;11;4;3;2	ATP-dependent 6-phosphofruct	PFKP
O76031;H0YM48;H0YK	O76031 5;2;1	5;2;1	5;2;1	5;2;1	ATP-dependent Clp protease	CLPX
M0R208;Q16740;M0QY	M0R208;Q 3;3;1	3;3;1	3;3;1	3;3;1	ATP-dependent Clp protease	CLPP
P46063	P46063	3	3	3	ATP-dependent DNA helicase	RECQL
Q08211;Q08211-2	Q08211 26;6	26;6	26;6	26;6	ATP-dependent RNA helicase	DHX9
F1T0B3;A0A087X2G1;Q	F1T0B3;A0 10;10;10;9	10;10;10;9	10;10;10;9	10;10;10;9	ATP-dependent RNA helicase	DDX1
Q9NVP1;H7C452	Q9NVP1 9;3	9;3	9;3	9;3	ATP-dependent RNA helicase	DDX18
I3L0H8;F6QDS0;H3BQK	I3L0H8;F6C 2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	ATP-dependent RNA helicase	DDX19A;DI
G3V529;Q9GZR7-2;Q9G	G3V529;Q 6;6;6;4;4;1	6;6;6;4;4;1	6;6;6;4;4;1	6;6;6;4;4;1	ATP-dependent RNA helicase	DDX24
O00148;K7EPJ3;O0014	O00148;K7 8;5;5;5;4;3	1;1;1;1;1;0	1;1;1;1;1;0	1;1;1;1;1;0	ATP-dependent RNA helicase	DDX39A
A0A0D9SFB3;A0A0D9S	A0A0D9SFC 14;14;14;1	13;13;13;1	13;13;13;1	13;13;13;1	ATP-dependent RNA helicase	DDX3X;DD
A0A0A0MSJ0;Q86XP3-2	A0A0A0MS 1;1;1	1;1;1	1;1;1	1;1;1	ATP-dependent RNA helicase	DDX42
Q8TDD1;Q8TDD1-2;H0Y	Q8TDD1;Q 6;6;1	6;6;1	6;6;1	6;6;1	ATP-dependent RNA helicase	DDX54
Q8IYB8	Q8IYB8	2	2	2	ATP-dependent RNA helicase	SUPV3L1
J3KRJ2;J3KRF8;J3QR41	J3KRJ2;J3K 1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Aurora kinase B	AURKB
O95816	O95816	1	1	1	BAG family molecular chaperone	BAG2
O95817	O95817	3	3	3	BAG family molecular chaperone	BAG3
A0A0C4DH22;Q9H4G0	A0A0C4DH 2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	Band 4.1-like protein 1	EPB41L1
O75531	O75531	1	1	1	Barrier-to-autointegration factor	BANF1
P98160	P98160	1	1	1	Basement membrane-specific	HSPG2
Q7L1Q6-2;Q7L1Q6;Q7L	Q7L1Q6-2; 4;4;4;4;3;2	4;4;4;4;3;2	4;4;4;4;3;2	4;4;4;4;3;2	Basic leucine zipper and W2	BZW1
Q75MG1;E7ETZ4;Q9Y6	Q75MG1;E 3;3;3;2;2;2	3;3;3;2;2;2	3;3;3;2;2;2	3;3;3;2;2;2	Basic leucine zipper and W2	BZW2
P35613-4;P35613-2;P3	P35613-4;F 8;8;8;7;7;6	8;8;8;7;7;6	8;8;8;7;7;6	8;8;8;7;7;6	Basigin	BSG
P51572;P51572-2;C9JS	P51572;P5 6;6;2;2;2;1	6;6;2;2;2;1	6;6;2;2;2;1	6;6;2;2;2;1	B-cell receptor-associated protein	BCAP31
Q16611-2;Q16611	Q16611-2;( 1;1	1;1	1;1	1;1	Bcl-2 homologous antagonist	BAK1
E9PJA7;A0A1W2PQ43;E	E9PJA7;A0 4;4;4;4;4;4	4;4;4;4;4;4	4;4;4;4;4;4	4;4;4;4;4;4	Bcl-2-associated transcription factor	BCLAF1
A0A087WTL4;A0A087W	A0A087WT 3;3;3;3	3;3;3;3	3;3;3;3	3;3;3;3	Bcl-2-like protein 13	BCL2L13
P61769;H0YLF3;F5H6I0	P61769;H0 3;2;2	3;2;2	3;2;2	3;2;2	Beta-2-microglobulin;Beta-	B2M
Q13425	Q13425	1	1	1	Beta-2-syntrophin	SNTB2
P42025	P42025	1	1	1	Beta-centractin	ACTR1B
Q53H82	Q53H82	3	3	3	Beta-lactamase-like protein	LACTB2
P55957;P55957-2;B2ZP	P55957;P5 3;3;1;1	3;3;1;1	3;3;1;1	3;3;1;1	BH3-interacting domain de	BID
Q13057;Q13057-2;K7EF	Q13057;Q1 3;3;1;1;1;1	3;3;1;1;1;1	3;3;1;1;1;1	3;3;1;1;1;1	Bifunctional coenzyme A sy	COASY
P07814;V9GYZ6;V9GZ7	P07814;V9 22;13;1	22;13;1	22;13;1	22;13;1	Bifunctional glutamate/prol	EPRS
P13995-2;P13995;B9A0	P13995-2;F 2;2;1	2;2;1	2;2;1	2;2;1	Bifunctional methylenetetra	MTHFD2

P31939-2;P31939;H7C1	P31939-2;F 13;13;5;3;2	13;13;5;3;2	13;13;5;3;2	Bifunctional purine biosynt	ATIC
Q8NFC6	Q8NFC6	1	1	1	Biorientation of chromosom
A0A087WZT3;Q9H3K6;I	A0A087WZ 2;2;1;1;1;1	2;2;1;1;1;1	2;2;1;1;1;1	2;2;1;1;1;1	BolA-like protein 2
F5GXW6;O95415	F5GXW6;O 1;1	1;1	1;1	1;1	Brain protein I3
Q9UHR4	Q9UHR4	4	4	4	Brain-specific angiogenesis
P54687-2;P54687-3;P54	P54687-2;F 1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Branched-chain-amino-acid
Q9P287-4;Q9P287-3;Q9	Q9P287-4;( 2;2;2;2	2;2;2;2	2;2;2;2	2;2;2;2	BRCA2 and CDKN1A-interac
Q8WY22	Q8WY22	2	2	2	BRI3-binding protein
Q9NRL2-2;Q9NRL2	Q9NRL2-2;( 2;2	2;2	2;2	2;2	Bromodomain adjacent to z
Q96CX2	Q96CX2	4	4	4	BTB/POZ domain-containin
H3BSS5;Q9NXV2	H3BSS5;Q9 1;1	1;1	1;1	1;1	BTB/POZ domain-containin
J3QRS9;X6R4W8;O4367	J3QRS9;X6I 4;4;4;4;3	4;4;4;4;4;3	4;4;4;4;4;3	4;4;4;4;4;3	BUB3-interacting and GLEB
F5H2F4;P11586;V9GYY	F5H2F4;P1 15;15;3	15;15;3	15;15;3	15;15;3	C-1-tetrahydrofolate syntha
O75844	O75844	4	4	4	CAAX prenyl protease 1 hor
E9PKA7;E9PI08;Q9Y256	E9PKA7;E9 1;1;1	1;1;1	1;1;1	1;1;1	CAAX prenyl protease 2
F8VPD4;P27708;H7C2E	F8VPD4;P2 20;20;3;2;1	20;20;3;2;1	20;20;3;2;1	20;20;3;2;1	CAD protein;Glutamine-dep
A0A087WXI5;P12830-2	A0A087WX 2;2;2	2;2;2	2;2;2	2;2;2	Cadherin-1;E-Cad/CTF1;E-C
P22223-2;P22223	P22223-2;F 4;4	4;4	4;4	4;4	Cadherin-3
Q99653;H0YLY7;H0YKE	Q99653;HC 3;2;2;2;2	3;2;2;2;2	3;2;2;2;2	3;2;2;2;2	Calcineurin B homologous p
Q8IU85-2;Q8IU85	Q8IU85-2;( 1;1	1;1	1;1	1;1	Calcium/calmodulin-depen
Q9UJS0;Q9UJS0-2;O757	Q9UJS0;Q9 17;17;4;4;2	17;17;4;4;2	17;17;4;4;2	17;17;4;4;2	Calcium-binding mitochond
Q6NUK1-2;Q6NUK1	Q6NUK1-2; 6;6	6;6	6;6	6;6	Calcium-binding mitochond
B4E2Q0;P98194-4;P981	B4E2Q0;P9 7;7;7;6;6;6	7;7;7;6;6;6	7;7;7;6;6;6	7;7;7;6;6;6	Calcium-transporting ATPas
Q9HB71-3;Q9HB71	Q9HB71-3; 6;6	6;6	6;6	6;6	Calcyclin-binding protein
P27824;P27824-2;P278	P27824;P2 21;21;14;1	21;21;14;1	21;21;14;1	21;21;14;1	Calnexin
K7EM73;K7EIV0;A0A07	K7EM73;K7 4;4;4;4;4;3	4;4;4;4;4;3	4;4;4;4;4;3	4;4;4;4;4;3	Calpain small subunit 1
P07384;E9PLX0;E9PJ3	P07384 8;2;2;2;2;2	8;2;2;2;2;2	8;2;2;2;2;2	8;2;2;2;2;2	Calpain-1 catalytic subunit
P17655;P17655-2	P17655;P1 6;4	6;4	6;4	6;4	Calpain-2 catalytic subunit
E7EQ12;E7EQA0;H0Y7F	E7EQ12;E7 5;5;5;5;5;5	5;5;5;5;5;5	5;5;5;5;5;5	5;5;5;5;5;5	Calpastatin
B4DDF4;B4DUT8;Q994	B4DDF4;B4 8;8;8;7;6;5	8;8;8;7;6;5	8;8;8;7;6;5	8;8;8;7;6;5	Calponin;Calponin-2
P27797;K7EJB9;K7EL50	P27797;K7I 15;10;3	15;10;3	15;10;3	15;10;3	Calreticulin
O43852-10;O43852-6;C	O43852-10 3;3;3;3;2;2	3;3;3;3;2;2	3;3;3;3;2;2	3;3;3;3;2;2	Calumenin
P10644;K7EM13;P1064	P10644;K7I 3;2;2;1	3;2;2;1	3;2;2;1	3;2;2;1	cAMP-dependent protein ki
H7C1L0;P13861-2;P138	H7C1L0;P1 1;1;1	1;1;1	1;1;1	1;1;1	cAMP-dependent protein ki
G3V153;Q14444-2;Q14	G3V153;Q1 4;4;4;3	4;4;4;3	4;4;4;3	4;4;4;3	Caprin-1
P00918;E5RID5;E5RK37	P00918 4;1;1	4;1;1	4;1;1	4;1;1	Carbonic anhydrase 2
P16152;E9PQ63;A8MTM	P16152;E9I 12;6;6;6;2	12;6;6;6;2	12;6;6;6;2	12;6;6;6;2	Carbonyl reductase [NADPH
O75976;O75976-2;J3QC	O75976;O7 8;5;2	8;5;2	8;5;2	8;5;2	Carboxypeptidase D
P50416-2;P50416;H3BP	P50416-2;F 9;9;2;2;1;1	9;9;2;2;1;1	9;9;2;2;1;1	9;9;2;2;1;1	Carnitine O-palmitoyltransf
P23786;A0A1B0GTB8;A	P23786;A0 6;5;5;5;4;1	6;5;5;5;4;1	6;5;5;5;4;1	6;5;5;5;4;1	Carnitine O-palmitoyltransf
D6REM4;E7ETM0;P487	D6REM4;E7 3;3;3;3;3;2	3;3;3;3;3;2	3;3;3;3;3;2	3;3;3;3;3;2	Casein kinase I isoform alph
E7EU96;Q8NEV1;P6840	E7EU96;Q8 2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	Casein kinase II subunit alp
Q5SRQ3;Q5SRQ6;N0E4	Q5SRQ3;Q5 2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	Casein kinase II subunit bet
F5GX99;H0YGM0;Q9H0	F5GX99;H0 2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	Caseinolytic peptidase B pr
Q9BXW7-2;Q9BXW7	Q9BXW7-2 2;2	2;2	2;2	2;2	Cat eye syndrome critical re
P04040	P04040	9	9	9	Catalase
P21964-2;P21964;E7EM	P21964-2;F 6;6;4;3;2;1	6;6;4;3;2;1	6;6;4;3;2;1	6;6;4;3;2;1	Catechol O-methyltransfera
P35221;P35221-2;G3XA	P35221;P3 21;21;18;1	21;21;18;1	21;21;18;1	21;21;18;1	Catenin alpha-1
B4DGU4;P35222	B4DGU4;P3 7;7	5;5	5;5	5;5	Catenin beta-1
C9JZR2;O60716-21;O60	C9JZR2;O6 14;14;14;1	14;14;14;1	14;14;14;1	14;14;14;1	Catenin delta-1



A0A1B0GW44;A0A1B0C	A0A1B0GW	6;6;6;6;6	6;6;6;6;6	6;6;6;6;6	Cathepsin D;Cathepsin D lig	CTSD
P20645;H0YGT2;F5GX3	P20645;H0	3;2;2;1;1;1	3;2;2;1;1;1	3;2;2;1;1;1	Cation-dependent mannose	M6PR
P11717	P11717	8	8	8	Cation-independent manno	IGF2R
Q03135;E9PCT5;C9JKI3	Q03135;E9	8;6;5;5;1	8;6;5;5;1	8;6;5;5;1	Caveolin-1;Caveolin	CAV1
Q03701	Q03701	2	2	2	CCAAT/enhancer-binding pr	CEBPZ
Q6YHK3-2;Q6YHK3;Q6Y	Q6YHK3-2;	3;3;2;2	3;3;2;2	3;3;2;2	CD109 antigen	CD109
H7C543;F5GXJ9;Q1374	H7C543;F5	3;3;3;3;3	3;3;3;3;3	3;3;3;3;3	CD166 antigen	ALCAM
A0A0C4DGH0;Q5ZPR3-	A0A0C4DG	2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	CD276 antigen	CD276
H0YD13;H0Y2P0;P1607	H0YD13;HC	6;6;6;6;6	6;6;6;6;6	6;6;6;6;6	CD44 antigen	CD44
E9PNW4;E9PR17;P1398	E9PNW4;E	3;3;3;1	3;3;3;1	3;3;3;1	CD59 glycoprotein	CD59
P27701-2;P27701;E9PJ	P27701-2;F	3;3;1	3;3;1	3;3;1	CD82 antigen	CD82
P48960-2;P48960-3;P4	P48960-2;F	3;3;3	3;3;3	3;3;3	CD97 antigen;CD97 antigen	CD97
I3L1N9;Q8N5K1	I3L1N9;Q8	2;2	2;2	2;2	CDGSH iron-sulfur domain-c	CISD2
B3KY94;O14735-3;O147	B3KY94;O1	2;2;2;1	2;2;2;1	2;2;2;1	CDP-diacylglycerol--inositol	CDIPT
Q8N163-2;Q8N163;G3V	Q8N163-2;	4;4;3;3;2;1	4;4;3;3;2;1	4;4;3;3;2;1	Cell cycle and apoptosis reg	CCAR2
P60953;Q5JYX0;P60953	P60953;Q5	5;4;4	4;3;3	4;3;3	Cell division control protein	CDC42
Q99459	Q99459	4	4	4	Cell division cycle 5-like pro	CDC5L
Q9NX58;D6RDJ1	Q9NX58;D	2;1	2;1	2;1	Cell growth-regulating nucle	LYAR
P62633-2;P62633;P626	P62633-2;F	5;5;4;4;4	5;5;4;4;4	1;1;1;1;0;0	Cellular nucleic acid-binding	CNBP
Q5JVD3;Q7Z7A1-5;Q7Z	Q5JVD3;Q7	1;1;1	1;1;1	1;1;1	Centriolin	CNTRL
Q7Z7K6-2;Q7Z7K6-3;Q7	Q7Z7K6-2;(	2;2;2	2;2;2	2;2;2	Centromere protein V	CENPV
A0A1B0GW73;H3BNF1; A0A1B0GW	A0A1B0GW	2;2;2;2;2	2;2;2;2;2	2;2;2;2;2	Ceroid-lipofuscinosis neuro	CLN6
M0R1L7;M0R1T5;O436	M0R1L7;M	1;1;1	1;1;1	1;1;1	Charged multivesicular bod	CHMP2A
Q9H444;Q96CF2	Q9H444	5;1	5;1	5;1	Charged multivesicular bod	CHMP4B
O00299	O00299	9	9	9	Chloride intracellular chann	CLIC1
Q8WWI5-3;Q8WWI5-2; Q8WWI5-3	Q8WWI5-3	3;3;3	3;3;3	3;3;3	Choline transporter-like pro	SLC44A1
Q8IWA5-3;Q8IWA5;Q8I	Q8IWA5-3;	1;1;1	1;1;1	1;1;1	Choline transporter-like pro	SLC44A2
A0A0C4DGS9;Q9Y6K0	A0A0C4DG	1;1	1;1	1;1	Choline/ethanolaminephos	CEPT1
H7BZN1;H7C1T3;C9J05	H7BZN1;H7	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Choline-phosphate cytidyl	PCYT1A;PC
A0A087X1B7;X6R700;Q	A0A087X1	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Chromatin target of PRMT1	CHTOP
Q13185;S4R2Y4;C9JMV	Q13185;S4	6;3;2;2;1;1	6;3;2;2;1;1	6;3;2;2;1;1	Chromobox protein homolo	CBX3
F5GWX5;A0A0C4DGG9; F5GWX5;A	F5GWX5;A	2;2;2;2;1;1	2;2;2;2;1;1	2;2;2;2;1;1	Chromodomain-helicase-D	CHD4;CHD
B4DJV2;O75390;A0A0C	B4DJV2;O7	9;9;8;5;3;3	9;9;8;5;3;3	8;8;8;5;2;2	Citrate synthase;Citrate syn	CS
A0A087WVQ6;Q00610- A0A087WV	A0A087WV	46;46;46;1	46;46;46;1	35;35;35;1	Clathrin heavy chain;Clathri	CLTC
P09496-2;F8WF69;P094	P09496-2;F	3;2;2;2;2;2	3;2;2;2;2;2	3;2;2;2;2;2	Clathrin light chain A	CLTA
P09497-2;P09497	P09497-2;F	2;2	2;2	2;2	Clathrin light chain B	CLTB
K7EP40;F5H496;I3L3X1; K7EP40;F5	K7EP40;F5	2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	Claudin;Claudin-7	CLDN7
O95832	O95832	3	3	3	Claudin-1	CLDN1
P56749	P56749	1	1	1	Claudin-12	CLDN12
O14493;O95484;P5674	O14493;O	2;1;1;1	2;1;1;1	2;1;1;1	Claudin-4;Claudin-9;Claudin	CLDN4;CLD
O43809;H3BV41;H3BN	O43809;H3	3;2;2	3;2;2	3;2;2	Cleavage and polyadenylati	NUDT21
F8WJN3;Q16630-3;Q16	F8WJN3;Q	4;4;4;4;1	4;4;4;4;1	4;4;4;4;1	Cleavage and polyadenylati	CPSF6
J3QT54;F5H6M0;F5H04	J3QT54;F5	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Cleavage and polyadenylati	CPSF7
A0A0A0MT56;E9PID8;E	A0A0A0MT	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Cleavage stimulation factor	CSTF2
O96005;O96005-4;K7EC	O96005;O	5;4;3;2;1	5;4;3;2;1	5;4;3;2;1	Cleft lip and palate transme	CLPTM1
G5E9Z2;Q96KA5-2;Q96	G5E9Z2;Q9	3;3;3	3;3;3	3;3;3	Cleft lip and palate transme	CLPTM1L
I3L2B0;K7EIG1;O75153	I3L2B0;K7E	3;2;2	3;2;2	3;2;2	Clustered mitochondria pro	CLUH
Q14019;H3BT58	Q14019	5;2	5;2	5;2	Coactosin-like protein	COTL1
Q9NQP5;A6PVK5;P004	Q9NQP5;A	1;1;1	1;1;1	1;1;1	Coagulation factor XIII A ch	F13A1
P53621;P53621-2	P53621;P5	10;10	10;10	10;10	Coatomer subunit alpha;Xe	COPA

P53618;E9PP73	P53618	5;2	5;2	5;2	Coatomer subunit beta	COPB1
P35606-2;P35606;D6R9	P35606-2;F	10;10;3;2;2	10;10;3;2;2	10;10;3;2;2	Coatomer subunit beta	COPB2
P48444;B0YIW6;Q6P1Q	P48444;B0'	7;6;4;4;2	7;6;4;4;2	7;6;4;4;2	Coatomer subunit delta	ARCN1
M0QXB4;O14579;O145	M0QXB4;O	3;3;2;2;1	3;3;2;2;1	3;3;2;2;1	Coatomer subunit epsilon	COPE
Q9Y678;H0Y8X7	Q9Y678	4;1	4;1	4;1	Coatomer subunit gamma-1	COPG1
P23528;G3V1A4;E9PP5	P23528;G3	14;13;13;1	14;13;13;1	13;12;12;1	Cofilin-1	CFL1
Q68DW7;Q8WVM7-2;C	Q68DW7;C	1;1;1	1;1;1	1;1;1	Cohesin subunit SA-1	DKFZp781E
Q96A33-2;Q96A33	Q96A33-2;	5;5	5;5	5;5	Coiled-coil domain-containing	CCDC47
Q96ER9-2;Q96ER9	Q96ER9-2;	1;1	1;1	1;1	Coiled-coil domain-containing	CCDC51
C9JQ41;H7C525;Q4VC3	C9JQ41;H7	1;1;1	1;1;1	1;1;1	Coiled-coil domain-containing	CCDC58
H0YG79;Q9H6F5	H0YG79;Q	1;1	1;1	1;1	Coiled-coil domain-containing	CCDC86
Q9Y6H1;Q5T1J5	Q9Y6H1;Q	3;2	3;2	3;2	Coiled-coil-helix-coiled-coil-	CHCHD2;C
O75534-2;O75534;O75	O75534-2;	5;5;5;5;4;1	5;5;5;5;4;1	5;5;5;5;4;1	Cold shock domain-containing	CSDE1
Q9UMD9-2;Q9UMD9;A	Q9UMD9-2	11;11;8	11;11;8	11;11;8	Collagen alpha-1(XVII) chain	COL17A1
Q07021;I3L3Q7;I3L3B0	Q07021;I3L	8;6;6	8;6;6	8;6;6	Complement component 1	C1QBP
Q15021	Q15021	1	1	1	Condensin complex subunit	NCAPD2
E9PHA2;Q15003;C9J47	E9PHA2;Q14	4;4;3;3;2;1	4;4;3;3;2;1	4;4;3;3;2;1	Condensin complex subunit	NCAPH
Q9BPX3;H0Y9Z8	Q9BPX3	3;1	3;1	3;1	Condensin complex subunit	NCAPG
Q96JB2-2;Q96JB2	Q96JB2-2;	1;1	1;1	1;1	Conserved oligomeric Golgi	COG3
Q9NZB2;Q9NZB2-6;Q9N	Q9NZB2;Q	8;8;6;4;2;2	8;8;6;4;2;2	8;8;6;4;2;2	Constitutive coactivator of I	FAM120A
C9JFE4;A0A096LP07;A0	C9JFE4;A0	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	COP9 signalosome complex	GPS1
D6RAX7;Q9BT78-2;Q9B	D6RAX7;Q	2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	COP9 signalosome complex	COPS4
E9PGT6;Q99627-2;Q99	E9PGT6;Q9	2;2;2;1	2;2;2;1	2;2;2;1	COP9 signalosome complex	COPS8
O75131;A0A087WYQ3;	O75131;A0	10;5;3;3;3	10;5;3;3;3	9;5;3;3;3	Copine-3	CPNE3
E7ENV7;Q8IYJ1;Q86YQ	E7ENV7;Q	2;2;2;1;1	1;1;1;1;1	1;1;1;1;1	Copine-9;Copine-8;Copine-	CPNE8;CPN
O75367-2;O75367-3;O7	O75367-2;	10;10;10;8	10;10;10;8	9;9;9;7;1	Core histone macro-H2A.1;	H2AFY
I3L1U7;I3L0X9;I3L3T0	P I3L1U7;I3L	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Coronin;Mitochondrial imp	PAM16;CO
Q9BR76	Q9BR76	2	2	2	Coronin-1B	CORO1B
Q9ULV4;Q9ULV4-2;Q9L	Q9ULV4;Q	6;6;6;3;3	6;6;6;3;3	6;6;6;3;3	Coronin-1C;Coronin	CORO1C
Q92828	Q92828	1	1	1	Coronin-2A	CORO2A
Q5SZC9;Q9P1F3	Q5SZC9;Q9	1;1	1;1	1;1	Costars family protein ABR	ABRACL
P78310-2;P78310-6;P7	P78310-2;F	4;4;4;3;2	4;4;4;3;2	4;4;4;3;2	Coxsackievirus and adenovi	CXADR
P12532;P12532-2;C9JIX	P12532;P1	3;3;1;1;1	3;3;1;1;1	3;3;1;1;1	Creatine kinase U-type, mit	CKMT1A
P46109	P46109	2	2	2	Crk-like protein	CRKL
X6RI56;O94886	X6RI56;O9	1;1	1;1	1;1	CSC1-like protein 1	TMEM63A
Q5SQP8;P56545;P5654	Q5SQP8;P5	2;2;2;2	2;2;2;2	2;2;2;2	C-terminal-binding protein	CTBP2
P17812;P17812-2	P17812	5;2	5;2	5;2	CTP synthase 1	CTPS1
Q9H5V8;Q9H5V8-2;Q9	Q9H5V8;Q	3;2;1	3;2;1	3;2;1	CUB domain-containing pro	CDCP1
G5EA30;Q92879-5;Q92	G5EA30;Q	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	CUGBP Elav-like family men	CELF1
K4DI93;Q13620-3;Q136	K4DI93;Q1	1;1;1;1	1;1;1;1	1;1;1;1	Cullin-4B	CUL4B
Q86VP6;Q86VP6-2;A0A	Q86VP6;Q	7;6;5;1;1	7;6;5;1;1	7;6;5;1;1	Cullin-associated NEDD8-di	CAND1
A0A024QZP7;P06493;E	A0A024QZ	5;5;4;4;1	4;4;3;3;4	4;4;3;3;4	Cyclin-dependent kinase 1	CDC2;CDK1
Q00534	Q00534	6	6	5	Cyclin-dependent kinase 6	CDK6
P01040	P01040	1	1	1	Cystatin-A;Cystatin-A, N-ter	CSTA
P04080;A0A1W2PS52	P04080;A0	3;2	3;2	3;2	Cystatin-B	CSTB
P01034	P01034	1	1	1	Cystatin-C	CST3
P21291;E9PS42;E9PP21	P21291;E9I	6;4;4;3	6;4;4;3	6;4;4;3	Cysteine and glycine-rich pr	CSRP1
Q9UHD1;E9PIZ4;E9PSD	Q9UHD1;E	2;1;1;1;1	2;1;1;1;1	2;1;1;1;1	Cysteine and histidine-rich	CHORDC1
Q9H1C7	Q9H1C7	1	1	1	Cysteine-rich and transmem	CYSTM1
Q9NZV1;H7C1Z0;H7C2T	Q9NZV1	3;1;1	3;1;1	3;1;1	Cysteine-rich motor neuron	CRIM1

H0YFA4;P52943;P52943	H0YFA4;P5	1;1;1	1;1;1	1;1;1	Cysteine-rich protein 2	CRIP2
Q6UXH1-4;Q6UXH1;Q6UXH1-4	Q6UXH1-4;1;1;1;1	1;1;1;1	1;1;1;1	1;1;1;1	Cysteine-rich with EGF-like	CRELD2
P00167-2;P00167-3;P00167-2	P00167-2;F	1;1;1	1;1;1	1;1;1	Cytochrome b5	CYB5A
H3BUX2;J3KNF8;O4316	H3BUX2;J3	2;2;2;1	2;2;2;1	2;2;2;1	Cytochrome b5 type B	CYB5B
P31930	P31930	14	14	13	Cytochrome b-c1 complex s	UQCRC1
P22695;H3BRG4;H3BSJ	P22695;H3	13;12;11;9	13;12;11;9	13;12;11;9	Cytochrome b-c1 complex s	UQCRC2
P07919;A0A096LP55	P07919	3;1	3;1	3;1	Cytochrome b-c1 complex s	UQCRH
P14927;E5RHG9;B7Z2R	P14927;E5I	2;1;1;1	2;1;1;1	2;1;1;1	Cytochrome b-c1 complex s	UQCRB
Q9UDW1	Q9UDW1	1	1	1	Cytochrome b-c1 complex s	UQCR10
P47985;P0C7P4	P47985;P0	5;4	5;4	5;4	Cytochrome b-c1 complex s	UQCRFS1;L
C9JFR7;P99999;CON__	C9JFR7;P9	2;2;1	2;2;1	2;2;1	Cytochrome c	CYCS
Q9Y2R0;K7EPV0	Q9Y2R0;K7	3;2	3;2	3;2	Cytochrome c oxidase asser	COA3
Q7KZN9-2;Q7KZN9	Q7KZN9-2;	1;1	1;1	1;1	Cytochrome c oxidase asser	COX15
C9J8T6;Q14061	C9J8T6;Q1	1;1	1;1	1;1	Cytochrome c oxidase copp	COX17
P00403	P00403	3	3	3	Cytochrome c oxidase subu	MT-CO2
P13073;Q86WV2;H3BN	P13073;Q8	4;3;3;3;2;1	4;3;3;3;2;1	4;3;3;3;2;1	Cytochrome c oxidase subu	COX4I1
H3BNX8;P20674;H3BRN	H3BNX8;P2	2;2;1;1	2;2;1;1	2;2;1;1	Cytochrome c oxidase subu	COX5A
P10606	P10606	5	5	5	Cytochrome c oxidase subu	COX5B
P14854	P14854	4	4	4	Cytochrome c oxidase subu	COX6B1
P09669	P09669	3	3	3	Cytochrome c oxidase subu	COX6C
D6RIE3;D6RGV5;H0UI0	D6RIE3;D6I	2;2;2;2;1	2;2;2;2;1	2;2;2;2;1	Cytochrome c oxidase subu	COX7A2
O14548;E5RJZ1;H0YBD	O14548;E5	2;1;1	2;1;1	2;1;1	Cytochrome c oxidase subu	COX7A2L
D6R9Z7;P15954	D6R9Z7;P1	2;2	2;2	2;2	Cytochrome c oxidase subu	COX7C
O00483	O00483	2	2	2	Cytochrome c oxidase subu	NDUFA4
P08574	P08574	2	2	2	Cytochrome c1, heme prote	CYC1
P53701	P53701	4	4	4	Cytochrome c-type heme ly	HCCS
Q14204;H0YJ21	Q14204	41;2	41;2	41;2	Cytoplasmic dynein 1 heavy	DYNC1H1
Q13409-6;Q13409-3;Q1	Q13409-6;(3;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	Cytoplasmic dynein 1 intern	DYNC1I2
J3KRI4;O43237-2;O432	J3KRI4;O43	3;3;3;2	3;3;3;2	3;3;3;2	Cytoplasmic dynein 1 light i	DYNC1LI2
Q7L576;A0A0G2JR96;A	Q7L576;A0	4;3;3;2;2;2	4;3;3;2;2;2	4;3;3;2;2;2	Cytoplasmic FMR1-interacti	CYFIP1;CYF
Q07065	Q07065	22	22	22	Cytoskeleton-associated pr	CKAP4
P28838-2;P28838;H0Y9	P28838-2;F	3;3;2	3;3;2	3;3;2	Cytosol aminopeptidase	LAP3
O00154-2;O00154-3;OC	O00154-2;(2;2;2;1;1;1	2;2;2;1;1;1	2;2;2;1;1;1	2;2;2;1;1;1	Cytosolic acyl coenzyme A t	ACOT7
Q96KP4;Q96KP4-2;J3QF	Q96KP4;Q	5;4;1;1	5;4;1;1	5;4;1;1	Cytosolic non-specific dipep	CNDP2
Q5JUV6;P49902-2;P499	Q5JUV6;P4	2;2;2	2;2;2	2;2;2	Cytosolic purine 5-nucleotic	NT5C2
A0A286YF22;A0A2C9F2	A0A286YF2	10;10;10;7	10;10;10;7	10;10;10;7	D-3-phosphoglycerate dehy	PHGDH
K7EQ02;K7EQ55;K7EK3	K7EQ02;K7	3;3;3;3;3	3;3;3;3;3	3;3;3;3;3	DAZ-associated protein 1	DAZAP1
Q5BKZ1-2;Q5BKZ1;E2Q	Q5BKZ1-2;(2;2;1;1	2;2;1;1	2;2;1;1	2;2;1;1	DBIRD complex subunit ZNF	ZNF326
Q9H773	Q9H773	2	2	2	dCTP pyrophosphatase 1	DCTPP1
A0A087WT20;Q9NV06; A0A087WT	A0A087WT	2;2;1	2;2;1	2;2;1	DDB1- and CUL4-associated	DCAF13
P30046;J3KQ18;B5MC8	P30046;J3	4;3;3;3;3;1	4;3;3;3;3;1	4;3;3;3;3;1	D-dopachrome decarboxyla	DDT;DDTL
A0A0A0MRX2;Q96HY6- A0A0A0MF	A0A0A0MF	2;2;2	2;2;2	2;2;2	DDR GK domain-containing	DDR GK1
Q9Y394-2;Q9Y394;H0YJ	Q9Y394-2;(3;3;2;2;2	3;3;2;2;2	3;3;2;2;2	3;3;2;2;2	Dehydrogenase/reductase	DHRS7
Q3LIE7;Q15392-2;Q153	Q3LIE7;Q1	5;5;5;2	5;5;5;2	5;5;5;2	Delta(24)-sterol reductase	Nbla03646
Q13011;M0R248;M0QZ	Q13011;M	4;3;2	3;2;1	3;2;1	Delta(3,5)-Delta(2,4)-dieno	ECH1
P30038-3;P30038;Q5TF	P30038-3;F	2;2;1;1	2;2;1;1	2;2;1;1	Delta-1-pyrroline-5-carboxy	ALDH4A1
P54886-2;P54886	P54886-2;F	15;15	15;15	15;15	Delta-1-pyrroline-5-carboxy	ALDH18A1
O43583	O43583	1	1	1	Density-regulated protein	DENR
J3KP30;Q5QJE6;E9PRB3	J3KP30;Q5	3;3;1	3;3;1	3;3;1	Deoxynucleotidyltransferas	DNTTIP2
G3V158;E9PPM8;Q9Y31	G3V158;E9	1;1;1	1;1;1	1;1;1	Deoxyribose-phosphate ald	DERA

A0A0C4DGL3;H0YNW5; A0A0C4DG	5;5;5;5;4;3	5;5;5;5;4;3	5;5;5;5;4;3	Deoxyuridine 5-triphosphat	DUT	
E5RGY0;B4E1G1;Q9BUN	E5RGY0;B4 1;1;1;1	1;1;1;1	1;1;1;1	Derlin-1	DERL1	
I3L1T3;Q9GZP9	I3L1T3;Q9C 1;1	1;1	1;1	Derlin-2	DERL2	
Q02487-2;Q02487	Q02487-2;(1;1	1;1	1;1	Desmocollin-2	DSC2	
Q14574-2;Q14574;J3QF	Q14574-2;(4;4;1	4;4;1	4;4;1	Desmocollin-3	DSC3	
Q14126	Q14126	12	12	12	Desmoglein-2	DSG2
P32926	P32926	12	12	12	Desmoglein-3	DSG3
P15924;P15924-3;P159	P15924;P1 46;40;39	46;40;39	46;40;39	Desmoplakin	DSP	
P60981;F6RFD5;P60981	P60981;F6 8;7;7	7;6;6	7;6;6	Destrin	DSTN	
Q9Y295	Q9Y295	2	2	2	Developmentally-regulated	DRG1
P09622;E9PEX6;P09622	P09622;E9 5;4;4;4;1;1	5;4;4;4;1;1	5;4;4;4;1;1	Dihydrolipoyl dehydrogenase	DLD	
P10515;H0YDD4;E9PEJ4	P10515;H0 5;4;4	5;4;4	5;4;4	Dihydrolipoyllysine-residue	DLAT	
P36957;P36957-2;Q86S	P36957;P3 8;7;5;1;1;1	8;7;5;1;1;1	8;7;5;1;1;1	Dihydrolipoyllysine-residue	DLST	
G3V1D3;G3V180;Q9NY	G3V1D3;G 1;1;1;1	1;1;1;1	1;1;1;1	Dipeptidyl peptidase 3	DPP3	
O14672	O14672	2	2	2	Disintegrin and metalloprot	ADAM10
F8WC54;A0AVL1;Q134	F8WC54;A 5;5;5;5	5;5;5;5	5;5;5;5	Disintegrin and metalloprot	ADAM9	
Q05BS2;Q96SL1-2;Q96	Q05BS2;Q 1;1;1	1;1;1	1;1;1	Disrupted in renal carcinom	DIRC2	
Q16531;F5GY55;F5H2L	Q16531;F5 9;8;3;3;2;2	9;8;3;3;2;2	9;8;3;3;2;2	DNA damage-binding prote	DDB1	
Q6UX65	Q6UX65	1	1	1	DNA damage-regulated aut	DRAM2
B0QYD3;Q9UH17-3;Q9	B0QYD3;Q 5;5;5;3;2;2	5;5;5;3;2;2	5;5;5;3;2;2	DNA dC->dU-editing enzym	APOBEC3B	
B1AHB1;P33992;B1AHB	B1AHB1;P3 5;5;1;1	5;5;1;1	5;5;1;1	DNA helicase;DNA replicati	MCM5	
E9PHA6;P43246-2;P432	E9PHA6;P4 3;3;3;1	3;3;3;1	3;3;3;1	DNA mismatch repair prote	MSH2	
P52701-4;P52701-3;P52	P52701-4;F 4;4;4;3;3;1	4;4;4;3;3;1	4;4;4;3;3;1	DNA mismatch repair prote	MSH6	
E5RFF9;Q9BRT9	E5RFF9;Q9 1;1	1;1	1;1	DNA replication complex GI	GIN54	
H0Y8E6;P49736	H0Y8E6;P4 12;12	12;12	12;12	DNA replication licensing fa	MCM2	
P25205;P25205-2;J3KQ	P25205;P2 8;7;6;1	8;7;6;1	8;7;6;1	DNA replication licensing fa	MCM3	
P33991;E5RG31;E5RFJ8	P33991 11;3;2	11;3;2	11;3;2	DNA replication licensing fa	MCM4	
Q14566	Q14566	8	8	8	DNA replication licensing fa	MCM6
P33993;P33993-3;P339	P33993;P3 16;14;8;4	16;14;8;4	16;14;8;4	DNA replication licensing fa	MCM7	
P11387;E5RIC7;Q969P6	P11387 14;1;1;1	14;1;1;1	14;1;1;1	DNA topoisomerase 1	TOP1	
P11388;P11388-2;P113	P11388;P1 14;14;14;1	14;14;14;1	14;14;14;1	DNA topoisomerase 2-alpha	TOP2A	
G3V5Q1;G3V3M6;P276	G3V5Q1;G 5;5;5;4;4;4	5;5;5;4;4;4	5;5;5;4;4;4	DNA-(apurinic or apyrimidir	APEX1	
P78527;P78527-2	P78527;P7 56;55	56;55	56;55	DNA-dependent protein kin	PRKDC	
O95602;B9ZVN9	O95602;B9 2;1	2;1	2;1	DNA-directed RNA polymer	POLR1A	
O15446;O15446-2	O15446;O1 2;2	2;2	2;2	DNA-directed RNA polymer	CD3EAP	
P24928-2;P24928	P24928-2;F 1;1	1;1	1;1	DNA-directed RNA polymer	POLR2A	
K7EMH3;O00411	K7EMH3;O 1;1	1;1	1;1	DNA-directed RNA polymer	POLRMT	
C9J2Y9;P30876;C9J4M6	C9J2Y9;P3 2;2;1;1	2;2;1;1	2;2;1;1	DNA-directed RNA polymer	POLR2B	
O15160-2;O15160;D6RI	O15160-2;(2;2;1;1;1	2;2;1;1;1	2;2;1;1;1	DNA-directed RNA polymer	POLR1C	
A0A087WVZ9;A0A0A0N	A0A087WV 1;1;1	1;1;1	1;1;1	DNA-directed RNA polymer	POLR2E	
P31689-2;P31689	P31689-2;F 3;3	3;3	3;3	DnaJ homolog subfamily A r	DNAJA1	
O60884;A0A087WT48;I	O60884;A0 4;3;1	4;3;1	4;3;1	DnaJ homolog subfamily A r	DNAJA2	
Q96EY1-2;Q96EY1;Q96	Q96EY1-2;(3;3;2	3;3;2	3;3;2	DnaJ homolog subfamily A r	DNAJA3	
P25685;M0R080;P2568	P25685;MC 4;3;3;1;1;1	4;3;3;1;1;1	4;3;3;1;1;1	DnaJ homolog subfamily B r	DNAJB1	
Q9UBS4;H7C2Y5	Q9UBS4;H 4;2	4;2	4;2	DnaJ homolog subfamily B r	DNAJB11	
V9GY70;V9GYN7;J3KPS	V9GY70;V9 1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	DnaJ homolog subfamily B r	DNAJB12	
Q9NVH1-3;Q9NVH1;Q9	Q9NVH1-3;4;4;2	4;4;2	4;4;2	DnaJ homolog subfamily C r	DNAJC11	
H0YA63;O75165	H0YA63;O7 1;1	1;1	1;1	DnaJ homolog subfamily C r	DNAJC13	
X6R9L0;Q13217	X6R9L0;Q1 3;3	3;3	3;3	DnaJ homolog subfamily C r	DNAJC3	
Q9H3Z4	Q9H3Z4	1	1	1	DnaJ homolog subfamily C r	DNAJC5



Q99615-2;Q99615;K7EC	Q99615-2;(4;4;1;1;1;1	4;4;1;1;1;1	4;4;1;1;1;1	DnaJ homolog subfamily C r	DNAJC7
Q8WXX5	Q8WXX5	1	1	DnaJ homolog subfamily C r	DNAJC9
Q5QPK2;H0Y368;O6076	Q5QPK2;H(3;3;3;1	3;3;3;1	3;3;3;1	Dolichol-phosphate mannosyl	DPM1
Q9P2X0;Q9P2X0-2	Q9P2X0;Q(2;2	2;2	2;2	Dolichol-phosphate mannosyl	DPM3
A0A0C4DGS1;P39656;P	A0A0C4DG 8;8;7;6;5	8;8;7;6;5	8;8;7;6;5	Dolichyl-diphosphooligosaccharide	DDOST
P04843;B7Z4L4;F8WF3	P04843;B7(24;18;5	24;18;5	24;18;5	Dolichyl-diphosphooligosaccharide	RPN1
P04844;P04844-2;Q5JYI	P04844;P0(11;10;3;2;2	11;10;3;2;2	11;10;3;2;2	Dolichyl-diphosphooligosaccharide	RPN2
F5GXX5;P61803;F5H89	F5GXX5;P6 4;4;2;2	4;4;2;2	4;4;2;2	Dolichyl-diphosphooligosaccharide	DAD1
P46977;P46977-2;A0A0	P46977;P4(5;4;1;1;1	5;4;1;1;1	5;4;1;1;1	Dolichyl-diphosphooligosaccharide	STT3A
Q8TCJ2	Q8TCJ2	2	2	Dolichyl-diphosphooligosaccharide	STT3B
Q9Y673-2;Q9Y673	Q9Y673-2;(1;1	1;1	1;1	Dolichyl-phosphate beta-glucosyl	ALG5
A0A087X1A5;Q5JW30;C	A0A087X1(2;2;2;2;2	2;2;2;2;2	2;2;2;2;2	Double-stranded RNA-binding	STAU1
H0YCK3;P55265-5;P552	H0YCK3;P5 3;3;3;3;3	3;3;3;3;3	3;3;3;3;3	Double-stranded RNA-specific	ADAR
A8MY26;A8MTY9;O149	A8MY26;A(1;1;1;1	1;1;1;1	1;1;1;1	Down syndrome critical reg	DSCR3
H0Y5J4;B4DDD6;Q9UJU	H0Y5J4;B4(3;3;3;3;3	3;3;3;3;3	3;3;3;3;3	Drebrin-like protein	DBNL
Q02750-2;Q02750	Q02750-2;(1;1	1;1	1;1	Dual specificity mitogen-act	MAP2K1
P36507	P36507	1	1	Dual specificity mitogen-act	MAP2K2
P46734-2;P46734;P467	P46734-2;F 3;3;3;2;1;1	3;3;3;2;1;1	3;3;3;2;1;1	Dual specificity mitogen-act	MAP2K3
E7EX90;Q14203-5;Q142	E7EX90;Q1 2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	Dynactin subunit 1	DCTN1;DKF
G8JLD5;O00429-4;O004	G8JLD5;O0 3;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	Dynamamin-1-like protein	DNM1L
E5KLJ9;O60313-13;O60	E5KLJ9;O6(3;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	Dynamamin-like 120 kDa prote	OPA1
A0A075B6F3;Q96JB1-2; A0A075B6	F 1;1;1	1;1;1	1;1;1	Dynein heavy chain 8, axonal	DNAH8
P63167;F8VXI7;F8VXL2; P63167	3;1;1;1	1;1;1;1	1;1;1;1	Dynein light chain 1, cytoplasmic	DYNLL1
Q96FJ2	Q96FJ2	3	3	Dynein light chain 2, cytoplasmic	DYNLL2
Q9NP97;B1AKR6;Q8TFC	Q9NP97;B1(3;2;2;1;1;1	3;2;2;1;1;1	3;2;2;1;1;1	Dynein light chain roadblock	DYNLRB1;D
Q6P0N6;E7ETB9;E9PHV	Q6P0N6;E7 1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Dystonin	DST
Q14118	Q14118	2	2	Dystroglycan;Alpha-dystrog	DAG1
P49792;J3KNE0;Q7Z3J3	P49792 22;5;5;5;4; 22;5;5;5;4; 21;5;5;5;4;			E3 SUMO-protein ligase Rar	RANBP2
Q14258	Q14258	7	7	E3 ubiquitin/ISG15 ligase TF	TRIM25
H3BUD0;H3BS86;Q9UN	H3BUD0;H(1;1;1;1	1;1;1;1	1;1;1;1	E3 ubiquitin-protein ligase (	STUB1
Q7Z6Z7-2;Q7Z6Z7-3;Q7	Q7Z6Z7-2;(5;5;5;1	5;5;5;1	5;5;5;1	E3 ubiquitin-protein ligase H	HUWE1
F8WCD0;Q8NC42	F8WCD0;Q 3;3	3;3	3;3	E3 ubiquitin-protein ligase F	RNF149
Q5JYV0;Q13049	Q5JYV0;Q1 1;1	1;1	1;1	E3 ubiquitin-protein ligase 1	TRIM32
Q9C037-3;Q9C037-2;Q9	Q9C037-3;(2;2;2	2;2;2	2;2;2	E3 ubiquitin-protein ligase 1	TRIM4
A0A087WVR3;A0A087V	A0A087WV 3;3;3;3;2	3;3;3;3;2	3;3;3;3;2	E3 ubiquitin-protein ligase U	UHRF1
Q96C19;H0Y4Y4;A0A08	Q96C19;HC 7;4;1;1;1	7;4;1;1;1	7;4;1;1;1	EF-hand domain-containing	EFHD2
O43854-2;O43854	O43854-2;(2;2	2;2	2;2	EGF-like repeat and discoidin	EDIL3
C9J2Z4;A0A024R571;Q9	C9J2Z4;A0(2;2;2	2;2;2	1;1;1	EH domain-containing prote	EHD1
Q9H223;Q9NZN3-2	Q9H223 6;1	6;1	5;0	EH domain-containing prote	EHD4
Q15717;Q15717-2;M0C	Q15717;Q1(7;7;4;2	7;7;4;2	7;7;4;2	ELAV-like protein 1	ELAVL1
H0YKF0;H0YLU7;P1380	H0YKF0;H0 6;6;6;5;5;4	6;6;6;5;5;4	6;6;6;5;5;4	Electron transfer flavoprote	ETFA
P38117;P38117-2;M0Q	P38117;P3(10;10;5	10;10;5	10;10;5	Electron transfer flavoprote	ETFB
Q05639	Q05639	9	1	Elongation factor 1-alpha 2	EEF1A2
P24534;F2Z2G2;C9JZW	P24534 5;2;2;1	5;2;2;1	5;2;2;1	Elongation factor 1-beta	EEF1B2
E9PK01;P29692;A0A08	E9PK01;P2(8;8;7;7;6	8;8;7;7;6	1;1;1;1;1;1	Elongation factor 1-delta	EEF1D
P29692-3;E9PL71;E9PN	P29692-3;E 8;6;5	1;1;1	1;1;1	Elongation factor 1-delta	EEF1D
P26641;P26641-2	P26641;P2(16;15	16;15	16;15	Elongation factor 1-gamma	EEF1G
P13639	P13639	34	34	Elongation factor 2	EEF2
C9IZ01;Q96RP9;Q96RP	C9IZ01;Q9(5;5;5;4	5;5;5;4	5;5;5;4	Elongation factor G, mitoch	GFM1
P43897;P43897-2;C9JG	P43897;P4(3;2;1;1;1;1	3;2;1;1;1;1	3;2;1;1;1;1	Elongation factor Ts, mitoch	TSFM

P49411;H3BNU3	P49411	19;1	19;1	19;1	Elongation factor Tu, mitoc	TUFM
Q9BW60	Q9BW60		1	1	Elongation of very long chain	ELOVL1
A0A0A0MTI6;Q9NYP7-3	A0A0A0MT1;1;1;1	1;1;1;1	1;1;1;1	1;1;1;1	Elongation of very long chain	ELOVL5
F5H2T0;O95163	F5H2T0;O91;1	1;1	1;1	1;1	Elongator complex protein	IKBKAP
P50402;Q5HY57	P50402;Q55;3	5;3	5;3	5;3	Emerin	EMD
O94919	O94919	3	3	3	Endonuclease domain-cont	ENDOD1
MOQYE0;MOR0I3;Q9990	MOQYE0;M1;1;1;1	1;1;1;1	1;1;1;1	1;1;1;1	Endophilin-A2	SH3GL1
Q9NZ08;Q9NZ08-2;D6R	Q9NZ08;Q7;7;2;1	7;7;2;1	7;7;2;1	7;7;2;1	Endoplasmic reticulum amin	ERAP1
E7ER77;Q7Z2K6;A0A0C	E7ER77;Q74;4;1;1	4;4;1;1	4;4;1;1	4;4;1;1	Endoplasmic reticulum met	ERMP1
P30040;F8VY02;P30040	P30040;F87;5;1	7;5;1	6;5;1	6;5;1	Endoplasmic reticulum resic	ERP29
Q9BS26	Q9BS26	6	6	6	Endoplasmic reticulum resic	ERP44
H0Y621;H0Y5K5;Q9Y28	H0Y621;H03;3;3;3;2;2	3;3;3;3;2;2	3;3;3;3;2;2	3;3;3;3;2;2	Endoplasmic reticulum-Golgi	ERGIC3
P14625;Q96GW1;A0A1	P1462528;10;10;5	26;8;8;5;5	26;8;8;5;5	26;8;8;5;5	Endoplasmin	HSP90B1
O60869-2;O60869-3;O6	O60869-2;2;2;2	2;2;2	2;2;2	2;2;2	Endothelial differentiation-i	EDF1
P84090;G3V279	P84090;G33;2	3;2	3;2	3;2	Enhancer of rudimentary hc	ERH
P42126-2;P42126;Q96C	P42126-2;F5;5;4;3	5;5;4;3	5;5;4;3	5;5;4;3	Enoyl-CoA delta isomerase	ECI1;DCI
A0A0C4DGA2;O75521-2	A0A0C4DG4;4;4;3;3;3	4;4;4;3;3;3	4;4;4;3;3;3	4;4;4;3;3;3	Enoyl-CoA delta isomerase	ECI2
P30084	P30084	8	8	8	Enoyl-CoA hydratase, mitoc	ECHS1
P98172	P98172	1	1	1	Ephrin-B1	EFNB1
P00533;E9PFD7;Q504U	P00533;E9I30;29;25;1	30;29;25;1	30;29;25;1	30;29;25;1	Epidermal growth factor rec	EGFR
G3V2V8;J3KMY5;G3V3E	G3V2V8;J33;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	Epididymal secretory protei	NPC2
B5MCA4;P16422;C9JKY	B5MCA4;P6;6;3	6;6;3	6;6;3	6;6;3	Epithelial cell adhesion mol	EPCAM
H0YBR2;H0YBB3;Q6NX	H0YBR2;HC2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	Epithelial splicing regulato	ESRP1
P07099	P07099	6	6	6	Epoxide hydrolase 1	EPHX1
Q99808;Q99808-2	Q99808;Q91;1	1;1	1;1	1;1	Equilibrative nucleoside tra	SLC29A1
MOR1Y2;P33947-2;P339	MOR1Y2;P52;2;2;2;1	2;2;2;2;1	2;2;2;2;1	2;2;2;2;1	ER lumen protein-retaining	KDELRL1;KD
Q8N766-3;Q8N766-2;Q	Q8N766-3;3;3;3;2	3;3;3;2	3;3;3;2	3;3;3;2	ER membrane protein comp	EMC1
Q15006;H0YAS9	Q15006;HC3;2	3;2	3;2	3;2	ER membrane protein comp	EMC2
S4R3U9;Q9P0I2-2;Q9P0	S4R3U9;Q91;1;1	1;1;1	1;1;1	1;1;1	ER membrane protein comp	EMC3
O43402;MOR1B0;O434	O43402;M2;1;1	2;1;1	2;1;1	2;1;1	ER membrane protein comp	EMC8
O75477;B0QZ43;O9490	O75477;B05;4;1;1	2;1;0;0	2;1;0;0	2;1;0;0	Erlin-1	ERLIN1
E5RHW4;O94905;E5RJ0	E5RHW4;O6;6;2	6;6;2	3;3;1	3;3;1	Erlin-2	ERLIN2
Q96HE7;G3V3E6;G3V5C	Q96HE7;G512;7;5;5;2	12;7;5;5;2	12;7;5;5;2	12;7;5;5;2	ERO1-like protein alpha	ERO1L
A0A096LP73;A0A096LN	A0A096LP72;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	ES1 protein homolog, mitoc	C21orf33
Q9H501	Q9H501	1	1	1	ESF1 homolog	ESF1
Q92506	Q92506	1	1	1	Estradiol 17-beta-dehydrog	HSD17B8
P60842;J3KT12;P60842	P60842;J3K20;17;17;1	20;17;17;1	16;13;13;1	16;13;13;1	Eukaryotic initiation factor	EIF4A1;EIF4
P38919;I3L3H2	P38919	8;3	4;1	4;1	Eukaryotic initiation factor	EIF4A3
P15170-2;P15170-3;H3I	P15170-2;F7;7;5;5;2;1	7;7;5;5;2;1	7;7;5;5;2;1	7;7;5;5;2;1	Eukaryotic peptide chain re	GSPT1
B7Z7P8;P62495-2;P624	B7Z7P8;P66;6;6;2;1;1	6;6;6;2;1;1	6;6;6;2;1;1	6;6;6;2;1;1	Eukaryotic peptide chain re	ETF1
D6RBD7;C9J1V9;O4332	D6RBD7;C92;2;2;2;1;1	2;2;2;2;1;1	2;2;2;2;1;1	2;2;2;2;1;1	Eukaryotic translation elong	EEF1E1;EEF
K7EM18;P41567;O6073	K7EM18;P42;2;2;1	2;2;2;1	2;2;2;1	2;2;2;1	Eukaryotic translation initia	EIF1;EIF1B
P47813;X6RAC9;A6NJH	P47813;X6I3;2;2;2	3;2;2;2	3;2;2;2	3;2;2;2	Eukaryotic translation initia	EIF1AX;EIF
P05198;H0YJS4;G3V4T5	P05198;H05;3;3	5;3;3	5;3;3	5;3;3	Eukaryotic translation initia	EIF2S1
P20042	P20042	7	7	7	Eukaryotic translation initia	EIF2S2
P41091;Q2VIR3;F8W81	P41091;Q28;6;4;4;1	8;6;4;4;1	8;6;4;4;1	8;6;4;4;1	Eukaryotic translation initia	EIF2S3;EIF2
C9IZE1;F8WAE5;Q9BY4	C9IZE1;F8V2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	Eukaryotic translation initia	EIF2A
Q14152;Q14152-2	Q14152;Q111;10	11;10	11;10	11;10	Eukaryotic translation initia	EIF3A
P55884;P55884-2;C9JQ	P55884;P58;8;3;3	8;8;3;3	8;8;3;3	8;8;3;3	Eukaryotic translation initia	EIF3B
Q99613-2;Q99613;B5M	Q99613-2;7;7;6;1;1	7;7;6;1;1	7;7;6;1;1	7;7;6;1;1	Eukaryotic translation initia	EIF3C;EIF3C

O15371-2;O15371-3;O1	O15371-2;(9;9;9;3;1;1	9;9;9;3;1;1	9;9;9;3;1;1	Eukaryotic translation initia	EIF3D	
P60228;E5RGA2;H0YAM	P60228;E5I 7;6;3;2;2;1	7;6;3;2;2;1	7;6;3;2;2;1	Eukaryotic translation initia	EIF3E	
O00303;H0YDT6	O00303	3;1	3;1	3;1	Eukaryotic translation initia	EIF3F
K7EL20;O75821;K7ER9C	K7EL20;O7 4;4;3;2;1	4;4;3;2;1	4;4;3;2;1	Eukaryotic translation initia	EIF3G	
A0A087WZK9;B3KS98;C	A0A087WZ 4;4;4;2;1;1	4;4;4;2;1;1	4;4;4;2;1;1	Eukaryotic translation initia	EIF3H	
Q13347;Q5TFK1	Q13347	10;3	10;3	10;3	Eukaryotic translation initia	EIF3I
H0YGJ7;H0YLP3;O75821	H0YGJ7;H0 2;2;2;2;1	2;2;2;2;1	2;2;2;2;1	Eukaryotic translation initia	EIF3J	
K7ES31;K7ERF1;Q9UBQ	K7ES31;K7I 1;1;1;1	1;1;1;1	1;1;1;1	Eukaryotic translation initia	EIF3K	
B0QY89;Q9Y262;Q9Y26	B0QY89;Q9 7;7;6;5;3;3	7;7;6;5;3;3	7;7;6;5;3;3	Eukaryotic translation initia	EIF3L	
E9PRY0;J3KNJ2;H0YCQ8	E9PRY0;J3K 1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Eukaryotic translation initia	EIF3M	
Q04637-5;Q04637-4;QC	Q04637-5;(16;16;16;1	16;16;16;1	16;16;16;1	Eukaryotic translation initia	EIF4G1	
H0YCH5;H0Y3P2;D3DQ\	H0YCH5;HC 2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	Eukaryotic translation initia	EIF4G2	
E7EX17;P23588-2;P235	E7EX17;P2 4;4;4;1	4;4;4;1	4;4;4;1	Eukaryotic translation initia	EIF4B	
Q15056-2;Q15056	Q15056-2;(6;6	6;6	6;6	Eukaryotic translation initia	EIF4H	
P55010;H0YMJ8;H0YME	P55010;H0 2;1;1;1;1	2;1;1;1;1	2;1;1;1;1	Eukaryotic translation initia	EIF5	
I3L397;I3L504;P63241;F	I3L397;I3L 8;8;8;5;4	8;8;8;5;4	8;8;8;5;4	Eukaryotic translation initia	EIF5A;EIF5	
A0A087WUT6;O60841	A0A087WL 5;5	5;5	5;5	Eukaryotic translation initia	EIF5B	
P56537;B7ZBH1;P56537	P56537;B7 5;3;3;1;1;1	5;3;3;1;1;1	5;3;3;1;1;1	Eukaryotic translation initia	EIF6	
R4GNH9;R4GMQ7;B1A	R4GNH9;R4 1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Exosome complex compone	EXOSC1	
Q5RKV6	Q5RKV6	4	4	4	Exosome complex compone	EXOSC6
Q13868-3;Q13868	Q13868-3;(1;1	1;1	1;1	Exosome complex compone	EXOSC2	
Q15024	Q15024	2	2	2	Exosome complex compone	EXOSC7
F2Z2C0;G3V1J5;Q9Y2L1	F2Z2C0;G3' 2;2;2;2	2;2;2;2	2;2;2;2	Exosome complex exonucle	DIS3	
O14980;C9J673;C9JKM	O14980	9;3;3;2;2;2	9;3;3;2;2;2	9;3;3;2;2;2	Exportin-1	XPO1
P55060-3;P55060;P550	P55060-3;F 12;12;11;2	12;12;11;2	12;12;11;2	Exportin-2	CSE1L	
Q9HAV4;H0Y3Q8;E2QR	Q9HAV4;H0 2;1;1	2;1;1	2;1;1	Exportin-5	XPO5	
Q9BSJ8;Q9BSJ8-2	Q9BSJ8;Q9 11;11	11;11	11;11	Extended synaptotagmin-1	ESYT1	
E7EQR4;P15311;P35241	E7EQR4;P1 14;14;5;5;3	9;9;0;0;0;0	9;9;0;0;0;0	Ezrin	EZR	
Q9Y5B9;G3V5A4;G3V4C	Q9Y5B9	10;1;1;1	10;1;1;1	10;1;1;1	FACT complex subunit SPT1	SUPT16H
Q08945;E9PMD4;E9PP2	Q08945	10;4;1;1	10;4;1;1	10;4;1;1	FACT complex subunit SSRP	SSRP1
P52907	P52907	7	7	6	F-actin-capping protein sub	CAPZA1
P47755;C9JUG7;F8W9N	P47755;C9 6;5;5;5;4	5;4;4;4;3	5;4;4;4;3	F-actin-capping protein sub	CAPZA2	
P47756-2;B1AK87;B1AK	P47756-2;E 10;9;9;9;7	10;9;9;9;7	10;9;9;9;7	F-actin-capping protein sub	CAPZB	
Q96AE4-2;E9PEB5;Q96	Q96AE4-2;I 12;11;11;6	11;10;10;6	11;10;10;6	Far upstream element-bind	FUBP1	
A0A087WTP3;Q92945;I	A0A087WT 14;14;7;5;3	14;14;7;5;3	13;13;6;5;3	Far upstream element-bind	KHSRP	
Q96I24;Q96I24-2	Q96I24;Q9 8;5	7;4	7;4	Far upstream element-bind	FUBP3	
P14324-2;P14324;A0A0	P14324-2;F 3;3;2;2;2;1	3;3;2;2;2;1	3;3;2;2;2;1	Farnesyl pyrophosphate syr	FDPS	
Q96CS3	Q96CS3	6	6	6	FAS-associated factor 2	FAF2
Q16658;C9JFC0;A0A0A	Q16658	19;4;4;2	19;4;4;2	19;4;4;2	Fascin	FSCN1
A0A0U1RQF0;P49327;A	A0A0U1RQ 49;49;5;1;1	49;49;5;1;1	49;49;5;1;1	Fatty acid synthase;[Acyl-ca	FASN	
Q01469;I6L8B7;A8MUU	Q01469;I6L 4;3;1	4;3;1	4;3;1	Fatty acid-binding protein, ε	FABP5	
E9PNW8;Q8WVX9	E9PNW8;Q 3;3	3;3	3;3	Fatty acyl-CoA reductase 1	FAR1	
J3QRD1;P51648;P5164	J3QRD1;P5 7;7;7;4;3;1	7;7;7;4;3;1	7;7;7;4;3;1	Fatty aldehyde dehydrogen	ALDH3A2	
G3V1L6;Q9BQL6;Q9BQI	G3V1L6;Q9 4;4;3;3;1	4;4;3;3;1	4;4;3;3;1	Fermitin family homolog 1	FERMT1	
P02794;G3V1D1;G3V19	P02794;G3 6;4;4;3;3;2	6;4;4;3;3;2	6;4;4;3;3;2	Ferritin heavy chain;Ferritin	FTH1	
Q4ZHG4-2;Q4ZHG4	Q4ZHG4-2; 1;1	1;1	1;1	Fibronectin type III domain-	FNDCC1	
P21333-2;P21333;Q5HY	P21333-2;F 88;88;87;8	88;88;87;8	80;80;79;7	Filamin-A	FLNA	
O75369-2;O75369-9;O7	O75369-2;(48;48;48;4	43;43;43;4	41;41;41;4	Filamin-B	FLNB	
Q8WUP2-3;Q8WUP2;Q	Q8WUP2-3 2;2;2	2;2;2	2;2;2	Filamin-binding LIM protein	FBLIM1	
P39748;P39748-2;F5H1	P39748;P3 6;4;3;2	6;4;3;2	6;4;3;2	Flap endonuclease 1	FEN1	

P30043;M0R192;M0QZ	P30043;MC	5;4;3	5;4;3	5;4;3	Flavin reductase (NADPH)	BLVRB
O75955-2;O75955;A0A	O75955-2;(5;5;4;4;2;2	5;5;4;4;2;2	5;5;4;4;2;2	5;5;4;4;2;2	Flotillin-1	FLOT1
J3QLD9;E7EMK3;Q1425	J3QLD9;E7I6;6;6;3	6;6;6;3	6;6;6;3	6;6;6;3	Flotillin-2	FLOT2
J3KNW4;A0A0A0MSG2;J3KNW4;A	(2;2;2	2;2;2	2;2;2	2;2;2	Four and a half LIM domain	FHL2
B4DXZ6;P51114-2;P511	B4DXZ6;P5	6;6;6;5;4;4	6;6;6;5;4;4	6;6;6;5;4;4	Fragile X mental retardation	FXR1
H7C585;C9JAX1;Q1659	H7C585;C9	2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	Frataxin, mitochondrial;Fra	FXN
O60353-2;O60353	O60353-2;(1;1	1;1	1;1	1;1	Frizzled-6	FZD6
P04075;P04075-2;H3BC	P04075;P0	23;22;21;2	23;22;21;2	17;16;15;1	Fructose-bisphosphate aldo	ALDOA
P09972;K7EKH5;C9J8F3	P09972;K7I8;4;4;4;4	2;2;2;2;2	2;2;2;2;2	2;2;2;2;2	Fructose-bisphosphate aldo	ALDOC
P07954-2;P07954	P07954-2;F	11;11	11;11	11;11	Fumarate hydratase, mitoc	FH
S4R445;Q14802;Q1480	S4R445;Q1	1;1;1;1	1;1;1;1	1;1;1;1	FXD domain-containing ior	FXD3
E9PN19;O00214;O0021	E9PN19;OC	5;5;5;4;3;2	5;5;5;4;3;2	5;5;5;4;3;2	Galectin;Galectin-8	LGALS8
P09382;F8WEI7	P09382	8;2	8;2	8;2	Galectin-1	LGALS1
P17931;G3V3R6	P17931;G3	2;1	2;1	2;1	Galectin-3;Galectin	LGALS3
Q08380;K7EJY8;K7ESM	Q08380	4;1;1;1;1	4;1;1;1;1	4;1;1;1;1	Galectin-3-binding protein	LGALS3BP
P60520;H3BQ50;F5GZY	P60520;H3	2;1;1;1;1;1	2;1;1;1;1;1	2;1;1;1;1;1	Gamma-aminobutyric acid	GABARAPL
O75223-3;O75223;M0C	O75223-3;(3;3;2;1;1;1	3;3;2;1;1;1	3;3;2;1;1;1	3;3;2;1;1;1	Gamma-glutamylcyclotrans	GGCT
Q16666-3;Q16666-2;Q1	Q16666-3;(9;9;9;8;4;3	9;9;9;8;4;3	9;9;9;8;4;3	9;9;9;8;4;3	Gamma-interferon-inducibl	IFI16
Q9H488;Q9H488-2	Q9H488;Q	2;1	2;1	2;1	GDP-fucose protein O-fucos	POFUT1
CON__Q3SX14;A0A0A0	CON__Q3S	12;9;9;9;9;9	12;9;9;9;9;9	12;9;9;9;9;9	Gelsolin	GSN
Q12789-3;Q12789	Q12789-3;(1;1	1;1	1;1	1;1	General transcription factor	GTF3C1
P78347-2;P78347-4;P7	P78347-2;F	8;8;8;8;2	8;8;8;8;2	8;8;8;8;2	General transcription factor	GTF2I
O60763;O60763-2	O60763;O	2;2	2;2	2;2	General vesicular transport	USO1
G3V4P8;P60983	G3V4P8;P	6;1;1	1;1	1;1	Glia maturation factor beta	GMFB
Q9NZM5	Q9NZM5	2	2	2	Glioma tumor suppressor c	GLTSCR2
G3V5E4;G3V4W4;Q96E	G3V5E4;G3	1;1;1	1;1;1	1;1;1	Glucosamine 6-phosphate	GNPNAT1
D6RAY7;D6R9P4;P4692	D6RAY7;D	5;5;5;4;4;3	5;5;5;4;4;3	5;5;5;4;4;3	Glucosamine-6-phosphate	GNPDA1
P11413;P11413-3;P114	P11413;P1	15;15;15;9	15;15;15;9	15;15;15;9	Glucose-6-phosphate 1-deh	G6PD
A0A0A0MTS2;P06744;P	A0A0A0MT	10;10;10;9	10;10;10;9	10;10;10;9	Glucose-6-phosphate isom	GPI
K7ELL7;P14314-2;P1431	K7ELL7;P14	16;15;15;6	16;15;15;6	16;15;15;6	Glucosidase 2 subunit beta	PRKCSH
P00367;P00367-3;P003	P00367;P0	18;16;14;1	18;16;14;1	18;16;14;1	Glutamate dehydrogenase	GLUD1;GLL
E1CEI4;P48506;H0Y9I7	E1CEI4;P48	2;2;1;1	2;2;1;1	2;2;1;1	Glutamate--cysteine ligase	GCLC
P48507-2;P48507	P48507-2;F	1;1	1;1	1;1	Glutamate--cysteine ligase	GCLM
Q9BQ67;M0QX71	Q9BQ67;M	3;2	3;2	3;2	Glutamate-rich WD repeat	GRWD1
O94925-3;O94925;B8ZZ	O94925-3;(10;8;3;2;2	10;8;3;2;2	10;8;3;2;2	10;8;3;2;2	Glutaminase kidney isoform	GLS
Q06210-2;Q06210	Q06210-2;(4;4	4;4	4;4	4;4	Glutamine--fructose-6-phos	GFPT1
P47897-2;P47897;A0A0	P47897-2;F	6;6;3;3;3;3	6;6;3;3;3;3	2;2;2;2;2;2	Glutamine--tRNA ligase	QARS
O76003	O76003	2	2	2	Glutaredoxin-3	GLRX3
Q86SX6	Q86SX6	1	1	1	Glutaredoxin-related protei	GLRX5
P00390-4;P00390-2;P0	P00390-4;F	4;4;4;3;3;1	4;4;4;3;3;1	4;4;4;3;3;1	Glutathione reductase, mitc	GSR
E9PFN5;Q9Y2Q3-4;Q9Y	E9PFN5;Q9	3;3;3;2;2	3;3;3;2;2	3;3;3;2;2	Glutathione S-transferase k	GSTK1
P78417;Q5TA02;P7841	P78417;Q5	6;5;5;5;4	6;5;5;5;4	6;5;5;5;4	Glutathione S-transferase o	GSTO1
P09211;A8MX94;A0A0	P09211;A8	9;7;4;1	9;7;4;1	9;7;4;1	Glutathione S-transferase P	GSTP1
P04406-2;P04406;E7EU	P04406-2;F	15;15;13;1	15;15;13;1	15;15;13;1	Glyceraldehyde-3-phosphat	GAPDH
Q53EU6	Q53EU6	1	1	1	Glycerol-3-phosphate acyltr	AGPAT9
P43304;P43304-2;F5GY	P43304;P4	8;7;2	8;7;2	8;7;2	Glycerol-3-phosphate dehy	GPD2
A0A1W2PQV2;H3BUH9	A0A1W2PC	2;2;2	2;2;2	2;2;2	Glycine cleavage system H	GCSH
P41250;H7C443;F8WCK	P41250	5;1;1	5;1;1	5;1;1	Glycine--tRNA ligase	GARS
P49841;P49841-2	P49841;P4	1;1	1;1	1;1	Glycogen synthase kinase-3	GSK3B
G5E9W8;C9JQ42;P4697	G5E9W8;C	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Glycogenin-1	GYG1



F6TLX2;Q9HC38-2;Q9H1	F6TLX2;Q9H1	3;3;3;1;1;1	3;3;3;1;1;1	3;3;3;1;1;1	Glyoxalase domain-containing	GLOD4
U3KQ56;Q9UBQ7	U3KQ56;Q9UBQ7	1;1	1;1	1;1	Glyoxylate reductase/hydro	GRHPR
P35052;H7C410;H7C02	P35052;H7C410;H7C02	7;6;4;4;3;2	7;6;4;4;3;2	7;6;4;4;3;2	Glypican-1;Secreted glypica	GPC1
P49915-2;P49915	P49915-2;P49915	7;7	7;7	7;7	GMP synthase [glutamine-h	GMPS
Q92896;Q92896-3;Q928	Q92896;Q92896-3;Q928	6;6;6;4;1;1	6;6;6;4;1;1	6;6;6;4;1;1	Golgi apparatus protein 1	GLG1
F8W785;O00461	F8W785;O00461	3;3	3;3	3;3	Golgi integral membrane pr	GOLIM4
Q9H4A6;Q9H4A5	Q9H4A6;Q9H4A5	2;1	2;1	2;1	Golgi phosphoprotein 3;Gol	GOLPH3;G
Q9H8Y8-2;Q9H8Y8;Q9H	Q9H8Y8-2;Q9H8Y8;Q9H	4;4;4	4;4;4	4;4;4	Golgi reassembly-stacking p	GORASP2
Q9H3P7	Q9H3P7	1	1	1	Golgi resident protein GCP6	ACBD3
F6RU00;B4DQA8;K7EJC	F6RU00;B4DQA8;K7EJC	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Golgi SNAP receptor compl	GOSR1
Q08379-2;Q08379;A0A	Q08379-2;Q08379;A0A	4;4;2	4;4;2	4;4;2	Golgin subfamily A member	GOLGA2
Q7Z5G4-3;Q7Z5G4	Q7Z5G4-3;Q7Z5G4	1;1	1;1	1;1	Golgin subfamily A member	GOLGA7
D6R9J9;E7EM50;D6RFE	D6R9J9;E7EM50;D6RFE	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	GPI ethanolamine phosphat	PIGG
Q9Y653-5;Q9Y653-2;Q9	Q9Y653-5;Q9Y653-2;Q9	2;2;2;2;1;1	2;2;2;2;1;1	2;2;2;2;1;1	G-protein coupled receptor	GPR56;ADC
H0Y8R1;F5H5I6;H0YAK1	H0Y8R1;F5H5I6;H0YAK1	2;2;2;2;2	2;2;2;2;2	2;2;2;2;2	G-rich sequence factor 1	GRSF1
Q9H3K2	Q9H3K2	2	2	2	Growth hormone-inducible	GHITM
Q9HAV7	Q9HAV7	5	5	5	GrpE protein homolog 1, mi	GRPEL1
Q9UIJ7-2;Q9UIJ7-3;Q9L	Q9UIJ7-2;Q9UIJ7-3;Q9L	1;1;1	1;1;1	1;1;1	GTP:AMP phosphotransfer	AK3
P01116-2;P01116;P011	P01116-2;P01116;P011	2;2;2;1;1;1	2;2;2;1;1;1	2;2;2;1;1;1	GTPase KRas;GTPase KRas,	KRAS;NRAS
B5MDF5;P62826;J3KQE	B5MDF5;P62826;J3KQE	7;7;6;5;3;3	7;7;6;5;3;3	7;7;6;5;3;3	GTP-binding nuclear protei	RAN
C9J931;Q15382	C9J931;Q15382	1;1	1;1	1;1	GTP-binding protein Rheb	RHEB
H0Y5E8;Q9NR31-2;Q9N	H0Y5E8;Q9NR31-2;Q9N	1;1;1	1;1;1	1;1;1	GTP-binding protein SAR1a	SAR1A
P52735-3;P52735-2;P52	P52735-3;P52735-2;P52	2;2;2	2;2;2	2;2;2	Guanine nucleotide exchan	VAV2
P63096;P63096-2;C9JPF	P63096;P63096-2;C9JPF	8;7;4;1	4;4;4;1	4;4;4;1	Guanine nucleotide-binding	GNAI1
P04899;P04899-4;P048	P04899;P04899-4;P048	8;8;7;7;7	4;4;4;4;4	4;4;4;4;4	Guanine nucleotide-binding	GNAI2
Q9UBI6	Q9UBI6	5	5	5	Guanine nucleotide-binding	GNG12
P62873;P62873-2;B1AK	P62873;P62873-2;B1AK	7;6;5;5;3;2	4;4;3;3;1;1	4;4;3;3;1;1	Guanine nucleotide-binding	GNB1
P62879;C9JIS1;C9JXA5;	P62879;C9JIS1;C9JXA5;	9;8;8;7;5;5	9;8;8;7;5;5	6;6;6;5;2;3	Guanine nucleotide-binding	GNB2;GNB
P08754;P11488;P09471	P08754;P11488;P09471	8;2;2;2;2;1	8;2;2;2;2;1	4;0;0;0;0;0	Guanine nucleotide-binding	GNAI3
P50148;B1AM21	P50148;B1AM21	2;1	2;1	1;1	Guanine nucleotide-binding	GNAQ
P63092-3;P63092-2;P63	P63092-3;P63092-2;P63	4;4;4;4;4;4	3;3;3;3;3;3	3;3;3;3;3;3	Guanine nucleotide-binding	GNAS
P29992;O95837	P29992;O95837	2;1	1;0	1;0	Guanine nucleotide-binding	GNA11;GN
Q14344-2;Q14344	Q14344-2;Q14344	1;1	1;1	1;1	Guanine nucleotide-binding	GNA13
P63244;J3KPE3;H0YAF8	P63244;J3KPE3;H0YAF8	14;13;10;1	14;13;10;1	14;13;10;1	Guanine nucleotide-binding	GNB2L1
Q9BVP2-2;Q9BVP2	Q9BVP2-2;Q9BVP2	2;2	2;2	2;2	Guanine nucleotide-binding	GNL3
H0Y2M6;P51798-2;P51	H0Y2M6;P51798-2;P51	1;1;1	1;1;1	1;1;1	H(+)/Cl(-) exchange transpo	CLCN7
Q9NY12-2;Q9NY12	Q9NY12-2;Q9NY12	2;2	2;2	2;2	H/ACA ribonucleoprotein cc	GAR1
Q9NX24;J3QSY4;D6RC5	Q9NX24;J3QSY4;D6RC5	4;3;3;3	4;3;3;3	4;3;3;3	H/ACA ribonucleoprotein cc	NHP2
O60832;O60832-2;H7C	O60832;O60832-2;H7C	6;4;2;2;2;1	6;4;2;2;2;1	6;4;2;2;2;1	H/ACA ribonucleoprotein cc	DKC1
Q5T3Q7;Q9H583;Q6P6	Q5T3Q7;Q9H583;Q6P6	10;10;1	10;10;1	10;10;1	HEAT repeat-containing pro	HEATR1
Q0VDF9	Q0VDF9	1	1	1	Heat shock 70 kDa protein	HSPA14
A0A0G2JIW1;P0DMV9;A0A	A0A0G2JIW1;P0DMV9;A0A	29;29;29;2	15;15;15;1	15;15;15;1	Heat shock 70 kDa protein	HSPA1B;HS
P34932;A0A087WYC1;A	P34932;A0A087WYC1;A	19;16;11;4	18;15;10;4	18;15;10;4	Heat shock 70 kDa protein	HSPA4
P17066;P48741	P17066;P48741	10;6	1;1	1;1	Heat shock 70 kDa protein	HSPA6;HSP
P11142;E9PKE3;P11142	P11142;E9PKE3;P11142	28;27;22;1	24;23;19;1	18;17;13;1	Heat shock cognate 71 kDa	HSPA8
O75506	O75506	1	1	1	Heat shock factor-binding p	HSPB1
Q92598-2;Q92598;Q92	Q92598-2;Q92598;Q92	21;21;20;2	21;21;20;2	20;20;19;1	Heat shock protein 105 kDa	HSPH1
Q12931-2;Q12931;J3L0	Q12931-2;Q12931;J3L0	13;13;9;3	13;13;9;3	13;13;9;3	Heat shock protein 75 kDa,	TRAP1
P04792;F8WE04;C9J3N	P04792;F8WE04;C9J3N	14;6;3	14;6;3	14;6;3	Heat shock protein beta-1	HSPB1
P07900;P07900-2;G3V2	P07900;P07900-2;G3V2	34;34;10;7	19;19;5;2	219;19;5;2	Heat shock protein HSP 90-	HSP90AA1

P08238;Q58FF7	P08238	39;16	39;16	19;6	Heat shock protein HSP 90- $\alpha$	HSP90AB1
P54652	P54652	11	1	1	Heat shock-related 70 kDa $\gamma$	HSPA2
J3KT51;Q9UK76;Q9UK7	J3KT51;Q9UK7	4;4;4;3;3	4;4;4;3;3	4;4;4;3;3	Hematological and neurological	HN1
H3BMT0;H3BTV5;H3BU	H3BMT0;H3BTV5	2;2;2;2;2	2;2;2;2;2	2;2;2;2;2	Hematological and neurological	HN1L
P30519;A0A087WT44;P	P30519;A0A087WT44	4;3;3;2;2;1	4;3;3;2;2;1	4;3;3;2;2;1	Heme oxygenase 2	HMOX2
Q5THN1;Q9Y5Z4	Q5THN1;Q9Y5Z4	1;1	1;1	1;1	Heme-binding protein 2	HEBP2
CON__P01966;G3V1N2	CON__P01966;G3V1N2	5;3;3;1	5;3;3;1	5;3;3;1	Hemoglobin subunit alpha	HBA2;HBA3
P68871;F8W6P5	P68871;F8W6P5	3;2	2;2	2;2	Hemoglobin subunit beta;L	HBB
CON__ENSEMBL:ENSBT	CON__ENSEMBL:ENSBT	3;2;2	3;2;2	3;2;2	Hepatocyte growth factor a	HGFAC
I3L1P5;O14964-2;O149	I3L1P5;O14964-2;O149	1;1;1	1;1;1	1;1;1	Hepatocyte growth factor-r	HGS
P51858;P51858-2;P518	P51858;P51858-2;P518	5;3;3	5;3;3	5;3;3	Hepatoma-derived growth f	HDGF
B0QZK4;Q5SSJ5-2;Q5SS	B0QZK4;Q5SSJ5-2;Q5SS	6;6;6;5;5;5	6;6;6;5;5;5	6;6;6;5;5;5	Heterochromatin protein 1-	HP1BP3
D6R9P3;D6RD18;D6RBZ	D6R9P3;D6RD18;D6RBZ	4;4;4;4;4;3	4;4;4;4;4;3	4;4;4;4;4;3	Heterogeneous nuclear ribc	HNRNPAB
Q13151	Q13151	5	5	5	Heterogeneous nuclear ribc	HNRNPA0
F8W6I7;P09651-3;P096	F8W6I7;P09651-3;P096	11;11;11;1	10;10;10;1	10;10;10;1	Heterogeneous nuclear ribc	HNRNPA1;I
P51991-2;P51991;H7C1	P51991-2;P51991;H7C1	8;7;1	8;7;1	8;7;1	Heterogeneous nuclear ribc	HNRNPA3
H0YA96;Q14103-4;Q14	H0YA96;Q14103-4;Q14	7;7;7;6;6;6	7;7;7;6;6;6	7;7;7;6;6;6	Heterogeneous nuclear ribc	HNRNPD
A0A087WUK2;O14979-	A0A087WUK2;O14979-	3;3;3;3	3;3;3;3	3;3;3;3	Heterogeneous nuclear ribc	HNRNPDL
P52597;A0A1B0GW42	P52597;A0A1B0GW42	11;2	11;2	9;2	Heterogeneous nuclear ribc	HNRNPF
E9PCY7;G8JLB6;P31943	E9PCY7;G8JLB6;P31943	10;10;10;7	8;8;8;5;4;5	4;4;4;2;2;2	Heterogeneous nuclear ribc	HNRNPH1
P55795	P55795	9	4	4	Heterogeneous nuclear ribc	HNRNPH2
P31942-2;P31942;P319	P31942-2;P31942;P319	7;7;6;4;3;3	7;7;6;4;3;3	7;7;6;4;3;3	Heterogeneous nuclear ribc	HNRNPH3
P61978-3;P61978;P619	P61978-3;P61978;P619	17;16;16;1	17;16;16;1	17;16;16;1	Heterogeneous nuclear ribc	HNRNPK
P14866;M0QXS5;P1486	P14866;M0QXS5;P1486	14;11;11;3	14;11;11;3	8;5;5;0;0;1	Heterogeneous nuclear ribc	HNRNPL
P52272-2;P52272;A0A0	P52272-2;P52272;A0A0	23;23;22;1	23;23;22;1	23;23;22;1	Heterogeneous nuclear ribc	HNRNPM
O60506-4;O60506-3;O6	O60506-4;O60506-3;O6	16;16;16;1	16;16;16;1	11;11;11;1	Heterogeneous nuclear ribc	SYNCRIP
O43390;O43390-2;O43	O43390;O43390-2;O43	14;13;11;1	9;8;7;6;5	9;8;7;6;5	Heterogeneous nuclear ribc	HNRNPR
Q00839;A0A1W2PPS1;(	Q00839;A0A1W2PPS1;(	24;23;23;2	24;23;23;2	24;23;23;2	Heterogeneous nuclear ribc	HNRNPU
M0R3F1;A0A0A0MRA5;M	M0R3F1;A0A0A0MRA5;M	3;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	Heterogeneous nuclear ribc	HNRNPUL1
Q1KMD3;H3BQZ7	Q1KMD3;H3BQZ7	15;14	15;14	15;14	Heterogeneous nuclear ribc	HNRNPUL2
P22626;P22626-2;A0A0	P22626;P22626-2;A0A0	16;15;10	16;15;10	15;14;9	Heterogeneous nuclear ribc	HNRNPA2B
G3V4W0;B4DY08;B2R5	G3V4W0;B4DY08;B2R5	15;15;15;1	15;15;15;1	15;15;15;1	Heterogeneous nuclear ribc	HNRNPC
E9PB90;P52789	E9PB90;P52789	9;9	8;8	8;8	Hexokinase;Hexokinase-2	HK2
P19367-4;P19367-2;P19	P19367-4;P19367-2;P19	14;14;14;1	14;14;14;1	13;13;13;1	Hexokinase-1	HK1
P30825	P30825	2	2	2	High affinity cationic amino	SLC7A1
Q5T7C4;P09429;B2RPK	Q5T7C4;P09429;B2RPK	5;5;2	5;5;2	4;4;1	High mobility group protein	HMGB1
D6R9A6;P26583	D6R9A6;P26583	2;2	1;1	1;1	High mobility group protein	HMGB2
E9PES6;E7ES08;E7EQU1	E9PES6;E7ES08;E7EQU1	1;1;1;1	1;1;1;1	1;1;1;1	High mobility group protein	HMGB3
P17096;P17096-3;P170	P17096;P17096-3;P170	4;4;2;1	4;4;2;1	4;4;2;1	High mobility group protein	HMGA1
F5H2U8;F5H2A4;F5H6H	F5H2U8;F5H2A4;F5H6H	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	High mobility group protein	HMGA2
P49773;D6REP8;D6RE9	P49773;D6REP8;D6RE9	4;3;3;3;2	4;3;3;3;2	4;3;3;3;2	Histidine triad nucleotide-b	HINT1
D6RJE6;B3KWE1;P1208	D6RJE6;B3KWE1;P1208	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	Histidine--tRNA ligase, cyto	HARS2;HAF
O14929-2;O14929	O14929-2;O14929	1;1	1;1	1;1	Histone acetyltransferase ty	HAT1
Q92769-3;Q92769	Q92769-3;Q92769	4;4	4;4	2;2	Histone deacetylase 2	HDAC2
P07305;P07305-2	P07305;P07305-2	4;2	4;2	4;2	Histone H1.0;Histone H1.0,	H1F0
P16403	P16403	10	10	3	Histone H1.2	HIST1H1C
P10412;P16402;P22492	P10412;P16402;P22492	2;0;0;0	2;0;0;0	2;0;0;0	Histone H1.4;Histone H1.3	HIST1H1E;I
P16401	P16401	7	6	6	Histone H1.5	HIST1H1B
Q92522	Q92522	2	2	2	Histone H1x	H1FX
A0A0U1RR32;A0A0U1R	A0A0U1RR32;A0A0U1R	5;5;5;5;5;5	5;5;5;5;5;5	1;1;1;1;1;1	Histone H2A type 1-J;Hisor	HIST1H2AJ;

Q71UI9;P0C0S5;C9J0D1	Q71UI9;P04;4;3;3;3;3	2;2;1;2;2;1	2;2;1;2;2;1	Histone H2A.V;Histone H2A	H2AFV;H2A
Q5SQT3;Q9P0M6	Q5SQT3;Q5;2;2	1;1	1;1	Histone H2A;Core histone	n H2AFY2
P16104;Q96QV6;REV__	P16104;Q94;3;1;1;1;1	1;0;0;0;0;0	1;0;0;0;0;0	Histone H2AX;Histone H2A	H2AFX;HIST
Q99880;Q96A08	Q99880;Q5;8;5	1;1	0;0	Histone H2B type 1-L;Hist	HIST1H2BL
Q16778;P33778;P23527	Q16778;P37;7;7;7;2	1;1;1;1;1	0;0;0;0;0	Histone H2B type 2-E;Hist	HIST2H2BE
Q8N257	Q8N257	7	1	Histone H2B type 3-B	HIST3H2BB
U3KQK0;Q99879;Q9987	U3KQK0;Q5;8;8;8;8;8	8;8;8;8;8	0;0;0;0;0	Histone H2B;Histone H2B ty	HIST1H2BN
Q5TEC6	Q5TEC6	5	5	Histone H3	HIST2H3PS
P62805	P62805	8	8	Histone H4	HIST1H4A
Q09028-3;Q09028;Q090	Q09028-3;Q9;9;7;6;3;3	9;9;7;6;3;3	5;5;3;3;2;2	Histone-binding protein RBI	RBBP4
Q16576;Q16576-2;E9P0	Q16576;Q16;6;5;3	2;2;1;2	2;2;1;2	Histone-binding protein RBI	RBBP7
P16189;Q9GJ45;B0UXQ	P16189;Q912;10;10;1	2;0;1;0;0	1;0;0;0;0	HLA class I histocompatibili	HLA-A
P30453;A0A140T8Y4;P3	P30453;A012;11;11;1	12;11;11;1	0;0;0;0;0	HLA class I histocompatibili	HLA-A
Q8MH48;Q5RJ85;A0A00	Q8MH48;Q2;2;2;2;1	1;1;1;1;1	1;1;1;1;1	HLA class I histocompatibili	HLA-G
P30479;P30481;A0A140	P30479;P38;6;5;3;3	2;2;1;1;1	0;0;0;0;0	HLA class I histocompatibili	HLA-B
P30508;A0A1W2PRZ0;A	P30508;A09;8;8;8;8	5;4;4;4;5	0;0;0;0;0	HLA class I histocompatibili	HLA-C
Q95604	Q95604	8	2	0	HLA class I histocompatibili
P50502;Q3KNR6;Q8NFI	P50502;Q37;6;6;5;4;4	7;6;6;5;4;4	7;6;6;5;4;4	Hsc70-interacting protein;P	ST13;ST13F
Q16543;K7EQA9;K7EKC	Q16543;K78;6;5;3;2	8;6;5;3;2	8;6;5;3;2	Hsp90 co-chaperone Cdc37	CDC37
H3BRH5;O00219-2;O00	H3BRH5;O1;1;1	1;1;1	1;1;1	Hyaluronan synthase 3	HAS3
A0A0D9SFP2;E9PF18;Q	A0A0D9SFF5;5;5;5;4	5;5;5;5;4	5;5;5;5;4	Hydroxyacyl-coenzyme A de	HADH
P35914	P35914	2	2	2	Hydroxymethylglutaryl-CoA
Q01581;D6RIW1	Q01581	8;2	8;2	8;2	Hydroxymethylglutaryl-CoA
Q6YN16-2;Q6YN16	Q6YN16-2;5;5	5;5	5;5	5;5	Hydroxysteroid dehydrogen
P00492	P00492	5	5	5	Hypoxanthine-guanine phosph
A0A087X054;Q9Y4L1;E	A0A087X05;8;8;6;6;4	8;8;6;6;4	8;8;6;6;4	Hypoxia up-regulated prote	HYOU1
A0A1W2PNR9;Q9Y5U9	A0A1W2PN1;1	1;1	1;1	1;1	Immediate early response 3
P52292;J3QLL0;J3KS65;	P52292	9;4;4;1	9;4;4;1	9;4;4;1	Importin subunit alpha-1
O00629;H7C4F6	O00629	5;2	5;2	4;2	Importin subunit alpha-3
O00505	O00505	2	1	1	Importin subunit alpha-4
P52294;C9J352;C9JWD	P52294;C92;1;1;1;1;1	2;1;1;1;1	2;1;1;1;1	Importin subunit alpha-5;In	KPNA1;KPNA
Q14974;J3KTM9;Q1497	Q14974;J315;12;12;3	15;12;12;3	15;12;12;3	Importin subunit beta-1	KPNB1
H0Y8C6;O00410-2;O00	H0Y8C6;O010;10;10;1	10;10;10;1	10;10;10;1	Importin-5	IPO5
O95373	O95373	4	4	4	Importin-7
Q96P70	Q96P70	2	2	2	Importin-9
Q13308-3;Q13308-4;Q1	Q13308-3;Q2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	Inactive tyrosine-protein kin	PTK7
Q70UQ0;Q70UQ0-2	Q70UQ0;Q2;1	1;1	1;1	1;1	Inhibitor of nuclear factor k
Q70UQ0-4	Q70UQ0-4	2	2	1	Inhibitor of nuclear factor k
Q9NQS7-2;Q9NQS7	Q9NQS7-2;2;2	2;2	2;2	2;2	Inner centromere protein
Q9Y2U8	Q9Y2U8	2	2	2	Inner nuclear membrane pr
Q15181;Q5SQT6	Q15181;Q5;9;6	9;6	9;6	9;6	Inorganic pyrophosphatase
Q9BY32-2;Q9BY32;Q9B	Q9BY32-2;Q2;2;1	2;2;1	2;2;1	2;2;1	Inosine triphosphate pyroph
H0Y4R1;P12268;E7ETK	H0Y4R1;P112;12;4;1	12;12;4;1	11;11;3;0	Inosine-5-monophosphate c	IMPDH2
Q14573;B7ZMI3;Q1464	Q14573	6;1;1;1;1	6;1;1;1;1	6;1;1;1;1	Inositol 1,4,5-trisphosphate
O00425;O00425-2;F8W	O00425;O04;2;1;1;1	4;2;1;1;1	4;2;1;1;1	4;2;1;1;1	Insulin-like growth factor 2
Q9Y287;Q9Y287-2	Q9Y287;Q5;4;3	4;3	4;3	4;3	Integral membrane protein
J3QRY6;C9IYS7;A0A087	J3QRY6;C91;1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Integrator complex subunit
P17301;E7ESP4;E7EMF	P17301;E715;12;11;7	15;12;11;7	15;12;11;7	15;12;11;7	Integrin alpha-2
P26006;P26006-1;H0YA	P26006;P25;5;2;1	5;5;2;1	5;5;2;1	5;5;2;1	Integrin alpha-3;Integrin al
P23229-4;P23229-2;P2	P23229-4;F22;22;22;2	22;22;22;2	22;22;22;2	22;22;22;2	Integrin alpha-6;Integrin al

P06756-3;P06756-2;P06756-3;F5;5;5;1	5;5;5;1	5;5;5;1	Integrin alpha-V;Integrin alpha-V	ITGAV		
A0A087WXP3;E9PEE8;P0A0A087WX2;2;2;1	2;2;2;1	2;2;2;1	Integrin beta;Integrin beta-1	ITGB6		
P05556;P05556-2;P05556;P05556;P014;13;13;1	14;13;13;1	14;13;13;1	Integrin beta-1	ITGB1		
P16144-4;P16144-2;P16144-4;F36;36;36;3	36;36;36;3	36;36;36;3	Integrin beta-4	ITGB4		
P05362;E7ESS4	P05362;E7I2;1	2;1	2;1	Intercellular adhesion molecule		
P15260;Q5TFD1;Q5TFC	P15260	3;1;1;1	3;1;1;1	3;1;1;1	Interferon gamma receptor	IFNGR1
B1AJU4;O14896;O1489	B1AJU4;O13;3;2	3;3;2	3;3;2	3;3;2	Interferon regulatory factor	IRF6
H7BYV1;E9PS44;E9PQN	H7BYV1;E91;1;1;1;1	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Interferon-induced transmembrane	IFITM2;IFIT
P19525;P19525-2;F8WE	P19525;P15;4;1;1	5;4;1;1	5;4;1;1	5;4;1;1	Interferon-induced, double-stranded	EIF2AK2
B4DY09;Q12905;X6R6Z	B4DY09;Q18;8;3;2	8;8;3;2	8;8;3;2	8;8;3;2	Interleukin enhancer-binding	ILF2
Q12906;Q12906-7;Q12906;Q120;20;18;1	20;20;18;1	20;20;18;1	20;20;18;1	20;20;18;1	Interleukin enhancer-binding	ILF3
Q27J81-2;Q27J81	Q27J81-2;C1;1	1;1	1;1	1;1	Inverted formin-2	INF2
D6RGE2;Q96CN7	D6RGE2;Q91;1	1;1	1;1	1;1	Isochorismatase domain-containing	ISOC1
H0YL72;P50213;H0YLI6	H0YL72;P508;8;5;5;4	8;8;5;5;4	8;8;5;5;4	8;8;5;5;4	Isocitrate dehydrogenase [NADH3A	IDH3A
P51553;H7C1W2;E9PF8	P51553;H73;2;2;2;2	3;2;2;2;2	3;2;2;2;2	3;2;2;2;2	Isocitrate dehydrogenase [NADH3G	IDH3G
O75874;C9J4N6;C9JJE5	O75874	13;6;3;3;1	13;6;3;3;1	13;6;3;3;1	Isocitrate dehydrogenase [NADH1	IDH1
P41252;J3KR24;A0A0AC	P41252;J3K12;11;11;3	12;11;11;3	12;11;11;3	12;11;11;3	Isoleucine--tRNA ligase, cytoplasmic	IARS
Q9NSE4	Q9NSE4	7	7	7	Isoleucine--tRNA ligase, mitochondrial	IARS2
C9JD53;C9JKM8;Q1390	C9JD53;C9J1;1;1;1	1;1;1;1	1;1;1;1	1;1;1;1	Isopentenyl-diphosphate decarboxylase	IDI1
P14923;C9JTX4;C9J826	P14923	20;8;8;8;8	20;8;8;8;8	18;8;8;8;8	Junction plakoglobin	JUP
Q9Y624;A0A087WY82;C9Y624;A09;6;6	Q9Y624;A09;6;6	9;6;6	9;6;6	9;6;6	Junctional adhesion molecule	F11R
K7EM02;K7EIJ8;Q8IYT4	K7EM02;K71;1;1;1	1;1;1;1	1;1;1;1	1;1;1;1	Katanin p60 ATPase-containing	KATNAL2
CON__P13645;P13645;CON__P1367;7;1;1;1	4;4;1;1;1	4;4;1;1;1	4;4;1;1;1	4;4;1;1;1	Keratin, type I cytoskeletal	KRT10
CON__P13646-1;P13646	CON__P13627;26;25;2	25;24;23;2	11;10;9;9;9	9	Keratin, type I cytoskeletal	KRT13
CON__P19012;P19012;CON__P19016;16;10;1	7;7;5;5;4	5;5;3;3;2	5;5;3;3;2	5;5;3;3;2	Keratin, type I cytoskeletal	KRT15
P05783;F8VZY9;CON__P05783;F825;22;2;1	124;21;2;1	118;15;2;1	118;15;2;1	118;15;2;1	Keratin, type I cytoskeletal	KRT18
CON__P08727;P08727;CON__P0833;32;15;1	33;32;15;1	22;21;9;7;2	22;21;9;7;2	22;21;9;7;2	Keratin, type I cytoskeletal	KRT19
P35527;CON__P35527;P35527;CO5;4;2	4;3;2	4;3;2	4;3;2	4;3;2	Keratin, type I cytoskeletal	KRT9
CON__P04264;P04264	CON__P048;8	4;4	2;2	2;2	Keratin, type II cytoskeletal	KRT1
CON__P35908;P35908;CON__P357;7;4	1;1;1	1;1;1	1;1;1	1;1;1	Keratin, type II cytoskeletal	KRT2
CON__P13647;P13647;CON__P1328;28;10;9	24;24;6;9	7;5;5;0;2;1	7;5;5;0;2;1	7;5;5;0;2;1	Keratin, type II cytoskeletal	KRT5
CON__P02538;P02538;CON__P0223;23;21;2	12;12;10;1	2;2;1;0;1;0	2;2;1;0;1;0	2;2;1;0;1;0	Keratin, type II cytoskeletal	KRT6A;KRT
P04259	P04259	20	1	0	Keratin, type II cytoskeletal	KRT6B
CON__Q3KNV1;P08729	CON__Q3K37;37	37;37	3;3	3;3	Keratin, type II cytoskeletal	KRT7
CON__P05787;P05787;CON__P0536;36;36;2	33;33;33;2	29;29;29;1	29;29;29;1	29;29;29;1	Keratin, type II cytoskeletal	KRT8
Q07666-2;Q07666;Q07666-2;C3;3;2	3;3;2	3;3;2	3;3;2	3;3;2	KH domain-containing, RNA-binding	KHDRBS1
Q86UP2-2;Q86UP2-3;Q86UP2-2;5;5;5;5;2	5;5;5;5;2	5;5;5;5;2	5;5;5;5;2	5;5;5;5;2	Kinectin	KTN1
P33176;A0A0G2JMZ6;J3P33176	6;1;1;1;1	6;1;1;1;1	6;1;1;1;1	6;1;1;1;1	Kinesin-1 heavy chain	KIF5B
Q15058	Q15058	1	1	1	Kinesin-like protein	KIF14
H7BYN4;Q02241-2;Q02H7BYN4;Q5;5;5;4;2	15;5;5;4;2	15;5;5;4;2	15;5;5;4;2	15;5;5;4;2	Kinesin-like protein;Kinesin-like	KIF23
Q13601-2;Q13601	Q13601-2;C1;1	1;1	1;1	1;1	KRR1 small subunit processing	KRR1
K7EM91;O43291-2;O43K7EM91;O44;4;4;2	14;4;4;2;1	3;3;3;1;1	3;3;3;1;1	3;3;3;1;1	Kunitz-type protease inhibitor	SPINT2
Q16719	Q16719	1	1	1	Kynureninase	KYNU
Q04760-2;Q04760	Q04760-2;C2;2	2;2	2;2	2;2	Lactoylglutathione lyase	GLO1
E9PDI4;O00515;A0A0J9	E9PDI4;O07;7;4;4;3;1	7;7;4;4;3;1	7;7;4;4;3;1	7;7;4;4;3;1	Ladinin-1	LAD1
P42166;P42167-3	P42166;P411;7	4;0	4;0	4;0	Lamina-associated polypeptide	TMPO
P42167;G5E972;P42167	P42167;G513;11;10;6	13;11;10;6	6;4;3;4	6;4;3;4	Lamina-associated polypeptide	TMPO
Q14739;C9JXK0;C9JES9	Q14739;C94;2;1	4;2;1	4;2;1	4;2;1	Lamin-B receptor	LBR
P20700;E9PBF6;A0A0D9	P20700;E9I32;25;22;1	31;24;22;1	30;24;22;1	30;24;22;1	Lamin-B1	LMNB1
Q03252	Q03252	27	25	25	Lamin-B2	LMNB2



K7EIP4;A0A0A0MTS5;A1	K7EIP4;A0A0A0MTS5;A1	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Laminin subunit alpha-3	LAMA3
O15230;O15230-2	O15230	3;1	3;1	3;1	Laminin subunit alpha-5	LAMA5
Q13751;Q5THA1	Q13751	7;2	7;2	7;2	Laminin subunit beta-3	LAMB3
P11047	P11047	5	5	5	Laminin subunit gamma-1	LAMC1
Q13753-2;Q13753	Q13753-2;Q13753	7;7	7;7	7;7	Laminin subunit gamma-2	LAMC2
F8WDS9;E9PHS0;O4381	F8WDS9;E9PHS0;O4381	1;1;1	1;1;1	1;1;1	LanC-like protein 1	LANCL1
A0A0C4DFL7;Q16850;Q A0A0C4DFI6;6;5;2	A0A0C4DFL7;Q16850;Q A0A0C4DFI6;6;5;2	6;6;5;2	6;6;5;2	6;6;5;2	Lanosterol 14-alpha demethylase	CYP51A1
P48449-3;P48449;C9J31	P48449-3;P48449;C9J31	3;3;2;2;1	3;3;2;2;1	3;3;2;2;1	Lanosterol synthase	LSS
Q01650	Q01650	5	5	5	Large neutral amino acid transporter	SLC7A5
A0A0G2JL47;A0A024RC	A0A0G2JL47;A0A024RC	3;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	Large proline-rich protein B	BAT3;BAGE
Q14696	Q14696	2	2	2	LDLR chaperone	MESD
Q8NC56-2;Q8NC56;D6F	Q8NC56-2;Q8NC56;D6F	2;2;1;1;1	2;2;1;1;1	2;2;1;1;1	LEM domain-containing protein	LEM2
O95202	O95202	5	5	5	LETM1 and EF-hand domain	LETM1
P42704;B8ZZ38;A0A0C4	P42704	33;11;11;9	33;11;11;9	33;11;11;9	Leucine-rich PPR motif-containing	LRPPRC
Q32MZ4-3;Q32MZ4-2;C	Q32MZ4-3;Q32MZ4-2;C	5;5;5;1;1;1	5;5;5;1;1;1	5;5;5;1;1;1	Leucine-rich repeat flightless	LRRFIP1
O75473-3;O75473-2;O7	O75473-3;O75473-2;O7	1;1;1	1;1;1	1;1;1	Leucine-rich repeat-containing	LGR5
Q8N1G4	Q8N1G4	3	3	3	Leucine-rich repeat-containing	LRRC47
Q96AG4;I3L223	Q96AG4	8;1	8;1	8;1	Leucine-rich repeat-containing	LRRC59
Q9P2J5-2;Q9P2J5;Q9P2	Q9P2J5-2;Q9P2J5;Q9P2	5;5;3	5;5;3	5;5;3	Leucine--tRNA ligase, cytoplasmic	LARS
Q9UIQ6-3;Q9UIQ6-2;Q9	Q9UIQ6-3;Q9UIQ6-2;Q9	3;3;3	3;3;3	3;3;3	Leucyl-cystinyl aminopeptidase	LNPEP
P30740;P30740-2	P30740;P30740-2	4;3	4;3	4;3	Leukocyte elastase inhibitor	SERPINB1
Q08722-2;Q08722-3;Q0	Q08722-2;Q08722-3;Q0	3;3;3;3	3;3;3;3	3;3;3;3	Leukocyte surface antigen CD47	CD47
P09960;P09960-2;P099	P09960;P09960-2;P099	6;5;5;4;1	6;5;5;4;1	6;5;5;4;1	Leukotriene A-4 hydrolase	LTA4H
Q14847;Q14847-2;C9J9	Q14847;Q14847-2;C9J9	8;8;7;5;2;1	8;8;7;5;2;1	8;8;7;5;2;1	LIM and SH3 domain protein	LASP1
F8VQE1;Q9UHB6-2;Q9L	F8VQE1;Q9UHB6-2;Q9L	12;12;12;1	12;12;12;1	12;12;12;1	LIM domain and actin-binding	LIMA1
S4R3V8;Q86X29-6;Q86	S4R3V8;Q86X29-6;Q86	3;3;3;3;3;2	3;3;3;3;3;2	3;3;3;3;3;2	Lipolysis-stimulated lipoprotein	LSR
P00338;P00338-3;P003	P00338;P00338-3;P003	13;13;10;9	13;13;10;9	12;12;9;8;8	L-lactate dehydrogenase A	LDHA
P07195;A8MW50;C9J7	P07195;A8MW50;C9J7	8;5;5;4	8;5;5;4	8;5;5;4	L-lactate dehydrogenase B	LDHB
K7EJE8;K7EKE6;P36776	K7EJE8;K7EKE6;P36776	6;6;6;6;6;3	6;6;6;6;6;3	6;6;6;6;6;3	Lon protease homolog, mitochondrial	LONP1
Q6P1M0;Q6P1M0-2	Q6P1M0	4;1	4;1	4;1	Long-chain fatty acid transporter	SLC27A4
O95573;F5GWH2	O95573	12;1	12;1	10;1	Long-chain-fatty-acid--CoA	ACSL3
O60488-2;O60488;H0Y	O60488-2;O60488;H0Y	5;5;2	3;3;2	3;3;2	Long-chain-fatty-acid--CoA	ACSL4
P24666;F2Z2Q9;G5E9R	P24666;F2Z2Q9;G5E9R	3;2;2;2;2;2	3;2;2;2;2;2	3;2;2;2;2;2	Low molecular weight phosphatase	ACP1
J3KMZ9;P01130-2;P011	J3KMZ9;P01130-2;P011	5;5;5;5;5;5	5;5;5;5;5;5	5;5;5;5;5;5	Low-density lipoprotein receptor	LDLR
Q7Z4F1	Q7Z4F1	1	1	1	Low-density lipoprotein receptor	LRP10
J3KPP4;O95232;D6RDI2	J3KPP4;O95232;D6RDI2	3;3;2;1;1	3;3;2;1;1	3;3;2;1;1	Luc7-like protein 3	LUC7L3
P05455;E9PGX9;E7ERC	P05455	4;1;1	4;1;1	4;1;1	Lupus La protein	SSB
C9JY28;H7C4Q5;C9JRX8	C9JY28;H7C4Q5;C9JRX8	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	LYR motif-containing protein	LYRM4
Q15046;Q15046-2;J3KR	Q15046;Q15046-2;J3KR	8;8;1;1;1	8;8;1;1;1	8;8;1;1;1	Lysine--tRNA ligase	KARS
Q6UWP7-3;Q6UWP7;C	Q6UWP7-3;Q6UWP7;C	3;3;2;1;1	3;3;2;1;1	3;3;2;1;1	Lysocardiolipin acyltransferase	LCLAT1
A0A0G2JRI7;A0A0G2JQ	A0A0G2JRI7;A0A0G2JQ	2;2;2	2;2;2	2;2;2	Lysophosphatidylcholine acyltransferase	LPCAT1
Q7L5N7;Q7L5N7-2;H3B	Q7L5N7;Q7L5N7-2;H3B	3;2;1	3;2;1	3;2;1	Lysophosphatidylcholine acyltransferase	LPCAT2
Q6P1A2-2;Q6P1A2	Q6P1A2-2;Q6P1A2	1;1	1;1	1;1	Lysophospholipid acyltransferase	LPCAT3
Q96N66-2;Q96N66;Q9	Q96N66-2;Q96N66;Q9	4;4;3	4;4;3	4;4;3	Lysophospholipid acyltransferase	MBOAT7
D6RDG0;A0A1W2PS70;D	D6RDG0;A0A1W2PS70;D	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Lysosome membrane protein	SCARB2
P11279;P11279-2	P11279;P11279-2	4;3	4;3	4;3	Lysosome-associated membrane	LAMP1
P13473-2;P13473;P134	P13473-2;P13473;P134	2;2;2	2;2;2	2;2;2	Lysosome-associated membrane	LAMP2
H0YAR1;Q9Y4K0	H0YAR1;Q9Y4K0	2;2	2;2	2;2	Lysyl oxidase homolog 2	LOXL2
P14174	P14174	2	2	2	Macrophage migration inhibitory	MIF
P40121-2;P40121;H7C0	P40121-2;P40121;H7C0	4;4;2;2	4;4;2;2	4;4;2;2	Macrophage-capping protein	CAPG

A0A087WU53;Q9H0U3;A0A087WL3;3;2	3;3;2	3;3;2	Magnesium transporter protein	MAGT1		
P07199	P07199	4	4	4	Major centromere autoantigen	CENPB
D6RIZ4;D6RA47;D6RE79	D6RIZ4;D6I1;1;1;1	1;1;1;1	1;1;1;1	Major facilitator superfamily	MFSD10	
Q95460-3;Q95460-2;Q95460-3;(1;1;1	1;1;1	1;1;1	1;1;1	Major histocompatibility complex	MR1	
A2A2V1;P04156-2;P041	A2A2V1;P02;2;2	2;2;2	2;2;2	Major prion protein	PRNP	
Q14764;H3BP76;H3BUK	Q14764	11;2;2;2;2;2	11;2;2;2;2;2	11;2;2;2;2;2	Major vault protein	MVP
B9A041;P40925-2;P409	B9A041;P4	6;6;6;6;4;4	6;6;6;6;4;4	6;6;6;6;4;4	Malate dehydrogenase, cytoplasmic	MDH1
P40926;P40926-2;G3XA	P40926;P4	18;15;13	18;15;13	18;15;13	Malate dehydrogenase, mitochondrial	MDH2
Q14165;F5H1S8;H0YGO	Q14165;F5	4;3;2;2	4;3;2;2	4;3;2;2	Malectin	MLEC
Q9ULC4-2;Q9ULC4;Q9U	Q9ULC4-2;1;1;1	1;1;1	1;1;1	1;1;1	Malignant T-cell-amplified sequence	MCTS1
Q9Y5P6;Q9Y5P6-2	Q9Y5P6;Q9	1;1	1;1	1;1	Mannose-1-phosphate guanylyltransferase	GMPPB
J3KSI4;I3L1D2;I3L4E0;J3	J3KSI4;I3L1	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	Mannose-P-dolichol utilization	MPDU1
Q13724-2;Q13724;C9J8	Q13724-2;(6;6;4;2	6;6;4;2	6;6;4;2	6;6;4;2	Mannosyl-oligosaccharide glucosyltransferase	MOGS
Q8NDC0	Q8NDC0	1	1	1	MAPK-interacting and signaling protein	MAPK1IP11
P49006	P49006	2	2	2	MARCKS-related protein	MARCKSL1
A0A0R4J2E8;A8MXP9;P	A0A0R4J2E	17;17;17;1	17;17;17;1	17;17;17;1	Matrin-3	MATR3
P50281;F8W1B7	P50281	4;1	4;1	4;1	Matrix metalloproteinase-1	MMP14
Q14676-2;Q14676;Q14	Q14676-2;(8;8;6;1;1	8;8;6;1;1	8;8;6;1;1	8;8;6;1;1	Mediator of DNA damage checkpoint	MDC1
E9PGW7;Q5T8T7;E7EN9	E9PGW7;Q	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Mediator of RNA polymerase II transcription	MED22
B7Z9I1;Q5T4U5;P11310	B7Z9I1;Q5	12;2;2;2;1;1	12;2;2;2;1;1	12;2;2;2;1;1	Medium-chain specific acyl-CoA oxidase	ACADM
P08582	P08582	3	3	3	Melanotransferrin	MFI2
Q8N4V1;Q8N4V1-2	Q8N4V1;Q	1;1	1;1	1;1	Membrane magnesium transporter	MMGT1
O00264;O00264-2	O00264;O	4;2	3;2	3;2	Membrane-associated progesterone receptor	PGRMC1
O15173;O15173-2;U3K	O15173;O	14;4;1	4;4;1	3;3;0	Membrane-associated progesterone receptor	PGRMC2
I3L1H7;I3L4K3;I3L3P0;I	I3L1H7;I3L	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Membrane-associated tyrosine phosphatase	PKMYT1
A8K878;P55145;H7C2D	A8K878;P	54;4;1	4;4;1	4;4;1	Mesencephalic astrocyte-derived neurotrophic factor	MANF
B8ZZX6;Q658P3-4;Q658	B8ZZX6;Q	62;2;2;2;2	2;2;2;2;2	2;2;2;2;2	Metalloreductase STEAP3	STEAP3
P80297;P13640-2;P027	P80297;P	12;2;2;2;1;1	12;2;2;2;1;1	12;2;2;2;1;1	Metallothionein-1X;Metallothionein-2	MT1X;MT2
O94776;O94776-2	O94776;O	54;2	4;2	4;2	Metastasis-associated protein	MTA2
Q13505-3;Q13505;A0A	Q13505-3;(4;4;3;3	4;4;3;3	4;4;3;3	4;4;3;3	Metaxin-1	MTX1
C9JAZ1;O75431-2;O754	C9JAZ1;O	72;2;2;1	2;2;2;1	2;2;2;1	Metaxin-2	MTX2
H7C0X7;Q9NZL9-3;Q9N	H7C0X7;Q	91;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Methionine adenosyltransferase	MAT2B
P53582;H0YAI3;H0Y955	P53582	3;1;1	3;1;1	3;1;1	Methionine aminopeptidase	METAP1
G3V1U3;P50579-3;P505	G3V1U3;P	52;2;2;1;1;1	12;2;2;1;1;1	12;2;2;1;1;1	Methionine aminopeptidase	METAP2
P56192;P56192-2;H0YI	P56192;P	516;5;1;1;1;1	16;5;1;1;1;1	16;5;1;1;1;1	Methionine--tRNA ligase, cytoplasmic	MARS
X6RBL6;Q9UBB5-3;Q9U	X6RBL6;Q	91;1;1	1;1;1	1;1;1	Methyl-CpG-binding domain	MBD2
Q9HCC0-2;Q9HCC0;D6F	Q9HCC0-2;3;3;2;1;1	3;3;2;1;1	3;3;2;1;1	3;3;2;1;1	Methylcrotonoyl-CoA carboxyltransferase	MCCC2
G5E9X5;F5GYT8;E9PG3	G5E9X5;F	51;1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Methylcrotonoyl-CoA carboxyltransferase	MCCC1
Q9BQA1-2;Q9BQA1	Q9BQA1-2;1;1	1;1	1;1	1;1	Methylosome protein 50	WDR77
E9PMI6;J3KN38;P54105	E9PMI6;J	31;1;1	1;1;1	1;1;1	Methylosome subunit pICln	CLNS1A
F5H8H2;A0A1B0GWC2;F	F5H8H2;A	02;2;2;1	2;2;2;1	2;2;2;1	Mevalonate kinase	MVK
A0A087WU07;Q5TGZ0-	A0A087WL	2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	MICOS complex subunit MICOS1	MINOS1;MICOS1
C9JRZ6;Q9NX63;F8WAR	C9JRZ6;Q	916;6;5;3	6;6;5;3	6;6;5;3	MICOS complex subunit MICOS1	CHCHD3
J3QTB2;J3QTA6;Q9BRQ	J3QTB2;J	31;1;1	1;1;1	1;1;1	MICOS complex subunit MICOS1	CHCHD6
Q16891-2;Q16891;B9A	Q16891-2;(16;16;15;1	16;16;15;1	16;16;15;1	16;16;15;1	MICOS complex subunit MICOS1	IMMT
Q99735-2;Q99735	Q99735-2;(1;1	1;1	1;1	1;1	Microsomal glutathione S-transferase	MGST2
Q5VV89;O14880;Q5VV8	Q5VV89;O	2;2;1	2;2;1	2;2;1	Microsomal glutathione S-transferase	MGST3
P11137-3;P11137	P11137-3;F	1;1	1;1	1;1	Microtubule-associated protein	MAP2
Q15691	Q15691	8	8	8	Microtubule-associated protein	MAPRE1
H0Y2V1;H7C4C5;B5ME	H0Y2V1;H	73;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	Microtubule-associated protein	MAP4

E9PPJ5;E9PLM6;P21741	E9PPJ5;E9F 2;2;2;1	2;2;2;1	2;2;2;1	Midkine	MDK
Q9BTE3-2;Q9BTE3	Q9BTE3-2;(1;1	1;1	1;1	Mini-chromosome mainten	MCMBP
Q8TCT9-5;Q8TCT9;A0A0D	Q8TCT9-5;(3;3;2;2;2;1	3;3;2;2;2;1	3;3;2;2;2;1	Minor histocompatibility an	HM13
Q8N4C8-5;Q8N4C8-2;Q	Q8N4C8-5; 1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Misshapen-like kinase 1	MINK1
I3L1P8;Q02978-2;Q029	I3L1P8;Q025;5;5	5;5;5	5;5;5	Mitochondrial 2-oxoglutar	SLC25A11
Q7Z434-4;Q7Z434	Q7Z434-4;(3;3	3;3	3;3	Mitochondrial antiviral-sign	MAVS
H0Y8C3;Q9NZJ7-2;Q9N	H0Y8C3;Q94;4;4;1	4;4;4;1	4;4;4;1	Mitochondrial carrier homo	MTCH1
Q9Y6C9;E9PIE4	Q9Y6C9;E9 6;5	6;5	6;5	Mitochondrial carrier homo	MTCH2
Q9UBX3;Q9UBX3-2;F6R	Q9UBX3;Q94;4;2	1;1;1	1;1;1	Mitochondrial dicarboxylate	SLC25A10
Q9Y3D6	Q9Y3D6	2	2	Mitochondrial fission 1 prot	FIS1
E9PJH7;Q9H936;A0A0D	E9PJH7;Q9 2;2;1;1;1;1	2;2;1;1;1;1	2;2;1;1;1;1	Mitochondrial glutamate ca	SLC25A22;S
Q9Y5L4	Q9Y5L4	2	2	Mitochondrial import inner	TIMM13
O43615;M0QXU7;M0Q	O43615;M(6;4;1	6;4;1	6;4;1	Mitochondrial import inner	TIMM44
M0R047;Q3ZCQ8;Q3ZC	M0R047;Q9 1;1;1	1;1;1	1;1;1	Mitochondrial import inner	TIMM50
O60220	O60220	2	2	Mitochondrial import inner	TIMM8A
G3V2F3;A0A1W2PRH9;	G3V2F3;A0 1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Mitochondrial import inner	TIMM9
Q9NS69	Q9NS69	5	5	Mitochondrial import recep	TOMM22
Q15785	Q15785	4	4	Mitochondrial import recep	TOMM34
O96008;O96008-2;K7EJ	O96008;O9 9;8;6;4	9;8;6;4	9;8;6;4	Mitochondrial import recep	TOMM40
O94826	O94826	8	8	Mitochondrial import recep	TOMM70A
C9JC63;E7EVY0;S4R3Q9	C9JC63;E7E 1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Mitochondrial inner membr	OXA1L
Q99797	Q99797	1	1	Mitochondrial intermediate	MIPEP
C9JVB6;Q7L0Y3	C9JVB6;Q7 3;3	3;3	3;3	Mitochondrial ribonuclease	TRMT10C
Q10713;Q10713-2;Q5S	Q10713;Q16;3;1	6;3;1	6;3;1	Mitochondrial-processing p	PMPCA
O75439;G3V0E4;F8WE	O75439;G34;3;1;1;1	3;2;1;1;1	3;2;1;1;1	Mitochondrial-processing p	PMPCB
P28482-2;P28482	P28482-2;F 2;2	2;2	2;2	Mitogen-activated protein k	MAPK1
J3QT28;O43684-2;O436	J3QT28;O4 5;5;5;3	5;5;5;3	5;5;5;3	Mitotic checkpoint protein	BUB3
Q8IVT2	Q8IVT2	2	2	Mitotic interactor and subst	MISP
Q9BYG3;H7BZL0;C9J80	Q9BYG3;H7 3;2;2;1	3;2;2;1	3;2;2;1	MKI67 FHA domain-interact	NIFK
P26038;V9GZ54	P26038	21;4	16;2	Moesin	MSN
P53985	P53985	2	2	Monocarboxylate transport	SLC16A1
A0A087WVM4;B7ZM99	A0A087WV 3;3;3;1;1;1	3;3;3;1;1;1	3;3;3;1;1;1	Monofunctional C1-tetrahy	MTHFD1L
H3BVD1;B7Z5N5;P8402	H3BVD1;B7 2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	Mothers against decapenta	SMAD3;SM
E9PPG9;E9PQ57;P7840	E9PPG9;E9 5;5;5;2	5;5;5;2	5;5;5;2	mRNA export factor	RAE1
Q9UKD2	Q9UKD2	3	3	mRNA turnover protein 4 h	MRTO4
F8WCY8;O15440-5;O15	F8WCY8;O9 1;1;1	1;1;1	1;1;1	Multidrug resistance-associ	ABCC5
F5GYQ2;F5GX77;Q9UI3	F5GYQ2;F5 1;1;1;1	1;1;1;1	1;1;1;1	Multifunctional methyltran	TRMT112
E9PBS1;P22234;P22234	E9PBS1;P2 8;8;8;6	8;8;8;6	8;8;8;6	Multifunctional protein AD	PAICS
C9JP00;A0A0A0MQX8;C	C9JP00;A0 2;2;2;1;1;1	2;2;2;1;1;1	2;2;2;1;1;1	Muscleblind-like protein 1	MBNL1;ME
Q9BQG0;Q9BQG0-2;I3L	Q9BQG0;Q 15;15;13;2	15;15;13;2	15;15;13;2	Myb-binding protein 1A	MYBBP1A
Q9NUJ1;Q9NUJ1-2;Q9N	Q9NUJ1;Q9 2;1;1	2;1;1	2;1;1	Mycophenolic acid acyl-gluc	ABHD10
O95297-4;O95297-2;O9	O95297-4;(4;4;4;1;1;1	4;4;4;1;1;1	4;4;4;1;1;1	Myelin protein zero-like prc	MPZL1
O60487	O60487	1	1	Myelin protein zero-like prc	MPZL2
C9JIV6;C9JZL8;C9J5M0	C9JIV6;C9J 2;2;2;2;2	2;2;2;2;2	2;2;2;2;2	Myeloid-associated differer	MYADM
Q9NZM1-6;Q9NZM1;Q9	Q9NZM1-6 49;49;48;4	49;49;48;4	49;49;48;4	Myoferlin	MYOF
P05976-2;P05976;P085	P05976-2;F 1;1;1	1;1;1	1;1;1	Myosin light chain 1/3, skel	MYL1;MYL
F8W1R7;G3V1V0;P606	F8W1R7;G9 9;9;9;8;8	9;9;9;8;8	8;7;7;7;7;6	Myosin light polypeptide 6	MYL6
J3KSW8;H0Y2S9;Q6WC	J3KSW8;H0 2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	Myosin phosphatase Rho-in	MPRIP
J3QRS3;P19105;O1495	J3QRS3;P1 8;8;8;5;4;3	8;8;8;5;4;3	8;8;8;5;4;3	Myosin regulatory light chai	MYL12A;M
P35580;P35580-5;P355	P35580;P3 13;13;13;1	1;1;1;1;1	1;1;1;1;1	Myosin-10	MYH10

P35749-4;P35749-3;P35749-4;F 11;11;11;1 1;1;1;1 1;1;1;1	Myosin-11	MYH11
Q7Z406;Q7Z406-6;Q7Z406;Q79;9;9;7;6;5 2;2;2;1;1 2;2;2;1;1	Myosin-14	MYH14
P35579;P35579-2;Q5BK P35579;P3104;67;9;5 104;67;9;5;88;53;7;4;C	Myosin-9	MYH9
C9JL85;P58546 C9JL85;P582;2 2;2 2;2	Myotrophin	MTPN
P29966 P29966 8 8 8	Myristoylated alanine-rich C	MARCKS
O14745;J3QRP6;O14745;J3(2;1;1 2;1;1 2;1;1	Na(+)/H(+) exchange regula	SLC9A3R1
Q86SF2;H0YAK0;E9PBY; Q86SF2;H0 2;1;1;1 2;1;1;1 2;1;1;1	N-acetylgalactosaminyltran	GALNT7
Q9H0A0;Q9H0A0-2;A0A Q9H0A0;Q13;12;11;3 13;12;11;3 13;12;11;3	N-acetyltransferase 10	NAT10
A0A0G2JPB6;A0A0G2JL A0A0G2JPE 4;4;4;4;4 4;4;4;4;4 4;4;4;4;4	NACHT, LRR and PYD domai	NLRP2;NLR
Q13423;D6RHU2;D6RAI Q13423;D6 4;2;2;2 4;2;2;2 4;2;2;2	NAD(P) transhydrogenase, r	NNT
B4DLR8;H3BRK3;P1555 B4DLR8;H3 4;4;4;4;3 4;4;4;4;3 4;4;4;4;3	NAD(P)H dehydrogenase [q	NQO1
A0A1W2PQF8;A0A1W2 A0A1W2PC 4;4;4;4;4 4;4;4;4;4 4;4;4;4;4	NAD-dependent malic enzym	ME2
Q9BU61 Q9BU61 1 1 1	NADH dehydrogenase [ubiq	NDUFA3
F8WAS3;C9IZN5;A0A08 F8WAS3;C1 1;1;1;1;1 1;1;1;1;1 1;1;1;1;1	NADH dehydrogenase [ubiq	NDUFA5
F5H0J3;Q16795 F5H0J3;Q1 1;1 1;1 1;1	NADH dehydrogenase [ubiq	NDUFA9
H3BPJ9;O96000;H3BV1 H3BPJ9;O9 2;2;1;1 2;2;1;1 2;2;1;1	NADH dehydrogenase [ubiq	NDUFB10
E7EPT4;P19404 E7EPT4;P1 2;2 2;2 2;2	NADH dehydrogenase [ubiq	NDUFV2
O75306-2;O75306 O75306-2;(2;2 2;2 2;2	NADH dehydrogenase [ubiq	NDUFS2
O75489 O75489 1 1 1	NADH dehydrogenase [ubiq	NDUFS3
H7C0R7;Q9UHQ9 H7C0R7;Q1 1;1 1;1 1;1	NADH-cytochrome b5 reduc	CYB5R1
P00387-2;P00387;P003 P00387-2;F 6;6;6;3 6;6;6;3 6;6;6;3	NADH-cytochrome b5 reduc	CYB5R3
P48163-2;P48163 P48163-2;F 1;1 1;1 1;1	NADP-dependent malic enz	ME1
A0A0A0MTN9;J3QQX3; A0A0A0MT 3;3;3;3;3 3;3;3;3;3 3;3;3;3;3	NADPH:adrenodoxin oxidor	FDXR
P16435;E7EMD0;H0Y4R P16435;E7I 4;3;3 4;3;3 4;3;3	NADPH--cytochrome P450 r	POR
E7EQ69;Q9GZZ1;F8WCI E7EQ69;Q9 2;2;1;1;1 2;2;1;1;1 2;2;1;1;1	N-alpha-acetyltransferase 5	NAA50
F8VZJ2;F8W0W4;H0YH F8VZJ2;F8V 2;2;2;2;2 2;2;2;2;2 2;2;2;2;2	Nascent polypeptide-associ	NACA
Q9Y2A7;Q9Y2A7-2 Q9Y2A7;Q1 1;1 1;1 1;1	Nck-associated protein 1	NCKAP1
Q9BT67 Q9BT67 1 1 1	NEDD4 family-interacting pr	NDFIP1
H7C5F7;B4DGY6;A0A0C H7C5F7;B4 2;2;2;2 2;2;2;2 2;2;2;2	NEDD4 family-interacting pr	NDFIP2
P61081;M0QX69;M0QY P61081;M1 3;2;1 3;2;1 3;2;1	NEDD8-conjugating enzyme	UBE2M
Q9UMX5 Q9UMX5 2 2 2	Neudesin	NENF
Q09666;E9PJZ0;E9PKR9 Q09666 138;3;3;3 138;3;3;3 138;3;3;3	Neuroblast differentiation-e	AHNAK
H0YAK4;E9PCB6;Q9BYT H0YAK4;E9 1;1;1 1;1;1 1;1;1	Neurolysin, mitochondrial	NLN
Q9Y639-1;Q9Y639;H3BI Q9Y639-1;(3;3;2;2;2 3;3;2;2;2 3;3;2;2;2	Neuroplastin	NPTN;DKFZ
Q14697;F5H6X6 Q14697;F5 26;23 26;23 1;1	Neutral alpha-glucosidase A	GANAB
Q14697-2;E9PKU7;E9P Q14697-2;I 26;20;5;1 1;1;1;0 1;1;1;0	Neutral alpha-glucosidase A	GANAB
P43007;P43007-2 P43007;P4 2;1 2;1 2;1	Neutral amino acid transpo	SLC1A4
Q15758;M0QXM4;Q15 Q15758;M1 9;8;6;6;4;1 9;8;6;6;4;1 9;8;6;6;4;1	Neutral amino acid transpo	SLC1A5
A0A0R4J2G3;A0A0A0M A0A0R4J2C 4;4;4;3;2 4;4;4;3;2 4;4;4;3;2	Neutral cholesterol ester hy	NCEH1
X6R8F3;P80188;P80188 X6R8F3;P8 4;4;3 4;4;3 4;4;3	Neutrophil gelatinase-assoc	LCN2
B7Z5R6;Q14596-2;Q14 B7Z5R6;Q1 1;1;1 1;1;1 1;1;1	Next to BRCA1 gene 1 prote	NBR1
B1AHD1;P55769 B1AHD1;P5 3;3 3;3 3;3	NHP2-like protein 1;NHP2-li	NHP2L1
Q96TA1-2;Q96TA1 Q96TA1-2;(3;3 3;3 3;3	Niban-like protein 1	FAM129B
Q969V3-2;Q969V3;K7EI Q969V3-2;(4;4;1;1 4;4;1;1 4;4;1;1	Nicalin	NCLN
P43490;A0A0C4DFS8;C P43490;A0 8;6;1;1 8;6;1;1 8;6;1;1	Nicotinamide phosphoribos	NAMPT
Q6XQN6-3;Q6XQN6 Q6XQN6-3;1;1 1;1 1;1	Nicotinate phosphoribosylti	NAPRT
K7EQ23;O15118-2;O15 K7EQ23;O1 1;1;1 1;1;1 1;1;1	Niemann-Pick C1 protein	NPC1
J3KN36;A0A0G2JN29;A J3KN36;A0 6;6;6;6;6 6;6;6;6;6 6;6;6;6;6	Nodal modulator 2;Nodal r	NOMO3;N
P05204;A0A087WZE9;C P05204 3;1;1;1 3;1;1;1 3;1;1;1	Non-histone chromosomal	HMGN2
Q15233;Q15233-2;H7C Q15233;Q1 13;12;9;7;5 12;11;8;7;4 12;11;8;7;4	Non-POU domain-containin	NONO



P22307-6;P22307-2;P22307-6;F 4;4;4;4;4 4;4;4;4;4 4;4;4;4;4					Non-specific lipid-transfer p	SCP2
J3QRU1;P07947;P06241J3QRU1;P0 3;3;1;1;1,1 3;3;1;1;1,1 3;3;1;1;1,					Non-specific protein-tyrosir	YES1
Q9UNZ2;Q9UNZ2-5;F2Z Q9UNZ2;Q 6;6;5;5;3,2 6;6;5;5;3,2 6;6;5;5;3,2,					NSFL1 cofactor p47	NSFL1C
Q9BV86-2;Q9BV86 Q9BV86-2; 1;1 1;1 1;1					N-terminal Xaa-Pro-Lys N-m	NTMT1
H0YDS9;Q5T624;P4932 H0YDS9;Q 3;3;3;3;3 3;3;3;3;3 3;3;3;3;3;					Nuclear autoantigenic sperr	NASP
Q09161 Q09161 4 4 4					Nuclear cap-binding proteir	NCBP1
F8WE41;P52298-3;P522 F8WE41;P 1;1;1 1;1;1 1;1;1					Nuclear cap-binding proteir	NCBP2
D6RH30;P19838;P1983 D6RH30;P 1;1;1 1;1;1 1;1;1					Nuclear factor NF-kappa-B i	NFKB1
Q7Z417 Q7Z417 3 3 3					Nuclear fragile X mental ret	NUFIP2
Q9Y266;A0A0A0MSS4;A Q9Y266 5;1;1 5;1;1 5;1;1					Nuclear migration protein n	NUDC
Q14980-2;A0A087WY6 Q14980-2; 46;45;45;3 46;45;45;3 46;45;45;3					Nuclear mitotic apparatus p	NUMA1
P57740;P57740-3;P577 P57740;P 6;4;4;2;1 6;4;4;2;1 6;4;4;2;1					Nuclear pore complex prote	NUP107
Q8WUM0 Q8WUM0 6 6 6					Nuclear pore complex prote	NUP133
P49790-2;P49790;P497 P49790-2;F 6;6;6 6;6;6 6;6;6					Nuclear pore complex prote	NUP153
E9PF10;O75694;O7569 E9PF10;O 13;13;12;1 13;13;12;1 13;13;12;1					Nuclear pore complex prote	NUP155
G3V198;Q12769;E9PR1 G3V198;Q 17;7;6;2;1 7;7;6;2;1 7;7;6;2;1					Nuclear pore complex prote	NUP160
Q92621;U3KPX2 Q92621 9;4 9;4 9;4					Nuclear pore complex prote	NUP205
A0A0A0MSW3;P35658-A0A0A0MS 5;5;5;5;5 5;5;5;5;5 5;5;5;5;5;					Nuclear pore complex prote	NUP214
Q9UKX7-2;Q9UKX7 Q9UKX7-2; 1;1 1;1 1;1					Nuclear pore complex prote	NUP50
J3QL54;Q9BW27-2;Q9B J3QL54;Q 2;2;2;2;1,1 2;2;2;2;1,1 2;2;2;2;1,1					Nuclear pore complex prote	NUP85
J3KMX1;Q99567;I3L4K7 J3KMX1;Q 5;5;5;1;1 5;5;5;1;1 5;5;5;1;1					Nuclear pore complex prote	NUP88
H3BVG0;Q8N1F7;Q8N1 H3BVG0;Q 7;7;5;3;2,2 7;7;5;3;2,2 7;7;5;3;2,2					Nuclear pore complex prote	NUP93
P52948-6;P52948-5;P52 P52948-6;F 6;6;6;5;5,2 6;6;6;5;5,2 6;6;6;5;5,2					Nuclear pore complex prote	NUP98
P37198;MOQXN5 P37198;MC 3;2 3;2 3;2					Nuclear pore glycoprotein p	NUP62
Q8TEM1;Q8TEM1-2 Q8TEM1;Q 4;2 4;2 4;2					Nuclear pore membrane gly	NUP210
Q8TAT6;Q8TAT6-2 Q8TAT6;Q 1;1 1;1 1;1					Nuclear protein localization	NPLOC4
Q13772;Q13772-3;Q13 Q13772;Q 16;6;6;4;4,2 6;6;6;4;4,2 6;6;6;4;4,2					Nuclear receptor coactivatc	NCOA4
P61970;H3BRV9 P61970;H3 5;3 5;3 5;3					Nuclear transport factor 2	NUTF2
Q9H1E3;Q9H1E3-2 Q9H1E3 3;1 3;1 3;1					Nuclear ubiquitous casein a	NUCKS1
O15381-3;O15381-4;O1 O15381-3;( 1;1;1;1,1 1;1;1;1,1 1;1;1;1,1					Nuclear valosin-containing i	NVL
P67809;H0Y449;C9J5V9 P67809;H0 10;9;5;3 10;9;5;3 7;7;4;0					Nuclease-sensitive element	YBX1
Q02818;C9JKZ2 Q02818 3;1 3;1 3;1					Nucleobindin-1	NUCB1
A0A0A0MRM9;Q14978 A0A0A0MF 5;5;5;5;1,1 5;5;5;5;1,1 5;5;5;5;1,1					Nucleolar and coiled-body p	NOLC1
Q9Y3T9 Q9Y3T9 4 4 4					Nucleolar complex protein :	NOC2L
Q8WTT2 Q8WTT2 1 1 1					Nucleolar complex protein :	NOC3L
Q9BZE4;Q9BZE4-2;Q9B Q9BZE4;Q 10;9;7;5 10;9;7;5 10;9;7;5					Nucleolar GTP-binding proti	GTPBP4
O60287 O60287 1 1 1					Nucleolar pre-ribosomal-as	URB1
Q9H8H0;J3QLQ6;J3QR2 Q9H8H0;J3 2;1;1;1 2;1;1;1 2;1;1;1					Nucleolar protein 11	NOL11
E9PFK5;P78316-2;P783 E9PFK5;P 1;1;1 1;1;1 1;1;1					Nucleolar protein 14	NOP14
D6RC60;D6RIC3;A0A0C D6RC60;D6 1;1;1;1;1,1 1;1;1;1;1,1 1;1;1;1;1,1					Nucleolar protein 16	NOP16
O00567;H0Y653;H0YDU O00567;H0 10;5;5;4 10;5;5;4 10;5;5;4					Nucleolar protein 56	NOP56
Q9Y2X3;H7BZ72;F8WEL Q9Y2X3 10;3;1 10;3;1 10;3;1					Nucleolar protein 58	NOP58
Q9H6R4-4;Q9H6R4;A0A Q9H6R4-4; 2;2;1;1;1,1 2;2;1;1;1,1 2;2;1;1;1,1					Nucleolar protein 6	NOL6
Q9NR30;Q9NR30-2;A0A Q9NR30;Q 18;16;1 18;16;1 17;15;0					Nucleolar RNA helicase 2	DDX21
E9PKP7;P17480-2;P174 E9PKP7;P 3;3;3;1 3;3;3;1 3;3;3;1					Nucleolar transcription fact	UBTF
P19338;H7BY16;C9JYW P19338;H7 23;15;1;1,1 23;15;1;1,1 23;15;1;1,1					Nucleolin	

Q8NFH5-2;Q8NFH5;C9I	Q8NFH5-2; 5;5;3;3;2	5;5;3;3;2	5;5;3;3;2	Nucleoporin NUP53	NUP35	
Q7Z3B4-2;Q7Z3B4-3;Q7	Q7Z3B4-2;(3;3;3	3;3;3	3;3;3	Nucleoporin p54	NUP54	
Q96EE3;Q96EE3-1;K7EL	Q96EE3;Q95;5;4;3;3;1	5;5;4;3;3;1	5;5;4;3;3;1	Nucleoporin SEH1	SEH1L	
P12270;P12270-2	P12270	14;4	14;4	Nucleoprotein TPR	TPR	
A0A0G2JQK5;Q6DKJ4	A0A0G2JQI1;1	1;1	1;1	Nucleoredoxin	NXN	
P15531;P15531-2;E5RH	P15531;P15;5;2;1	1;1;0;0	1;1;0;0	Nucleoside diphosphate kin	NME1	
Q32Q12;P22392-2;P223	Q32Q12;P28;8;7;6;5;4	8;8;7;6;5;4	4;4;4;4;1;0	Nucleoside diphosphate kin	NME1-NMI	
H0YHC3;F8W020;F8W1	H0YHC3;F83;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	Nucleosome assembly prote	NAP1L1	
C9JZI7;Q99733;Q99733	C9JZI7;Q994;4;4;3;3;3	4;4;4;3;3;3	4;4;4;3;3;3	Nucleosome assembly prote	NAP1L4	
Q96RS6-3;Q96RS6-2;Q9	Q96RS6-3;(2;2;2	2;2;2	2;2;2	NudC domain-containing pr	NUDCD1	
E5RFP0;Q8WVJ2	E5RFP0;Q81;1	1;1	1;1	NudC domain-containing pr	NUDCD2	
C9JTK6;J3KQ32;Q9NTK5	C9JTK6;J3K1;1;1;1	1;1;1;1	1;1;1;1	Obg-like ATPase 1	OLA1	
Q56VL3;D6RD77;J3KPI9	Q56VL3;D63;2;2;2	3;2;2;2	3;2;2;2	OCIA domain-containing pr	OCIAD2	
A0A087WUD3;Q9NRPO	A0A087WL1;1;1	1;1;1	1;1;1	Oligosaccharyltransferase c	OSTC	
Q9NQR4;H7C579;F8WF	Q9NQR4;H7;6;1	7;6;1	7;6;1	Omega-amidase NIT2	NIT2	
Q99650-2;Q99650	Q99650-2;(1;1	1;1	1;1	Oncostatin-M-specific recep	OSMR	
F6WST4;A0A1B0GXE7;C	F6WST4;AC1;1;1;1	1;1;1;1	1;1;1;1	ORM1-like protein 1;ORM1	ORMDL1;O	
J3QRM9;Q8N138-4;Q8M	J3QRM9;Q81;1;1	1;1;1	1;1;1	ORM1-like protein 3	ORMDL3	
P04181;P04181-2	P04181;P010;5	10;5	10;5	Ornithine aminotransferase	OAT	
Q92882	Q92882	1	1	1	Osteoclast-stimulating factc	OSTF1
P36551;H0YA22;P36551	P36551	5;1;1	5;1;1	5;1;1	Oxygen-dependent copropc	CPOX
Q9NWT1	Q9NWT1	1	1	1	p21-activated protein kinas	PAK1IP1
Q15645;H0YAL2;Q1564	Q15645;HC3;2;1	3;2;1	3;2;1	Pachytene checkpoint prote	TRIP13	
E9PSE5;E9PIA8;A0A2C9	E9PSE5;E91;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Palmitoyl-protein thioester	PPT1	
B4DRN8;Q5W0Z9	B4DRN8;Q51;1	1;1	1;1	Palmitoyltransferase;Probal	ZDHHC20	
Q8WXF1-2;Q8WXF1;X6	Q8WXF1-2;3;3;2	3;3;2	3;3;2	Paraspeckle component 1	PSPC1	
O00151	O00151	10	10	10	PDZ and LIM domain protei	PDLIM1
O14908;K7ELJ2;K7EM1	O14908;K72;1;1;1;1	2;1;1;1;1	2;1;1;1;1	PDZ domain-containing pro	GIPC1	
Q96EY7;Q96EY7-2	Q96EY7;Q92;1	2;1	2;1	Pentatricopeptide repeat d	PTCD3	
P62937-2	P62937-2	8	1	1	Peptidyl-prolyl cis-trans isor	PPIA
P62937;F8WE65;C9J5S7	P62937;F811;7;7;2;2;11;7;7;2;2;4;4;4;1;1;1				Peptidyl-prolyl cis-trans isor	PPIA
P23284	P23284	10	10	10	Peptidyl-prolyl cis-trans isor	PPIB
P45877	P45877	1	1	1	Peptidyl-prolyl cis-trans isor	PPIC
P30405;R4GN99;P3040	P30405;R44;4;3;3;2;1;1	3;2;2;1;1;1	3;2;2;1;1;1	Peptidyl-prolyl cis-trans isor	PPIF	
P62942;Q5W0X3;A0A08	P62942;Q53;2;2;1;1;1	3;2;2;1;1;1	3;2;2;1;1;1	Peptidyl-prolyl cis-trans isor	FKBP1A	
P26885;F5H0N4	P26885;F512;1	2;1	2;1	Peptidyl-prolyl cis-trans isor	FKBP2	
Q00688	Q00688	3	3	3	Peptidyl-prolyl cis-trans isor	FKBP3
Q02790;H0YFG2;F5H1U	Q02790	12;3;3;1	12;3;3;1	12;3;3;1	Peptidyl-prolyl cis-trans isor	FKBP4
M0R2K9;Q14318;Q143	M0R2K9;Q11;1;1	1;1;1	1;1;1	Peptidyl-prolyl cis-trans isor	FKBP8	
Q9Y3C6	Q9Y3C6	2	2	2	Peptidyl-prolyl cis-trans isor	PPIL1
Q8WUA2	Q8WUA2	1	1	1	Peptidyl-prolyl cis-trans isor	PPIL4
J3KQ48;Q9Y3E5	J3KQ48;Q92;2	2;2	2;2	Peptidyl-tRNA hydrolase 2,	PTRH2	
E5RGQ4;E9PGW9;E7EV	E5RGQ4;E92;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	Pericentriolar material 1 pr	PCM1	
O60664-4;O60664-3;O6	O60664-4;(8;8;8;6;4;4	8;8;8;6;4;4	8;8;8;6;4;4	Perilipin-3	PLIN3	
Q15269;A0A0B4J2E5;C9	Q15269;A03;2;1	3;2;1	3;2;1	Periodic tryptophan protein	PWP2	
Q06830;A0A0A0MSI0;A	Q06830;A015;13;7	15;13;7	11;10;3	Peroxiredoxin-1	PRDX1	
P32119;A6NIW5;P3211	P32119	9;4;1	8;4;1	8;4;1	Peroxiredoxin-2	PRDX2
Q13162;H7C3T4;A6NG4	Q13162;H712;7;4;2	9;4;4;2	9;4;4;2	Peroxiredoxin-4	PRDX4	
P30044-2;P30044;P300	P30044-2;F6;6;5;2	6;6;5;2	6;6;5;2	Peroxiredoxin-5, mitochonc	PRDX5	
P30041	P30041	9	9	9	Peroxiredoxin-6	PRDX6

I3L2U4;K7ELT1;I3L0T4;C	I3L2U4;K7E	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Peroxisomal acyl-coenzyme A	ACOX1
Q92968	Q92968	1	1	1	Peroxisomal membrane protein	PEX13
O75381-2;O75381	O75381-2;	2;2	2;2	2;2	Peroxisomal membrane protein	PEX14
P51659;E7EWE5;P51659	P51659;E7I	17;14;14;1	17;14;14;1	17;14;14;1	Peroxisomal multifunctional	HSD17B4
M0QXB5;O95571	M0QXB5;O	1;1	1;1	1;1	Persulfide dioxygenase	ETH1
B5MCF9;O00541;B3KX	B5MCF9;O	8;8;7;7;2	8;8;7;7;2	8;8;7;7;2	Pescadillo homolog	PES1
C9JZE2;C9IZ09;Q8IYB4	C9JZE2;C9I	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	PEX5-related protein	PEX5L
Q7RTV0	Q7RTV0	2	2	2	PHD finger-like domain-con	PHF5A
K7ER00;Q9Y285;K7ER1	K7ER00;Q9	3;3;2;2;1	3;3;2;2;1	3;3;2;2;1	Phenylalanine--tRNA ligase	FARSA
Q9NSD9;Q9NSD9-2	Q9NSD9;Q	10;8	10;8	10;8	Phenylalanine--tRNA ligase	FARSB
Q8WWQ0	Q8WWQ0	2	2	2	PH-interacting protein	PHIP
Q00325-2;Q00325;F8V	Q00325-2;	8;8;7;2;2;2	8;8;7;2;2;2	8;8;7;2;2;2	Phosphate carrier protein, r	SLC25A3
O95674	O95674	1	1	1	Phosphatidate cytidyltran	CDS2
P30086	P30086	6	6	6	Phosphatidylethanolamine-	PEBP1
C9J3E3;F8WDN7;E9PGZ	C9J3E3;F8V	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Phosphatidylinositide phosph	SACM1L
A0A0A0MSW4;P48739; A0A0A0MS	A0A0A0MS	4;4;4;3;2	4;4;4;4;3;2	4;4;4;4;3;2	Phosphatidylinositol transfe	PITPNB;PIT
Q13492-4;Q13492-3;Q1	Q13492-4;	4;4;4;4;2	4;4;4;4;2	4;4;4;4;2	Phosphatidylinositol-bindin	PICALM
P48651-3;P48651-2;P4	P48651-3;F	1;1;1	1;1;1	1;1;1	Phosphatidylserine synthas	PTDSS1
Q16822;A0A0A0MS74;P	Q16822;A0	4;3;3;3;2;2	4;3;3;3;2;2	4;3;3;3;2;2	Phosphoenolpyruvate carb	PCK2
P36871;P36871-2;P368	P36871;P3	8;6;5	8;6;5	8;6;5	Phosphoglucomutase-1	PGM1
Q96G03-2;Q96G03	Q96G03-2;	1;1	1;1	1;1	Phosphoglucomutase-2	PGM2
P00558-2;P00558;P072	P00558-2;F	15;15;3	15;15;3	15;15;3	Phosphoglycerate kinase 1	PGK1
P18669;P15259;Q8NOY	P18669	11;3;3	11;3;3	11;3;3	Phosphoglycerate mutase 1	PGAM1
Q8IV08;M0R3G9	Q8IV08;MC	2;1	2;1	2;1	Phospholipase D3	PLD3
C9J7K9;O15162-2;O151	C9J7K9;O1	2;2;2;1;1;1	2;2;2;1;1;1	2;2;2;1;1;1	Phospholipid scramblase 1	PLSCR1
C9JDU5;C9JJS3;C9K0K7	C9JDU5;C9	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Phosphoribosyl pyrophosph	PRPSAP2
Q9Y617;Q9Y617-2	Q9Y617;Q	8;7	8;7	8;7	Phosphoserine aminotransf	PSAT1
C9JBI3;P78330	C9JBI3;P7	8;7	8;7	8;7	Phosphoserine aminotransf	PSAT1
Q9H307	Q9H307	3	3	3	Pinin	PNN
O00625	O00625	1	1	1	Pirin	PIR
Q13835-2;Q13835	Q13835-2;	2;2	2;2	2;2	Plakophilin-1	PKP1
Q99959-2;Q99959;A0A	Q99959-2;	2;2;1	2;2;1	2;2;1	Plakophilin-2	PKP2
Q9Y446-2;Q9Y446;E9PC	Q9Y446-2;	9;8;4;3;3;3	9;8;4;3;3;3	9;8;4;3;3;3	Plakophilin-3	PKP3
P20020-5;P20020-2;P2	P20020-5;F	3;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	Plasma membrane calcium-	ATP2B1;AT
Q8NC51-3;Q8NC51;Q8	Q8NC51-3;	11;11;10;1	11;11;10;1	11;11;10;1	Plasminogen activator inhib	SERBP1
P05120;H7C004;H7BYS	P05120;H7	6;4;4;1;1;1	6;4;4;1;1;1	6;4;4;1;1;1	Plasminogen activator inhib	SERPINB2;S
P13796;Q5TBN3;P1379	P13796	19;8;3;2	19;8;3;2	13;5;3;2	Plastin-2	LCP1
A0A0A0MSQ0;P13797-3	A0A0A0MS	16;16;16;1	10;10;10;1	10;10;10;1	Plastin-3	PLS3
P43034;I3L3N5;I3L495	P43034;I3L	5;3;1	5;3;1	5;3;1	Platelet-activating factor ac	PAFAH1B1
P68402-3;P68402-2;P6	P68402-3;F	1;1;1;1	1;1;1;1	1;1;1;1	Platelet-activating factor ac	PAFAH1B2
R4GND3;Q8WV24	R4GND3;Q	1;1	1;1	1;1	Pleckstrin homology-like do	PHLDA1
Q15149-4;Q15149-7;Q1	Q15149-4;	102;101;10	102;101;10	102;101;10	Plectin	PLEC
O43660-2;O43660;H0Y	O43660-2;	2;2;1	2;2;1	2;2;1	Pleiotropic regulator 1	PLRG1
O75051	O75051	1	1	1	Plexin-A2	PLXNA2
O15031;A6QRG9;A6QR	O15031	6;2;1;1	6;2;1;1	6;2;1;1	Plexin-B2	PLXNB2
P09874;Q5VX84;Q5VX8	P09874	17;1;1	17;1;1	17;1;1	Poly [ADP-ribose] polymera	PARP1
Q9NVV4;Q9NVV4-2	Q9NVV4;Q	1;1	1;1	1;1	Poly(A) RNA polymerase, m	MTPAP
Q15365;F8VTZ0	Q15365	9;1	9;1	7;0	Poly(rC)-binding protein 1	PCBP1
Q15366-6;Q15366-3;Q1	Q15366-6;	8;8;7;7;7;7	6;6;5;5;5;5	6;6;5;5;5;5	Poly(rC)-binding protein 2;P	PCBP2;PCB
A0A0J9YYL3;A0A0J9YVF	A0A0J9YYL	8;8;8;8;8;7	8;8;8;8;8;7	8;8;8;8;8;7	Poly(U)-binding-splicing fac	PUF60

P11940;A0A087WTT1;E P11940;A0.18;17;17;1	18;17;17;1	14;13;13;1	Polyadenylate-binding protein	PABPC1;PA
Q86U42-2;Q86U42;H0Y Q86U42-2;2;2;1;1;1;1	2;2;1;1;1;1	2;2;1;1;1;1	Polyadenylate-binding protein	PABPN1
B1ANR0;Q13310-2;Q13 B1ANR0;Q.7;7;7;7;4;3	3;3;3;3;2;1	3;3;3;3;2;1	Polyadenylate-binding protein	PABPC4
D6REB4;Q9H074-3;Q9H D6REB4;Q.2;2;2;2	2;2;2;2	2;2;2;2	Polyadenylate-binding protein	PAIP1
B4DEM9;Q9Y2S7 B4DEM9;Q.1;1	1;1	1;1	Polymerase delta-interacting protein	POLDIP2
F6VRR5;Q9BY77-2;Q9B F6VRR5;Q9.2;2;2;1;1;1	2;2;2;1;1;1	2;2;2;1;1;1	Polymerase delta-interacting protein	POLDIP3;PI
Q6NZI2;Q6NZI2-2;Q6NZ Q6NZI2;Q6.10;6;4	10;6;4	10;6;4	Polymerase I and transcript	PTRF
Q10471;Q10471-2;F8VL Q10471	9;2;1;1;1	9;2;1;1;1	Polypeptide N-acetylgalactosyltransferase	GALNT2
E7EUL0;Q14435;C9J2C3 E7EUL0;Q1.3;3;1	3;3;1	3;3;1	Polypeptide N-acetylgalactosyltransferase	GALNT3
A6NLN1;A0A0U1RRM4; A6NLN1;AC.10;10;10;1	10;10;10;1	8;8;8;8;8;4	Polypyrimidine tract-binding protein	PTBP1
O95758-7;O95758-1;O9 O95758-7;(8;8;8;8;8;8	6;6;6;6;6;6	6;6;6;6;6;6	Polypyrimidine tract-binding protein	PTBP3
Q8TCS8;H7BXF6;F8WBI Q8TCS8;H7.3;2;1;1	3;2;1;1	3;2;1;1	Polyribonucleotide nucleotidyltransferase	PNPT1
A6NP52;O60831 A6NP52;O.1;1	1;1	1;1	PRA1 family protein 2	PRAF2
E5RGS4;O60925 E5RGS4;O.6;1;1	1;1	1;1	Prefoldin subunit 1	PFDN1
Q9UHV9 Q9UHV9	1	1	Prefoldin subunit 2	PFDN2
E9PQY2;Q9NQP4 E9PQY2;Q.1;1	1;1	1;1	Prefoldin subunit 4	PFDN4
P02545;P02545-3;P025 P02545;P0.39;38;37;3	39;38;37;3	38;37;36;3	Prelamin-A/C;Lamin-A/C	LMNA
Q9UMS4;F5GY56;F5H2I Q9UMS4	10;3;2;2;1	10;3;2;2;1	Pre-mRNA-processing factor	PRPF19
O75400-2;O75400-3;O7 O75400-2;(2;2;2	2;2;2	2;2;2	Pre-mRNA-processing factor	PRPF40A
O94906;O94906-2 O94906;O.9;8	9;8	9;8	Pre-mRNA-processing factor	PRPF6
Q6P2Q9;I3L0J9;I3L3Z8 Q6P2Q9	16;4;2	16;4;2	Pre-mRNA-processing-splicing factor	PRPF8
Q8NAV1 Q8NAV1	1	1	Pre-mRNA-splicing factor 3B	PRPF38A
O43143 O43143	6	6	Pre-mRNA-splicing factor A	DHX15
Q9ULR0;Q9ULR0-2;Q9U Q9ULR0;Q.1;1;1	1;1;1	1;1;1	Pre-mRNA-splicing factor IS	ISY1
Q9UHG3-2;Q9UHG3;C9 Q9UHG3-2.2;2;1;1;1	2;2;1;1;1	2;2;1;1;1	Prenylcysteine oxidase 1	PCYOX1
Q8IY81 Q8IY81	7	7	pre-rRNA processing protein	FTSJ3
Q2NL82;I3L1Q5 Q2NL82;I3L.4;3	4;3	4;3	Pre-rRNA-processing protein	TSR1
Q5JRX3-3;Q5JRX3;Q5JR Q5JRX3-3;(6;6;6;2;1;1	6;6;6;2;1;1	6;6;6;2;1;1	Presequence protease, mitochondrial	PITRM1
Q96IZ0 Q96IZ0	1	1	PRKC apoptosis WT1 regulator	PAWR
P46087;P46087-4;P460 P46087;P4.14;14;13;1	14;14;13;1	14;14;13;1	Probable 28S rRNA (cytosolic)	NOP2
F5GYY1;F5GXL6;F5GXJ8 F5GYY1;F5.1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Probable ATP-dependent RNA helicase	DDX11;DD
A0A1X7SBZ2;A0A1W2P A0A1X7SB.18;18;18;1	18;18;18;1	11;11;11;1	Probable ATP-dependent RNA helicase	DDX17
B7Z6D5;Q96GQ7;A0A0 B7Z6D5;Q9.7;7;4;1	7;7;4;1	7;7;4;1	Probable ATP-dependent RNA helicase	DDX27
F8WAJ0;Q9H8H2-4;Q9 F8WAJ0;Q.2;2;2;2	2;2;2;2	2;2;2;2	Probable ATP-dependent RNA helicase	DDX31
A0A0C4DG89;Q7L014;C A0A0C4DG.7;7;5	7;7;5	7;7;5	Probable ATP-dependent RNA helicase	DDX46
Q9H0S4-2;Q9H0S4 Q9H0S4-2;(2;2	2;2	2;2	Probable ATP-dependent RNA helicase	DDX47
J3KTA4;P17844-2;P178 J3KTA4;P1.17;17;17;7	10;10;10;2	10;10;10;2	Probable ATP-dependent RNA helicase	DDX5
F8WDT8;G3V0G3;H7C3 F8WDT8;G.1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Probable ATP-dependent RNA helicase	DDX56
P26196;Q8IV96 P26196;Q.8.2;1	2;1	2;1	Probable ATP-dependent RNA helicase	DDX6
Q9HA77;H0YFV1;F5H62 Q9HA77;H.2;1;1	2;1;1	2;1;1	Probable cysteine--tRNA ligase	CARS2
A0A0A0MRP6;B7ZLQ5;F A0A0A0MF.3;3;3	2;2;2;2	2;2;2;2	Probable global transcription factor	SMARCA1
Q96K78 Q96K78	1	1	Probable G-protein coupled receptor	GPR128
H3BMQ2;Q9UHA3 H3BMQ2;C.1;1	1;1	1;1	Probable ribosome biogenesis factor	RSL24D1
Q9Y4C8 Q9Y4C8	2	2	Probable RNA-binding protein	RBM19
H7C2Q8;Q99848 H7C2Q8;Q.7;7	7;7	7;7	Probable rRNA-processing factor	EBNA1BP2
Q8NBJ5;M0QX72;M0Q Q8NBJ5	9;3;2	9;3;2	Procollagen galactosyltransferase	COLGALT1
Q02809;Q02809-2 Q02809;Q.4;4	4;4	4;4	Procollagen-lysine,2-oxoglutarate	PLOD1
E7ETU9;O00469;O0046 E7ETU9;O.2;2;2;1	2;2;2;1	2;2;2;1	Procollagen-lysine,2-oxoglutarate	PLOD2
O60568;H7C2V1;H7C2S O60568;H7.7;4;2;1	7;4;2;1	7;4;2;1	Procollagen-lysine,2-oxoglutarate	PLOD3
P07737;K7EJ44;CON__ F P07737;K7.10;8;4;3	10;8;4;3	10;8;4;3	Profilin-1	PFN1



Q8WUM4;Q8WUM4-2;Q8WUM4;7;7;4;2;2;2 7;7;4;2;2;2 7;7;4;2;2;2	Programmed cell death 6-in	PDCD6IP
Q53EL6-2;Q53EL6 Q53EL6-2;C 1;1 1;1 1;1	Programmed cell death pro	PDCD4
A0A024QZ42;O75340-2 A0A024QZ 2;2;2 2;2;2 2;2;2	Programmed cell death pro	PDCD6
P35232;C9JW96;C9JZ20 P35232;C9 13;12;10;1 13;12;10;1 13;12;10;1	Prohibitin	PHB
Q99623;J3KPX7;F5GY37 Q99623;J3 17;16;15;1 17;16;15;1 17;16;15;1	Prohibitin-2	PHB2
P12004 P12004 7 7 7	Proliferating cell nuclear an	PCNA
Q9UQ80;Q9UQ80-2;F8\ Q9UQ80;Q 16;13;9;6;5 16;13;9;6;5 16;13;9;6;5	Proliferation-associated pro	PA2G4
P13674-3;P13674-2;P13 P13674-3;F 6;6;6 6;6;6 6;6;6	Prolyl 4-hydroxylase subuni	P4HA1
O15460-2;O15460 O15460-2;C 3;3 3;3 3;3	Prolyl 4-hydroxylase subuni	P4HA2
P48147 P48147 3 3 3	Prolyl endopeptidase	PREP
C9JIZ6;P07602;P07602- C9JIZ6;P07 8;8;8;7;1 8;8;8;7;1 8;8;8;7;1	Prosaposin;Saposin-A;Sapo	PSAP
O14684 O14684 2 2 2	Prostaglandin E synthase	PTGES
X6RJ95;Q9H7Z7;A6NHH X6RJ95;Q9 3;3;2 3;3;2 3;3;2	Prostaglandin E synthase 2;	PTGES2
A0A087WYT3;Q15185-4 A0A087WY 5;5;5;4;3;3 5;5;5;4;3;3 5;5;5;4;3;3	Prostaglandin E synthase 3	PTGES3
Q9P2B2 Q9P2B2 2 2 2	Prostaglandin F2 receptor n	PTGFRN
Q14914-2;Q14914;F2Z3 Q14914-2;C 6;6;3;1 6;6;3;1 6;6;3;1	Prostaglandin reductase 1	PTGR1
Q16186;A0A087WX59 Q16186;A0 2;1 2;1 2;1	Proteasomal ubiquitin rece	ADRM1
Q06323-3;Q06323;Q06 Q06323-3;C 5;5;5;1 5;5;5;1 5;5;5;1	Proteasome activator comp	PSME1
H0YM70;A0A087X1Z3;C H0YM70;A 2;2;2;1 2;2;2;1 2;2;2;1	Proteasome activator comp	PSME2
K7ENH2;K9J957;P6128 K7ENH2;K9 3;3;3;3;2 3;3;3;3;2 3;3;3;3;2	Proteasome activator comp	PSME3
H0Y555;F5H4Z3;Q5QPN H0Y555;F5 1;1;1;1 1;1;1;1 1;1;1;1	Proteasome inhibitor PI31 s	PSMF1
C9JCK5;A0A024RA52;P2 C9JCK5;A0 2;2;2 2;2;2 2;2;2	Proteasome subunit alpha t	PSMA2
H0YMZ1;H0YN18;H0YL H0YMZ1;H 5;5;5;5;4;4 5;5;5;5;4;4 5;5;5;5;4;4	Proteasome subunit alpha t	PSMA4
G3V295;G3V5Z7;P6090 G3V295;G3 7;7;7;6;5;3 7;7;7;6;5;3 7;7;7;6;5;3	Proteasome subunit alpha t	PSMA6
P25786;P25786-2;F5GX P25786;P2 11;11;9;5 11;11;9;5 11;11;9;5	Proteasome subunit alpha t	PSMA1
P25788-2;P25788;G3V3 P25788-2;F 3;3;1;1;1 3;3;1;1;1 3;3;1;1;1	Proteasome subunit alpha t	PSMA3
P28066;P28066-2 P28066;P2 8;5 8;5 8;5	Proteasome subunit alpha t	PSMA5
O14818;O14818-2;H0Y O14818;O 19;7;6;4;4;4 9;7;6;4;4;4 9;7;6;4;4;4	Proteasome subunit alpha t	PSMA7
X5D2R7;P28062-2;P280 X5D2R7;P2 3;3;3;2;2 3;3;3;2;2 3;3;3;2;2	Proteasome subunit beta ty	PSM8;PSM
A2ACR0;A0A0G2JJQ0;A A2ACR0;A0 1;1;1;1;1;1 1;1;1;1;1;1 1;1;1;1;1;1	Proteasome subunit beta ty	PSMB9
P20618 P20618 5 5 5	Proteasome subunit beta ty	PSMB1
P49721;A0A087WVV1 P49721;A0 2;1 2;1 2;1	Proteasome subunit beta ty	PSMB2
A0A087WXQ8;A0A087 A0A087WX 2;2;2;2 2;2;2;2 2;2;2;2	Proteasome subunit beta ty	PSMB3
P28070 P28070 2 2 2	Proteasome subunit beta ty	PSMB4
P28074;P28074-3;H0YJI P28074;P2 7;5;3;3 7;5;3;3 7;5;3;3	Proteasome subunit beta ty	PSMB5
P28072;I3L3X7;A0A087 P28072 3;1;1 3;1;1 3;1;1	Proteasome subunit beta ty	PSMB6
Q99436;Q5TBG5;Q994 Q99436;Q5 2;1;1 2;1;1 2;1;1	Proteasome subunit beta ty	PSMB7
J3KN16;Q5VYK3;R4GM J3KN16;Q5 2;2;1;1 2;2;1;1 2;2;1;1	Proteasome-associated pro	KIAA0368;E
Q9NY61;A0A087WW41 Q9NY61 3;1;1 3;1;1 3;1;1	Protein AATF	AATF
Q99873-3;E9PKG1;Q99 Q99873-3;I 7;6;6;6;5;3 7;6;6;6;5;3 7;6;6;6;5;3	Protein arginine N-methyltr	PRMT1
H0YJX6;O14744-3;O147 H0YJX6;O1 2;2;2;2;2;1 2;2;2;2;2;1 2;2;2;2;2;1	Protein arginine N-methyltr	PRMT5
Q8TD16;Q8TD16-2 Q8TD16;Q8 1;1 1;1 1;1	Protein bicaudal D homolog	BICD2
P41223;P41223-2;C9JCI P41223;P4 2;2;1 2;2;1 2;2;1	Protein BUD31 homolog	BUD31
F8W031;F8VXJ7;Q9Y2B F8W031;F8 5;4;4;3;2;1 4;4;4;3;1;1 4;4;4;3;1;1	Protein canopy homolog 2	CNPY2
A0A0J9YYJ0;Q8N129 A0A0J9YYJ 2;2 2;2 2;2	Protein canopy homolog 4	CNPY4
Q9UKY7-2;Q9UKY7;D6R Q9UKY7-2; 3;3;2;2;2;2 3;3;2;2;2;2 3;3;2;2;2;2	Protein CDV3 homolog	CDV3
A6NLH6;Q9P003 A6NLH6;Q9 1;1 1;1 1;1	Protein cornichon homolog	CNIH4
C9IZG4;O60888-3;O608 C9IZG4;O6 1;1;1;1 1;1;1;1 1;1;1;1	Protein CutA	CUTA
Q99497;K7ELW0;K7EN2 Q99497;K7 6;5;3 6;5;3 6;5;3	Protein deglycase DJ-1	PARK7
P35659;B4DFG0;P3565 P35659;B4 5;4;4;2;2;2 5;4;4;2;2;2 5;4;4;2;2;2	Protein DEK	DEK

A0A140T8Z0;A0A0G2JH A0A140T8Z	9;9;9;9;8 9;9;9;9;8 9;9;9;9;8	Protein diaphanous homolo	DIAPH1
P07237;H7BZ94;HOY3Z	P07237;H7 22;20;12;1 22;20;12;1 22;20;12;1	Protein disulfide-isomerase	P4HB
P30101	P30101 22 22 17	Protein disulfide-isomerase	PDIA3
P13667	P13667 14 14 14	Protein disulfide-isomerase	PDIA4
Q15084-3;Q15084;Q15084-3;(13;13;13;1 13;13;13;1 13;13;13;1		Protein disulfide-isomerase	PDIA6
H3BPB3;B4DIE3;Q96JJ7 H3BPB3;B4 1;1;1;1 1;1;1;1 1;1;1;1		Protein disulfide-isomerase	TMX3
Q8WYP5;Q8WYP5-3;Q8 Q8WYP5;Q 4;4;4;1 4;4;4;1 4;4;4;1		Protein ELYS	AHCTF1
P49257	P49257 9 9 9	Protein ERGIC-53	LMAN1
H7C3D5;Q8NC44 H7C3D5;Q 1;1 1;1 1;1		Protein FAM134A	FAM134A
Q49AJ0-3;Q49AJ0-4;Q4 Q49AJ0-3;C 2;2;2;1 2;2;2;1 2;2;2;1		Protein FAM135B	FAM135B
F8W7Q4;Q96A26;E9PH F8W7Q4;Q 3;3;2 3;3;2 3;3;2		Protein FAM162A	FAM162A
K7ELZ8;K7EIY1;K7ENN5 K7ELZ8;K7 1;1;1;1;1 1;1;1;1;1 1;1;1;1;1		Protein FAM32A	FAM32A
Q92520;C9JP35;C9JMN Q92520 6;2;2 6;2;2 6;2;2		Protein FAM3C	FAM3C
Q9NUQ9;Q9NUQ9-2;E5 Q9NUQ9;Q 3;2;1;1;1;1 3;2;1;1;1;1 3;2;1;1;1;1		Protein FAM49B	FAM49B
Q6ZRV2;J3KPS2 Q6ZRV2;J3 22;19 22;19 22;19		Protein FAM83H	FAM83H
Q8NCA5-2;Q8NCA5 Q8NCA5-2; 1;1 1;1 1;1		Protein FAM98A	FAM98A
Q52LJ0;Q52LJ0-2 Q52LJ0;Q5 3;3 3;3 3;3		Protein FAM98B	FAM98B
Q13045-2;Q13045-3;Q1 Q13045-2;(2;2;2;1;1;1 2;2;2;1;1;1 2;2;2;1;1;1		Protein flightless-1 homolog	FLII
G5E994;Q5VW38-2;Q5 G5E994;Q5 1;1;1 1;1;1 1;1;1		Protein GPR107	GPR107
M0R2E1;M0QZW9;M0R M0R2E1;M 1;1;1;1;1 1;1;1;1;1 1;1;1;1;1		Protein GPR108	GPR108
P78504-2;P78504;Q9Y2 P78504-2;F 2;2;1;1 2;2;1;1 2;2;1;1		Protein jagged-1;Protein jag	JAG1;JAG2
A0A0U1RR22;Q9UNF0 A0A0U1RR 2;2;2;1;1;1 2;2;2;1;1;1 2;2;2;1;1;1		Protein kinase C and casein	PAC SIN2
E9PIE3;Q969G5 E9PIE3;Q9 2;2 2;2 2;2		Protein kinase C delta-bindin	PRKCDBP
P41743	P41743 1 1 1	Protein kinase C iota type	PRKCI
C9JEN3;C9IYT2;F8WDY4 C9JEN3;C9I 2;2;2;2;2 2;2;2;2;2 2;2;2;2;2		Protein lifeguard 3	TMBIM1
G3V1D4;Q9NUP9;HOYI9 G3V1D4;Q 2;2;1;1;1;1 2;2;1;1;1;1 2;2;1;1;1;1		Protein lin-7 homolog C;Pro	LIN7C;LIN7
Q9C0E8-3;Q9C0E8-2;Q9 Q9C0E8-3;(2;2;2;2 2;2;2;2 2;2;2;2		Protein lunapark	LNP
Q86UE4;E5RJU9;HOYB5 Q86UE4;E5 5;4;2 5;4;2 5;4;2		Protein LYRIC	MTDH
F5H6P7;P61326;Q96A7 F5H6P7;P6 2;2;2;1;1;1 2;2;2;1;1;1 2;2;2;1;1;1		Protein mago nashi homolog	MAGOHB;M
HOYBV6;Q9BXY0 HOYBV6;Q 1;1 1;1 1;1		Protein MAK16 homolog	MAK16
Q969L2	Q969L2 1 1 1	Protein MAL2	MAL2
Q92597;Q92597-3;Q92 Q92597;Q 9;8;8;4;3;2 9;8;8;4;3;2 9;8;8;4;3;2		Protein NDRG1	NDRG1
Q9BZQ8	Q9BZQ8 4 4 4	Protein Niban	FAM129A
Q9BPW8;F8WCR5;H7C2 Q9BPW8;F 2;1;1 2;1;1 2;1;1		Protein NipSnap homolog 1	NIPSNAP1
Q9UFN0	Q9UFN0 1 1 1	Protein NipSnap homolog 3	NIPSNAP3A
Q96C90	Q96C90 2 2 2	Protein phosphatase 1 regul	PPP1R14B
B5MBZ8;C9JD73;C9J17 B5MBZ8;C 1;1;1;1;1;1 1;1;1;1;1;1 1;1;1;1;1;1		Protein phosphatase 1 regul	PPP1R7
O15355	O15355 5 5 5	Protein phosphatase 1G	PPM1G
P29590-4;P29590-2;P29 P29590-4;F 12;12;12;1 12;12;12;1 12;12;12;1		Protein PML	PML
E7EPN9;Q9Y520-2;Q9Y E7EPN9;Q 2;2;2;2;2 2;2;2;2;2 2;2;2;2;2		Protein PRRC2C	PRRC2C
Q9P258	Q9P258 7 7 7	Protein RCC2	RCC2
Q5T092;A0A0A0MR06;Q5T092;A0 1;1;1;1 1;1;1;1 1;1;1;1		Protein RER1	RER1
Q14690	Q14690 6 6 6	Protein RRP5 homolog	PDCD11
R4GN98;P06703 R4GN98;P 2;2 2;2 2;2		Protein S100;Protein S100-4	S100A6
P60903	P60903 3 3 3	Protein S100-A10	S100A10
P31949	P31949 4 4 4	Protein S100-A11;Protein S	S100A11
Q99584	Q99584 1 1 1	Protein S100-A13	S100A13
Q9HCY8	Q9HCY8 5 5 5	Protein S100-A14	S100A14
Q96FQ6	Q96FQ6 2 2 2	Protein S100-A16	S100A16
P29034;R4GN49;Q5RHS P29034;R4 5;3;2 5;3;2 5;3;2		Protein S100-A2	S100A2

O43819	O43819	2	2	2	Protein SCO2 homolog, mitochondria	SCO2
P55735;P55735-2;P55735	P55735;P55735-2;P55735	4;3;3;3;2	4;3;3;3;2	4;3;3;3;2	Protein SEC13 homolog	SEC13
Q01105-2;A0A0C4DFV9	Q01105-2;A0A0C4DFV9	8;7;7;7;7;4	8;7;7;7;7;4	8;7;7;7;7;4	Protein SET;Protein SETSIP	SET;SETSIP
P18583-6;P18583-2;P18583	P18583-6;P18583-2;P18583	4;4;4;4;4;4	4;4;4;4;4;4	4;4;4;4;4;4	Protein SON	SON
H3BT44;H3BPQ9;H3BR6	H3BT44;H3BPQ9;H3BR6	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Protein spinster homolog 1	SPNS1
H7C4R5;Q969Z0-2;Q969	H7C4R5;Q969Z0-2;Q969	2;2;2	2;2;2	2;2;2	Protein TBRG4	TBRG4
Q92734-4;Q92734-3;Q92734	Q92734-4;Q92734-3;Q92734	4;4;4;4;3;3	4;4;4;4;3;3	4;4;4;4;3;3	Protein TFG	TFG
G5EA31;P53992-2;P539	G5EA31;P53992-2;P539	2;2;2	2;2;2	2;2;2	Protein transport protein Sec24C	SEC24C
D6RHZ5;H7BXG7;D6REX	D6RHZ5;H7BXG7;D6REX	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Protein transport protein Sec31A	SEC31A
B4DR61;P61619;P61619	B4DR61;P61619;P61619	4;4;3;2;2;2	4;4;3;2;2;2	4;4;3;2;2;2	Protein transport protein Sec61A1;Sec61B	SEC61A1;SEC61B
P60468;S4R3B5	P60468	3;1	3;1	3;1	Protein transport protein Sec61G	SEC61G
P60059	P60059	1	1	1	Protein unc-45 homolog A	UNC45A
A0A1W2PNX8;Q9H3U1	A0A1W2PNX8;Q9H3U1	1;1;1	1;1;1	1;1;1	Protein YIF1A	YIF1A
E9PS11;A6NGW1;O950	E9PS11;A6NGW1;O950	1;1;1	1;1;1	1;1;1	Protein YIPF5	YIPF5
Q969M3;Q969M3-3	Q969M3;Q969M3-3	1;1	1;1	1;1	Protein-L-isoaspartate O-methyltransferase	PCMT1
A0A0A0MRJ6;H7BY58;P	A0A0A0MRJ6;H7BY58;P	5;5;5;4;2	5;5;5;4;2	5;5;5;4;2	Protein-tyrosine-phosphatase	PTPRK
Q5TG12;E9PGC5;Q1526	Q5TG12;E9PGC5;Q1526	3;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	Prothymosin alpha;Prothymosin	PTMA
B8ZZQ6;P06454-2;P064	B8ZZQ6;P06454-2;P064	5;5;5;4;4;4	5;5;5;4;4;4	5;5;5;4;4;4	Protocadherin-1	PCDH1
Q08174;Q08174-2;D6R	Q08174;Q08174-2;D6R	7;7;2;1;1	7;7;2;1;1	7;7;2;1;1	Protocadherin-7	PCDH7
O60245;O60245-2;H0Y	O60245;O60245-2;H0Y	3;3;2;1	3;3;2;1	3;3;2;1	Purine nucleoside phosphorylase	PNP
P00491;G3V5M2;G3V2	P00491;G3V5M2;G3V2	7;5;3;1	7;5;3;1	7;5;3;1	Purine nucleoside phosphorylase	MTAP
J3QSB7;B4DUC8;Q1312	J3QSB7;B4DUC8;Q1312	4;4;4;4;4;4	4;4;4;4;4;4	4;4;4;4;4;4	Puromycin-sensitive aminopeptidase	NPEPPS;NP
E9PLK3;P55786;P55786	E9PLK3;P55786;P55786	8;8;6;4;2;1	8;8;6;4;2;1	8;8;6;4;2;1	Putative adenosylhomocysteinase	AHCYL1;AH
O43865-2;O43865;H0Y	O43865-2;O43865;H0Y	2;2;1;1;1;1	2;2;1;1;1;1	2;2;1;1;1;1	Putative ATP-binding cassette	ABCA11P
Q4W5N1	Q4W5N1	1	1	1	Putative ATP-dependent RNA helicase	DHX30
H7BXY3;Q7L2E3-3;Q7L2	H7BXY3;Q7L2E3-3;Q7L2	1;1;1;1	1;1;1;1	1;1;1;1	Putative elongation factor 1	EEF1A1P5;I
Q5VTE0;P68104;A0A08	Q5VTE0;P68104;A0A08	19;19;16;1	19;19;16;1	11;11;10;1	Putative heat shock protein	HSP90AB2F
Q58FF8	Q58FF8	10	1	1	Putative heat shock protein	HSP90AB4F
Q58FF6	Q58FF6	6	1	1	Putative helicase MOV-10	MOV10
Q5JR04;Q9HCE1;Q9HCE	Q5JR04;Q9HCE1;Q9HCE	3;3;1	3;3;1	3;3;1	Putative methyltransferase	C9orf114
Q5T280;R4GNG4	Q5T280;R4GNG4	2;1	2;1	2;1	Putative oxidoreductase GLYR1	GLYR1
K7EMM8;Q49A26-5;Q4	K7EMM8;Q49A26-5;Q4	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Putative RNA-binding protein	RBM15
A0A087WWP4;Q96T37	A0A087WWP4;Q96T37	2;2;2;2	2;2;2;2	2;2;2;2	Putative RNA-binding protein	LUC7L2
Q96HJ9-2;A0A0A6YYJ8	Q96HJ9-2;A0A0A6YYJ8	3;3;3;3;3;1	3;3;3;3;3;1	3;3;3;3;3;1	Putative transferase CAF17;IBA57	CAF17;IBA57
Q5T440	Q5T440	1	1	1	Putative uncharacterized protein	CRYM-AS1
A6NIL9	A6NIL9	1	1	1	Pyrroline-5-carboxylate reductase	PYCR2;PYC
A0A087WTV6;J3KR12;C	A0A087WTV6;J3KR12;C	2;2;2;1;1;1	2;2;2;1;1;1	2;2;2;1;1;1	Pyruvate carboxylase, mitochondrial	PC
P11498;E9PS68;P11498	P11498;E9PS68;P11498	8;4;3;2	8;4;3;2	8;4;3;2	Pyruvate dehydrogenase E1	PDHA1
P08559-3;P08559;P08559	P08559-3;P08559;P08559	3;3;3;3;2;2	3;3;3;3;2;2	3;3;3;3;2;2	Pyruvate dehydrogenase E1	PDHB
P11177-3;P11177-2;P11177	P11177-3;P11177-2;P11177	5;5;5;3;2	5;5;5;3;2	5;5;5;3;2	Pyruvate dehydrogenase protein	PDHX
O00330-3;O00330	O00330-3;O00330	1;1	1;1	1;1	Pyruvate kinase PKM;Pyruvate kinase	PKM
P14618;P14618-3;B4DN	P14618;P14618-3;B4DN	39;34;32;1	39;34;32;1	4;4;4;0;0;0	Pyruvate kinase PKM;Pyruvate kinase	PKM
P14618-2;H3BTN5;H3B	P14618-2;H3BTN5;H3B	36;33;22;2	1;1;0;1	1;1;0;1	Rab GDP dissociation inhibitor	GDI2
P50395;P50395-2;Q5SX	P50395;P50395-2;Q5SX	13;11;4;3;3	13;11;4;3;3	13;11;4;3;3	Rac GTPase-activating protein	RACGAP1
Q9H0H5;H0YIK5;F8VZ4	Q9H0H5;H0YIK5;F8VZ4	3;2;1;1	3;2;1;1	3;2;1;1	Ragulator complex protein I	LAMTOR1
Q6IAA8;H0YF11;F5H479	Q6IAA8;H0YF11;F5H479	4;2;2;2;2	4;2;2;2;2	4;2;2;2;2	Ragulator complex protein I	LAMTOR5
R4GMU8;E9PLX3;A0A0	R4GMU8;E9PLX3;A0A0	1;1;1;1	1;1;1;1	1;1;1;1	Ran GTPase-activating protein	RANGAP1
P46060;H0Y4Q3;B0QYT	P46060;H0Y4Q3;B0QYT	12;6;3;3;1	12;6;3;3;1	12;6;3;3;1	Ran-specific GTPase-activating protein	RANBP1
P43487-2;P43487;C9JJ3	P43487-2;P43487;C9JJ3	3;3;2;2;1;1	3;3;2;2;1;1	3;3;2;2;1;1	Ras GTPase-activating protein	G3BP1
Q13283;E5RIZ6;E5RI46	Q13283	9;3;2;2;2;2	9;3;2;2;2;2	9;3;2;2;2;2		

P46940;A0A0J9YXZ5;HC	P46940;A0.36;28;22;2	36;28;22;2	35;27;21;2	Ras GTPase-activating-like p	IQGAP1
Q15404-2;Q15404	Q15404-2;(2;2	2;2	2;2	Ras suppressor protein 1	RSU1
P63000;P63000-2;P607	P63000;P6.9;9;5	9;9;5	3;3;1	Ras-related C3 botulinum to	RAC1;RAC3
P15153;B1AH77;B1AH8	P15153;B1.8;7;7;6;3;3	2;2;2;1;0;0	2;2;2;1;0;0	Ras-related C3 botulinum to	RAC2
Q9HB90;Q9NQL2;Q9NC	Q9HB90;Q.2;2;1	2;2;1	2;2;1	Ras-related GTP-binding pro	RRAGC;RR/
P61026;P51153;A0A087	P61026 6;2;1	5;1;1	5;1;1	Ras-related protein Rab-10	RAB10
Q15907;Q15907-2;H3BI	Q15907;Q111;10;9;9;9	11;10;9;9;9	10;9;8;8;8;8	Ras-related protein Rab-11	RAB11B;RA
P61106;X6RFL8	P61106;X6.13;10	13;10	13;10	Ras-related protein Rab-14	RAB14
Q9NP72;Q9NP72-2;Q5V	Q9NP72;Q.7;6;5;5;4;4	7;6;5;5;4;4	7;6;5;5;4;4	Ras-related protein Rab-18	RAB18
P62820;E7END7;P6282	P62820;E7.11;9;8;6;2	11;9;8;6;2	4;4;4;3;0;0	Ras-related protein Rab-1A	RAB1A
Q9H0U4;E9PLD0;Q9292	Q9H0U4;E.11;10;5	4;4;2	3;3;1	Ras-related protein Rab-1B	RAB1B
Q9UL25	Q9UL25	4	4	Ras-related protein Rab-21	RAB21
P57735	P57735	2	1	Ras-related protein Rab-25	RAB25
H3BU81;H3BUD9;H3BS	H3BU81;H.1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Ras-related protein Rab-27	RAB27A
P61019;E9PKL7;P61019	P61019;E9.7;5;5;5;2;2	7;5;5;5;2;2	7;5;5;5;2;2	Ras-related protein Rab-2A	RAB2A;RAE
Q13637;P57729;H0YEA	Q13637 5;2;1	5;2;1	4;1;1	Ras-related protein Rab-32	RAB32
F5H157;Q15286;Q1528	F5H157;Q1.2;2;1	2;2;1	2;2;1	Ras-related protein Rab-35	RAB35
Q86YS6	Q86YS6	1	1	Ras-related protein Rab-43	RAB43
P51148;P51148-2;K7ER	P51148;P5.7;7;4;4;3;3	7;7;4;4;3;3	7;7;4;4;3;3	Ras-related protein Rab-5C	RAB5C
P20340-2;P20340;F5H3	P20340-2;F.5;5;3;3;3;2	5;5;3;3;3;2	5;5;3;3;3;2	Ras-related protein Rab-6A	RAB6A
P51149;C9J8S3;C9J4V0	P51149;C9.16;12;10;1	16;12;10;1	16;12;10;1	Ras-related protein Rab-7a	RAB7A
O14966;O14966-2;E9PL	O14966;O1.3;2;1;1	2;2;1;1	2;2;1;1	Ras-related protein Rab-7L1	RAB29
P61006-2;P61006	P61006-2;F.3;3	1;1	1;1	Ras-related protein Rab-8A	RAB8A
P51151;A0A1B0GUI0;Q	P51151 3;1;1	3;1;1	3;1;1	Ras-related protein Rab-9A	RAB9A
H7C3P7;P11233	H7C3P7;P1.4;4	4;4	3;3	Ras-related protein Ral-A	RALA
P61224-3;P61224;E7ES	P61224-3;F.6;6;5;5;5;4	6;6;5;5;5;4	2;2;2;2;1;1	Ras-related protein Rap-1b	RAP1B;RAP
P61225	P61225	4	4	Ras-related protein Rap-2b	RAP2B
P10301	P10301	3	1	Ras-related protein R-Ras	RRAS
P62070;P62070-4;E9PK	P62070;P6.4;4;3;3;2;1	4;4;3;3;2;1	2;2;2;2;2;0	Ras-related protein R-Ras2	RRAS2
P60602-2;P60602	P60602-2;F.1;1	1;1	1;1	Reactive oxygen species me	ROMO1
Q00765;B7Z332;B7Z51	Q00765 3;1;1;1;1;1	3;1;1;1;1;1	3;1;1;1;1;1	Receptor expression-enhanc	REEP5
Q96L35;P54760;P54753	Q96L35;P5.2;2;2	2;2;2	2;2;2	Receptor protein-tyrosine k	EPHB4;EPH
P10586-2;P10586;H0Y4	P10586-2;F.4;4;3;3;3;2	4;4;3;3;3;2	4;4;3;3;3;2	Receptor-type tyrosine-pro	PTPRF
Q9BRX8-2;Q9BRX8	Q9BRX8-2;.4;4	4;4	4;4	Redox-regulatory protein F	FAM213A
P18754;P18754-2;C9JW	P18754;P1.8;8;7;6;6;6	8;8;7;6;6;6	8;8;7;6;6;6	Regulator of chromosome c	RCC1
Q96DB5-2;Q96DB5;H0Y	Q96DB5-2; 3;3;2;2;2;2	3;3;2;2;2;2	3;3;2;2;2;2	Regulator of microtubule dy	RMDN1
H0YNE5;H0YLG5;Q96TC	H0YNE5;HC.1;1;1	1;1;1	1;1;1	Regulator of microtubule dy	RMDN3
Q92900-2;Q92900	Q92900-2;(1;1	1;1	1;1	Regulator of nonsense tran	UPF1
Q8WUF5;K7EN03	Q8WUF5;K.2;1	2;1	2;1	RelA-associated inhibitor	PPP1R13L
P35250;P35250-2;H7C5	P35250;P3.3;2;1;1;1;1	3;2;1;1;1;1	3;2;1;1;1;1	Replication factor C subunit	RFC2
P40938-2;P40938;A0A0	P40938-2;F.5;5;1	5;5;1	5;5;1	Replication factor C subunit	RFC3
C9JZI1;P35249-2;P3524	C9JZI1;P35.2;2;2;1;1;1	2;2;2;1;1;1	2;2;2;1;1;1	Replication factor C subunit	RFC4
P40937-2;P40937;F5H3	P40937-2;F.2;2;1;1;1	2;2;1;1;1	2;2;1;1;1	Replication factor C subunit	RFC5
B5MC59;P35244	B5MC59;P.3;3	3;3	3;3	Replication protein A 14 kD	RPA3
P15927;P15927-2;P159	P15927;P1.2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	Replication protein A 32 kD	RPA2
P27694;I3L4R8	P27694;I3L.2;1	2;1	2;1	Replication protein A 70 kD	RPA1
Q15293;Q15293-2	Q15293;Q19;7	9;7	9;7	Reticulocalbin-1	RCN1
H0YL43;Q14257;Q1425	H0YL43;Q1.3;3;3	3;3;3	3;3;3	Reticulocalbin-2	RCN2
Q9NQC3-2;Q9NQC3-5;C	Q9NQC3-2;7;7;7;6;5;4	7;7;7;6;5;4	7;7;7;6;5;4	Reticulon-4;Reticulon	RTN4
P06400	P06400	1	1	Retinoblastoma-associated	RB1



Q8NFJ5;F5GWG3	Q8NFJ5;F5	2;1	2;1	2;1	Retinoic acid-induced prote	GPRC5A
Q8IZV5;E5RK48	Q8IZV5	3;1	3;1	3;1	Retinol dehydrogenase 10	RDH10
Q8TC12;G3V2G6;Q8TC1	Q8TC12;G3	5;4;4;3;3;2	5;4;4;3;3;2	5;4;4;3;3;2	Retinol dehydrogenase 11	RDH11
Q9HBH5	Q9HBH5	2	2	2	Retinol dehydrogenase 14	RDH14
J3KRE2;J3KTF8;J3QQX2;J3KRE2;J3K	J3KRE2;J3K	3;3;3;3;2;2	3;3;3;3;2;2	3;3;3;3;2;2	Rho GDP-dissociation inhibi	ARHGDI
F5H2R5;F5H6Q0;F5H3P	F5H2R5;F5	2;2;2;2;1	2;2;2;2;1	2;2;2;2;1	Rho GDP-dissociation inhibi	ARHGDI
Q07960;H0YE29;E9PNR	Q07960;H0	5;4;1	5;4;1	5;4;1	Rho GTPase-activating prot	ARHGAP1
R4GNI4;R4GMS4;Q14C	R4GNI4;R4	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Rho GTPase-activating prot	ARHGAP19
Q5JR08;P08134;E9PQH	Q5JR08;P0	5;5;4;3;3;3	5;5;4;3;3;3	1;1;1;0;0;0	Rho-related GTP-binding pr	RHOC;RHO
P84095	P84095	6	5	5	Rho-related GTP-binding pr	RHOG
P13489;E9PIM9;E9PMJ	P13489;E9	10;6;5;5;4	10;6;5;5;4	10;6;5;5;4	Ribonuclease inhibitor	RNH1
P23921;E9PL69;E9PP77	P23921;E9	3;2;1;1	3;2;1;1	3;2;1;1	Ribonucleoside-diphosphat	RRM1
C9JXC1;A0A286YFD6;P3	C9JXC1;A0	4;4;4;4;1;1	4;4;4;4;1;1	4;4;4;4;1;1	Ribonucleoside-diphosphat	RRM2
P60891;B1ALA9;P60891	P60891;B1	3;2;2;1	2;1;1;1	2;1;1;1	Ribose-phosphate pyrophos	PRPS1
P11908;P11908-2;D3YT	P11908;P1	4;4;3;2;1;1	4;4;3;2;1;1	3;3;3;2;0;1	Ribose-phosphate pyrophos	PRPS2
Q9Y4W2-4;Q9Y4W2-2;C	Q9Y4W2-4	1;1;1	1;1;1	1;1;1	Ribosomal biogenesis prote	LAS1L
O76021;J3QSV6;O7602	O76021;J3	16;15;8;6;6	16;15;8;6;6	16;15;8;6;6	Ribosomal L1 domain-conta	RSL1D1
J3QR09;J3KTE4;P84098	J3QR09;J3	4;4;4;3	4;4;4;3	4;4;4;3	Ribosomal protein L19;60S	RPL19
P56182;D6RE82	P56182	5;2	5;2	5;2	Ribosomal RNA processing	RRP1
Q92979;A0A087WVM7	Q92979;A0	3;2;1;1	3;2;1;1	3;2;1;1	Ribosomal RNA small subun	EMG1
Q9Y3A4	Q9Y3A4	1	1	1	Ribosomal RNA-processing	RRP7A
Q14692	Q14692	5	5	5	Ribosome biogenesis protei	BMS1
Q14137;Q14137-2;A0A	Q14137;Q1	7;6;1	7;6;1	7;6;1	Ribosome biogenesis protei	BOP1
Q8TDN6	Q8TDN6	6	6	6	Ribosome biogenesis protei	BRX1
A0A0A0MQZ6;O95478;A0A0A0MC	A0A0A0MC	3;3;1	3;3;1	3;3;1	Ribosome biogenesis protei	NSA2
Q9GZL7	Q9GZL7	4	4	4	Ribosome biogenesis protei	WDR12
Q15050	Q15050	2	2	2	Ribosome biogenesis regula	RRS1
F8WE72;A0A087X020;C	F8WE72;A0	2;2;2	2;2;2	2;2;2	Ribosome maturation prote	SBDS
Q5VXN0;Q9H7B2;U3KQ	Q5VXN0;Q	4;4;1;1	4;4;1;1	4;4;1;1	Ribosome production facto	RPF2
A0A0A0MRV0;Q9P2E9	A0A0A0MR	17;17;17;1	17;17;17;1	17;17;17;1	Ribosome-binding protein 1	RRBP1
Q96E11-8;Q96E11-3;Q9	Q96E11-8;(	5;5;5;3;2;2	5;5;5;3;2;2	5;5;5;3;2;2	Ribosome-recycling factor,	MRRF
D6RAL1;Q969S9-5;Q96	D6RAL1;Q9	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Ribosome-releasing factor	GFM2
P38159;P38159-2;H3BT	P38159;P3	11;10;8;7;7	11;10;8;7;7	11;10;8;7;7	RNA-binding motif protein,	RBMX;RBM
Q96PK6;Q96PK6-2	Q96PK6	10;3	10;3	8;1	RNA-binding protein 14	RBM14
Q96PK6-5;A0A0A6YYI9	Q96PK6-5;	4;2;2;2;2;2	2;0;0;0;0;0	0;0;0;0;0;0	RNA-binding protein 14	RBM14;RBI
P49756;E9PQU5;P4975	P49756;E9	3;2;2;2;1;1	3;2;2;2;1;1	3;2;2;2;1;1	RNA-binding protein 25	RBM25
U3KPZ7;Q9P2N5	U3KPZ7;Q9	1;1	1;1	1;1	RNA-binding protein 27	RBM27
Q9NW13;Q9NW13-2;C9	Q9NW13;C	5;4;2;2	5;4;2;2	5;4;2;2	RNA-binding protein 28	RBM28
Q5TCT4;A2A2V2;P4269	Q5TCT4;A2	2;2;2;2	2;2;2;2	2;2;2;2	RNA-binding protein 34	RBM34
A0A0U1RQH7;G3XAC6;A0A0U1RQ	A0A0U1RQ	7;7;7;7;6	7;7;7;7;6	7;7;7;7;6	RNA-binding protein 39	RBM39
Q9Y5S9;Q9Y5S9-2;A0A	Q9Y5S9;Q9	3;2;1	3;2;1	3;2;1	RNA-binding protein 8A	RBM8A
B0QYK0;Q01844-6;Q01	B0QYK0;Q	6;6;6;6;5	6;6;6;6;5	6;6;6;6;5	RNA-binding protein EWS	EWSR1
H3BPE7;P35637-2;P356	H3BPE7;P3	5;5;5	3;3;3	3;3;3	RNA-binding protein FUS	FUS
H3BUR4;Q9ULX3	H3BUR4;Q	1;1	1;1	1;1	RNA-binding protein NOB1	NOB1
Q9NRX1;F8WBJ6	Q9NRX1;F8	2;1	2;1	2;1	RNA-binding protein PNO1	PNO1
Q5QPL9;Q9UKM9-2;Q9	Q5QPL9;Q	5;5;5;4;3;2	5;5;5;4;3;2	5;5;5;4;3;2	RNA-binding protein Raly	RALY
H3BV80;H3BMS0;H3BM	H3BV80;H3	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	RNA-binding protein with s	RNPS1
Q5TZA2-2;Q5TZA2;B1A	Q5TZA2-2;(	2;2;1	2;2;1	2;2;1	Rootletin	CROCC
M0R299;M0QXL5;P220	M0R299;M	5;5;5;4;2;2	5;5;5;4;2;2	5;5;5;4;2;2	rRNA 2-O-methyltransferas	FBL
Q6IN84	Q6IN84	1	1	1	rRNA methyltransferase 1,	MRM1

A6NHQ2	A6NHQ2	1	1	1	rRNA/tRNA 2-O-methyltran	FBLL1
G3V2M5;G3V5S9;G3V1	G3V2M5;G	1;1;1;1	1;1;1;1	1;1;1;1	rRNA-processing protein	FC FCF1
Q5JTH9-2;Q5JTH9-3;Q5	Q5JTH9-2;(	4;4;4;1	4;4;4;1	4;4;4;1	RRP12-like protein	RRP12
Q9Y3B9	Q9Y3B9	3	3	3	RRP15-like protein	RRP15
Q9Y265;Q9Y265-2;E7ET	Q9Y265;Q9	12;9;7;6;3;	12;9;7;6;3;	12;9;7;6;3;	RuvB-like 1	RUVBL1
Q9Y230-2;Q9Y230;M0R	Q9Y230-2;(	13;13;9;4;3	13;13;9;4;3	13;13;9;4;3	RuvB-like 2	RUVBL2
P31153;P31153-2	P31153;P3	5;4	5;4	5;4	S-adenosylmethionine synt	MAT2A
F8VZQ9;H0YHG0;P8297	F8VZQ9;H0	2;2;2	2;2;2	2;2;2	SAP domain-containing ribo	SARNP
P16615;P16615-5;P166	P16615;P1	22;21;21;2	22;21;21;2	22;21;21;2	Sarcoplasmic/endoplasmic	ATP2A2
Q15424-2;Q15424;Q15	Q15424-2;(	9;9;9;9;1	9;9;9;9;1	4;4;4;4;1	Scaffold attachment factor	SAFB
Q14151;Q14151-2	Q14151	8;1	3;1	3;1	Scaffold attachment factor	SAFB2
B7ZKQ9;F5H4X0;Q8WT	B7ZKQ9;F5	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Scavenger receptor class B	SCARB1
Q08AF3	Q08AF3	1	1	1	Schlafen family member 5	SLFN5
Q8WVM8;Q8WVM8-2;(	Q8WVM8;(	4;3;3;1;1;1	4;3;3;1;1;1	4;3;3;1;1;1	Sec1 family domain-contain	SCFD1
Q12765;Q12765-2;Q12	Q12765;Q1	3;3;2;1;1;1	3;3;2;1;1;1	3;3;2;1;1;1	Secernin-1	SCRN1
A0A087WZA6;O15126-	A0A087WZ	1;1;1	1;1;1	1;1;1	Secretory carrier-associatec	SCAMP1
O15127	O15127	1	1	1	Secretory carrier-associatec	SCAMP2
O14828;O14828-2	O14828;O1	4;3	4;3	4;3	Secretory carrier-associatec	SCAMP3
Q969E2-2;Q969E2	Q969E2-2;(	1;1	1;1	1;1	Secretory carrier-associatec	SCAMP4
P35270	P35270	1	1	1	Sepiapterin reductase	SPR
D6RDP1;D6R9Y6;D6RD	D6RDP1;D6	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Septin-6;Septin-11	SEPT11;SEF
Q13501;Q13501-2;E7E	Q13501;Q1	14;11;10;6	14;11;10;6	14;11;10;6	Sequestosome-1	SQSTM1
P83111-2;P83111	P83111-2;F	2;2	2;2	2;2	Serine beta-lactamase-like	LACTB
P34897-3;P34897;P348	P34897-3;F	15;15;14;8	15;15;14;8	14;14;13;7	Serine hydroxymethyltransf	SHMT2
Q9NRX5	Q9NRX5	4	4	4	Serine incorporator 1	SERINC1
O15269;O15269-2	O15269	7;3	7;3	7;3	Serine palmitoyltransferase	SPTLC1
O15270;H0YJV2	O15270;H0	2;1	2;1	2;1	Serine palmitoyltransferase	SPTLC2
M0R088;E9PCT1;A9Z1X	M0R088;E9	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Serine/arginine repetitive r	SRRM1
Q9UQ35;Q9UQ35-2;I3L	Q9UQ35	13;4;2;2;2;	13;4;2;2;2;	13;4;2;2;2;	Serine/arginine repetitive r	SRRM2
J3KTL2;Q07955;Q07955	J3KTL2;Q0	7;7;6;6;4;1	7;7;6;6;4;1	7;7;6;6;4;1	Serine/arginine-rich splicing	SRSF1
Q5JRI1;O75494-5;O754	Q5JRI1;O7	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	Serine/arginine-rich splicing	SRSF10;SR
Q5T760;Q05519-2;Q05	Q5T760;QC	1;1;1	1;1;1	1;1;1	Serine/arginine-rich splicing	SRSF11
J3KP15;Q01130;J3QL05	J3KP15;Q0	5;5;4;4;2;2	5;5;4;4;2;2	5;5;4;4;2;2	Serine/arginine-rich splicing	SRSF2
A0A087X2D0;P84103-2;A0A087X2	A0A087X2	4;4;4	3;3;3	3;3;3	Serine/arginine-rich splicing	SRSF3
Q13243-3;Q13243;B4D	Q13243-3;(	3;3;2;2;1;1	2;2;1;1;1;1	2;2;1;1;1;1	Serine/arginine-rich splicing	SRSF5
Q13247-3;Q13247;A0A	Q13247-3;(	5;5;3;3;1	5;5;3;3;1	4;4;2;2;1	Serine/arginine-rich splicing	SRSF6;SRSF
A0A0B4J1Z1;C9JAB2;Q1A0A0B4J1Z	A0A0B4J1Z	6;6;6;6;6;6	6;6;6;6;6;6	5;5;5;5;5;5	Serine/arginine-rich splicing	SRSF7
Q13242;H0YIB4;S4R3G	Q13242;HC	7;5;3	7;5;3	7;5;3	Serine/arginine-rich splicing	SRSF9
H0Y630;B4DR80;Q9Y6E	H0Y630;B4	2;2;2;2;1;1	2;2;2;2;1;1	1;1;1;1;1;1	Serine/threonine-protein ki	STK24
E7ETY4;E9PC69;Q7KZ17	E7ETY4;E9	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	Serine/threonine-protein ki	MARK2
C9JIG9;O95747	C9JIG9;O9	1;1	1;1	1;1	Serine/threonine-protein ki	OXSR1
Q13177;B1AKS5;H7C1X	Q13177	5;1;1;1;1;1	5;1;1;1;1;1	5;1;1;1;1;1	Serine/threonine-protein ki	PAK2
H0YJF7;Q99986	H0YJF7;Q9	1;1	1;1	1;1	Serine/threonine-protein ki	VRK1
P63151;P63151-2;E5RF	P63151;P6	2;2;1;1;1;1	2;2;1;1;1;1	2;2;1;1;1;1	Serine/threonine-protein pl	PPP2R2A;P
P30153;C9J9C1;B3KQV	P30153;C9	11;7;7;3;3;3	11;7;7;3;3;3	11;7;7;3;3;3	Serine/threonine-protein pl	PPP2R1A
A6PVN9;F6WIT2;A6PVN	A6PVN9;F6	3;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	Serine/threonine-protein pl	PPP2R4
P67775;P67775-2;P627	P67775;P6	7;6;6;3;3;2	7;6;6;3;3;2	6;5;5;3;2;2	Serine/threonine-protein pl	PPP2CA;PP
Q96HS1-2;Q96HS1;F5G	Q96HS1-2;(	5;5;1	5;5;1	5;5;1	Serine/threonine-protein pl	PGAM5
P62136-3;P62136;P621	P62136-3;F	8;8;8;5	2;2;2;1	2;2;2;1	Serine/threonine-protein pl	PPP1CA
P62140;E7ETD8;C9JP48	P62140;E7	19;5;4;3;1;1	9;5;4;3;1;1	3;1;2;2;0;0	Serine/threonine-protein pl	PPP1CB

E7ETC2;Q08209-5;Q082	E7ETC2;Q0 2;2;2;2;1	2;2;2;2;1	2;2;2;2;1	2;2;2;2;1	Serine/threonine-protein pl	PPP3CA;PP
H3BV22;H3BTA2;P6051	H3BV22;H3 4;4;4;2;1;1	3;3;3;2;1;1	3;3;3;2;1;1	3;3;3;2;1;1	Serine/threonine-protein pl	PPP4C
F8VYE8;P36873;P36873	F8VYE8;P3 8;8;8;7;7;4	2;2;2;2;1;2	2;2;2;2;1;2	2;2;2;2;1;2	Serine/threonine-protein pl	PPP1CC
Q9Y3F4;Q9Y3F4-2;H0YF	Q9Y3F4;Q9 5;5;2	5;5;2	5;5;2	5;5;2	Serine-threonine kinase rec	STRAP
Q5T5C7;P49591	Q5T5C7;P4 4;4	4;4	4;4	4;4	Serine--tRNA ligase, cytopla	SARS
M0QWZ7;M0R2C6;Q9N	M0QWZ7;M 2;2;2;2;1;1	2;2;2;2;1;1	2;2;2;2;1;1	2;2;2;2;1;1	Serine--tRNA ligase, mitoch	SARS2
F8WE70;A0A0A0MQW	F8WE70;A0 4;4;4;4;2	4;4;4;4;2	4;4;4;4;2	4;4;4;4;2	Serpin B13	SERPINB13
P36952;P36952-2;C9JL	P36952;P3 14;8;6	14;8;6	14;8;6	14;8;6	Serpin B5	SERPINB5
A0A024QZX5;A0A087X1	A0A024QZ 6;6;6;1;1;1	6;6;6;1;1;1	6;6;6;1;1;1	6;6;6;1;1;1	Serpin B6	SERPINB6
P50454;E9PR70;E9PPV	P50454;E9 13;10;10;8	13;10;10;8	13;10;10;8	13;10;10;8	Serpin H1	SERPINH1
Q9BXP5-5;Q9BXP5-4;Q	Q9BXP5-5; 3;3;3;3;3;2	3;3;3;3;3;2	3;3;3;3;3;2	3;3;3;3;3;2	Serrate RNA effector molec	SRRT
J3QT77;A0A0J9YYG4;AC	J3QT77;A0 1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Serum paraoxonase/arylest	PON2
U3KQT1;H7BZT7;X6RA1	U3KQT1;H7 1;1;1;1	1;1;1;1	1;1;1;1	1;1;1;1	S-formylglutathione hydroly	ESD
Q5T123;Q9H299	Q5T123;Q9 2;2	2;2	2;2	2;2	SH3 domain-binding glutam	SH3BGR13
Q9NR45	Q9NR45	2	2	2	Sialic acid synthase	NANS
A0A0A0MS41;A0A1P0A	A0A0A0MS 6;6;6;5	6;6;6;5	6;6;6;5	6;6;6;5	Sideroflexin;Sideroflexin-3	SFXN3
Q9H9B4;D6RDG7;S4R2	Q9H9B4;D6 6;3;3;3;1	6;3;3;3;1	6;3;3;3;1	6;3;3;3;1	Sideroflexin-1	SFXN1
H0YNG3;P67812-4;P67	H0YNG3;P6 2;2;2;2;1;1	2;2;2;2;1;1	2;2;2;2;1;1	2;2;2;2;1;1	Signal peptidase complex c	SEC11A
Q9Y6A9;C9JBL1;X6R2S6	Q9Y6A9;C9 3;2;2	3;2;2	3;2;2	3;2;2	Signal peptidase complex s	SPCS1
E9PL01;A0A087WUC6;E	E9PL01;A0 4;4;4;4;3	4;4;4;4;3	4;4;4;4;3	4;4;4;4;3	Signal peptidase complex s	SPCS2
P61009	P61009	3	3	3	Signal peptidase complex s	SPCS3
H0YLA2;P37108	H0YLA2;P3 4;4	4;4	4;4	4;4	Signal recognition particle 1	SRP14
A0A087WYR0;P09132;A	A0A087WY 2;2;1	2;2;1	2;2;1	2;2;1	Signal recognition particle 1	SRP19
P49458;E9PE20;P49458	P49458;E9 4;3;3	4;3;3	4;3;3	4;3;3	Signal recognition particle 9	SRP9
Q9Y5M8;H7C4H2	Q9Y5M8;H 6;5	6;5	6;5	6;5	Signal recognition particle r	SRPRB
Q9UHB9-4;Q9UHB9-2;C	Q9UHB9-4; 3;3;3;2	3;3;3;2	3;3;3;2	3;3;3;2	Signal recognition particle s	SRP68
O76094;D6RDY6;O7609	O76094;D6 3;2;2	3;2;2	3;2;2	3;2;2	Signal recognition particle s	SRP72
J3KPM9;P42224-2;P422	J3KPM9;P4 5;5;5;2;2;1	5;5;5;2;2;1	5;5;5;2;2;1	5;5;5;2;2;1	Signal transducer and activ	STAT1
Q92783-2;Q92783	Q92783-2; 1;1	1;1	1;1	1;1	Signal transducing adapter	STAM
O75886-2;O75886	O75886-2; 1;1	1;1	1;1	1;1	Signal transducing adapter	STAM2
Q04837;A0A0G2JLD8;E	Q04837;A0 4;3;3;2	4;3;3;2	4;3;3;2	4;3;3;2	Single-stranded DNA-bindin	SSBP1
G3V1B8;H0YEB6;O6023	G3V1B8;HC 1;1;1	1;1;1	1;1;1	1;1;1	Sjogren syndrome/sclerod	SSSCA1
K7EMD6;O43765	K7EMD6;O 2;2	2;2	2;2	2;2	Small glutamine-rich tetratr	SGTA
P62306	P62306	2	2	2	Small nuclear ribonucleoprc	SNRPF
P62314;J3QLR7;J3QLI9	P62314;J3 2;1;1	2;1;1	2;1;1	2;1;1	Small nuclear ribonucleoprc	SNRPD1
P62316-2;P62316;K7ER	P62316-2;F 3;3;2	3;3;2	3;3;2	3;3;2	Small nuclear ribonucleoprc	SNRPD2
P62318-2;P62318;H3BT	P62318-2;F 4;4;2	4;4;2	4;4;2	4;4;2	Small nuclear ribonucleoprc	SNRPD3
J3QLE5;P14678-2;P631	J3QLE5;P1 5;5;5;5;5;5	5;5;5;5;5;5	5;5;5;5;5;5	5;5;5;5;5;5	Small nuclear ribonucleoprc	SNRPN;SNF
O75691	O75691	3	3	3	Small subunit processome c	UTP20
B8ZZN6;P63165;B8ZZJ0	B8ZZN6;P6 3;3;2;2;1;1	3;3;2;2;1;1	3;3;2;2;1;1	3;3;2;2;1;1	Small ubiquitin-related moc	SUMO1
P61956-2;P61956;A8MI	P61956-2;F 2;2;1;1;1;1	2;2;1;1;1;1	2;2;1;1;1;1	2;2;1;1;1;1	Small ubiquitin-related moc	SUMO2;SU
G3V5R3;G3V3A4;Q1357	G3V5R3;G3 1;1;1	1;1;1	1;1;1	1;1;1	SNW domain-containing prc	SNW1
P05023-4;P05023;P050	P05023-4;F 28;28;25;1	28;28;25;1	27;27;24;1	27;27;24;1	Sodium/potassium-transpo	ATP1A1
P05026-2;P05026;V9GY	P05026-2;F 4;4;3	4;4;3	4;4;3	4;4;3	Sodium/potassium-transpo	ATP1B1
P54709;C9JXZ1;C9JA36	P54709;C9 3;2;2;2;1	3;2;2;2;1	3;2;2;2;1	3;2;2;2;1	Sodium/potassium-transpo	ATP1B3
F8VX04;Q9H2H9	F8VX04;Q9 2;2	2;2	2;2	2;2	Sodium-coupled neutral am	SLC38A1
Q96QD8;Q96QD8-2;F8	Q96QD8;Q 3;2;1;1	3;2;1;1	3;2;1;1	3;2;1;1	Sodium-coupled neutral am	SLC38A2
Q8WUX1;C9JJU1;C9JM	Q8WUX1;C 4;2;2;2;2;2	4;2;2;2;2;2	4;2;2;2;2;2	4;2;2;2;2;2	Sodium-coupled neutral am	SLC38A5
H7BZK4;Q8WUM9	H7BZK4;Q8 1;1	1;1	1;1	1;1	Sodium-dependent phosph	SLC20A1
G3XAL9;P55011-3;P550	G3XAL9;P5 2;2;2	2;2;2	2;2;2	2;2;2	Solute carrier family 12 mer	SLC12A2

P11166	P11166	3	3	3	Solute carrier family 2, facilitator	SLC2A1
Q9NQZ2	Q9NQZ2	1	1	1	Something about silencing factor	UTP3
Q00796;H0YLA4;H0YKB	Q00796;H0YLA4;H0YKB	8;6;3;3	8;6;3;3	8;6;3;3	Sorbitol dehydrogenase	SORD
C9J0K6;P30626-3;P3062	C9J0K6;P30626-3;P3062	5;5;5;3	5;5;5;3	5;5;5;3	Sorcin	SRI
Q9Y512	Q9Y512	2	2	2	Sorting and assembly machinery	SAMM50
Q9UMY4;A0A087X0R6;A0A087X0R6	Q9UMY4;A0A087X0R6;A0A087X0R6	2;1;1;1	2;1;1;1	2;1;1;1	Sorting nexin-12	SNX12
O60493-2;O60493;O60493	O60493-2;O60493;O60493	2;2;1;1	2;2;1;1	2;2;1;1	Sorting nexin-3	SNX3
Q9NUQ6-2;Q9NUQ6;B8Q9NUQ6-2	Q9NUQ6-2;Q9NUQ6;B8Q9NUQ6-2	10;10;9;9;9	10;10;9;9;9	10;10;9;9;9	SPATS2-like protein	SPATS2L
Q9BW04-2;Q9BW04	Q9BW04-2;Q9BW04	2;2	2;2	2;2	Specifically androgen-regulated	SARG
A0A0D9SF54;A0A0D9SF54	A0A0D9SF54;A0A0D9SF54	29;29;29;29	29;29;29;29	29;29;29;29	Spectrin alpha chain, non-erythrocyte	SPTAN1
A0A087WUZ3;Q01082;A0A087WL	A0A087WUZ3;Q01082;A0A087WL	17;17;14;1	17;17;14;1	17;17;14;1	Spectrin beta chain, non-erythrocyte	SPTBN1
E5RJR5;P63208;E5RGM	E5RJR5;P63208;E5RGM	3;3;1;1;1	3;3;1;1;1	3;3;1;1;1	S-phase kinase-associated protein	SKP1
H7BXF4;Q9NXE4-3;Q9NH7BXF4	H7BXF4;Q9NXE4-3;Q9NH7BXF4	2;2;2;2;1	2;2;2;2;1	2;2;2;2;1	Sphingomyelin phosphodiesterase	SMPD4
H0Y3V8;H7BXL7;O9547	H0Y3V8;H7BXL7;O9547	2;2;2	2;2;2	2;2;2	Sphingosine-1-phosphate lyase	SGPL1
Q13838;Q13838-2;A0A087X0R6	Q13838;Q13838-2;A0A087X0R6	9;9;7;7;5;5	9;9;7;7;5;5	2;2;2;2;1;1	Spliceosome RNA helicase	DDX39B
Q15637-4;Q15637-6;Q15637-4	Q15637-4;Q15637-6;Q15637-4	4;4;4;4;4	4;4;4;4;4	4;4;4;4;4	Splicing factor 1	SF1
Q15459;Q15459-2;H7C0	Q15459;Q15459-2;H7C0	3;2;1	3;2;1	3;2;1	Splicing factor 3A subunit 1	SF3A1
Q12874	Q12874	4	4	4	Splicing factor 3A subunit 3	SF3A3
O75533;F8WC19;B4DG	O75533;F8WC19;B4DG	9;1;1;1;1	9;1;1;1;1	9;1;1;1;1	Splicing factor 3B subunit 1	SF3B1
Q13435;E9PJT3;E9PJ04	Q13435;E9PJT3;E9PJ04	6;5;5;5;4;1	6;5;5;5;4;1	6;5;5;5;4;1	Splicing factor 3B subunit 2	SF3B2
Q15393;Q15393-3;Q15393	Q15393;Q15393-3;Q15393	10;3;2;1;1	10;3;2;1;1	10;3;2;1;1	Splicing factor 3B subunit 3	SF3B3
Q9Y3B4	Q9Y3B4	2	2	2	Splicing factor 3B subunit 6	SF3B6
P0DN76;Q01081;Q01081	P0DN76;Q01081;Q01081	4;4;3;2;2	4;4;3;2;2	4;4;3;2;2	Splicing factor U2AF 35 kDa	U2AF1;U2AF2
K7ENG2;P26368-2;P26368	K7ENG2;P26368-2;P26368	6;6;6	6;6;6	6;6;6	Splicing factor U2AF 65 kDa	U2AF2
P23246;P23246-2;H0Y9	P23246;P23246-2;H0Y9	17;15;4;1	17;15;4;1	16;14;4;1	Splicing factor, proline- and serine-rich	SFPQ
Q8WW59	Q8WW59	3	3	3	SPRY domain-containing protein	SPRYD4
E9PNM1;P37268;A0A11E9PNM1	E9PNM1;P37268;A0A11E9PNM1	11;11;10;1	11;11;10;1	11;11;10;1	Squalene synthase	FDFT1
F8VV04;Q15020-4;Q15020	F8VV04;Q15020-4;Q15020	1;1;1	1;1;1	1;1;1	Squamous cell carcinoma antigen	SART3
A0A087WUN7;H0YJ40;A0A087WL	A0A087WUN7;H0YJ40;A0A087WL	3;3;3;3;3	3;3;3;3;3	3;3;3;3;3	SRA stem-loop-interacting factor	SLIRP
Q14247;Q14247-3;Q14247	Q14247;Q14247-3;Q14247	17;16;15;5	17;16;15;5	17;16;15;5	Src substrate cortactin	CTTN
Q7KZF4;H7C597	Q7KZF4;H7C597	16;5	16;5	16;5	Staphylococcal nuclease domain	SND1
P16949;A2A2D0;P16949	P16949;A2A2D0;P16949	5;4;4	5;4;4	5;4;4	Stathmin	STMN1
E5RGX5;Q93045;Q9304	E5RGX5;Q93045;Q9304	1;1;1	1;1;1	1;1;1	Stathmin;Stathmin-2	STMN2
Q5K651;C9JKF1	Q5K651;C9JKF1	2;1	2;1	2;1	Sterile alpha motif domain-containing	SAMD9
A0A087X1T2;G3V0I8;Q01081	A0A087X1T2;G3V0I8;Q01081	1;1;1;1	1;1;1;1	1;1;1;1	Sterol regulatory element-binding	SREBF2
Q15738;C9JDR0	Q15738;C9JDR0	6;5	6;5	6;5	Sterol-4-alpha-carboxylate	NSDHL
A0A087WYB4;Q9UJZ1;A0A087WY	A0A087WYB4;Q9UJZ1;A0A087WY	8;8;7;3	8;8;7;3	8;8;7;3	Stomatin-like protein 2, mitochondrial	STOML2
Q8WXE9;Q8WXE9-3	Q8WXE9;Q8WXE9-3	1;1	1;1	1;1	Stonin-2	STON2
P38646;D6RJI2;H0YBG6	P38646;D6RJI2;H0YBG6	33;6;5;3;3	33;6;5;3;3	32;6;5;3;3	Stress-70 protein, mitochondrial	HSPA9
P31948;P31948-2;P31948	P31948;P31948-2;P31948	16;16;14;7	16;16;14;7	16;16;14;7	Stress-induced phosphoprotein	STIP1
Q9HCN8	Q9HCN8	2	2	2	Stromal cell-derived factor	SDF2L1
H0YDB2;E9PNJ4;G0XQ3	H0YDB2;E9PNJ4;G0XQ3	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Stromal interaction molecule	STIM1
O95347;O95347-2;Q5T8	O95347;O95347-2;Q5T8	6;5;1;1	6;5;1;1	6;5;1;1	Structural maintenance of chromosomes	SMC2
Q9UQE7	Q9UQE7	5	5	5	Structural maintenance of chromosomes	SMC3
G8JLG1;Q14683;H0Y7K8	G8JLG1;Q14683;H0Y7K8	4;4;1;1	4;4;1;1	4;4;1;1	Structural maintenance of chromosomes	SMC1A
E9PD53;Q9NTJ3-2;Q9NTJ3	E9PD53;Q9NTJ3-2;Q9NTJ3	6;6;6;3;2;2	6;6;6;3;2;2	6;6;6;3;2;2	Structural maintenance of chromosomes	SMC4
P31040-2;P31040;D6RF	P31040-2;P31040;D6RF	8;8;7;6;6;1	8;8;7;6;6;1	8;8;7;6;6;1	Succinate dehydrogenase [ubiquinol]	SDHA
P53597;H7C233	P53597;H7C233	4;1	4;1	4;1	Succinyl-CoA ligase [ADP-forming]	SUCLG1
Q9P2R7-2;Q9P2R7;A0A087X0R6	Q9P2R7-2;Q9P2R7;A0A087X0R6	5;5;3;3;1;1	5;5;3;3;1;1	5;5;3;3;1;1	Succinyl-CoA ligase [ADP-forming]	SUCLA2
Q96I99;H0Y852;E9PDQ8	Q96I99;H0Y852;E9PDQ8	4;2;2;2	4;2;2;2	4;2;2;2	Succinyl-CoA ligase [GDP-forming]	SUCLG2



P55809;E9PDW2;P5580	P55809;E9I6;4;2	6;4;2	6;4;2	Succinyl-CoA:3-ketoacid co	OXCT1
A8MXB9;J3KQJ1;Q8NBJ	A8MXB9;J33;3;3;2;2	3;3;3;2;2	3;3;3;2;2	Sulfatase-modifying factor 2	SUMF2
Q9Y6N5;H3BNX3;H3BM	Q9Y6N5;H312;7;6;4;4	12;7;6;4;4	12;7;6;4;4	Sulfide:quinone oxidoreduc	SQRDL
M0QX65;M0QZS6;B3KN	M0QX65;N1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	SUMO-activating enzyme su	SAE1
H3BPC4;H3BQ9;B0QY	H3BPC4;H33;3;3;3	3;3;3;3	3;3;3;3	SUMO-conjugating enzyme	UBE2I
H7C2K3;H0Y6N5;H0Y74	H7C2K3;H01;1;1;1;1	1;1;1;1;1	1;1;1;1;1	SUN domain-containing pro	SUN1
P42285;H0Y8U3	P42285;H02;1	2;1	2;1	Superkiller viralicidic activit	SKIV2L2
P00441;H7BYH4	P00441;H73;2	3;2	3;2	Superoxide dismutase [Cu-2	SOD1
P04179-4;P04179;F5H3	P04179-4;F55;5;4;4;4	5;5;4;4;4	5;5;4;4;4	Superoxide dismutase [Mn]	SOD2
Q9Y2Z0-2;Q9Y2Z0	Q9Y2Z0-2;(4;4	4;4	4;4	Suppressor of G2 allele of S	SUGT1
Q9BRV8;Q9BRV8-2	Q9BRV8;Q91;1	1;1	1;1	Suppressor of IKBKE 1	SIKE1
A8MV53;A0A0A6YYI3;A	A8MV53;A14;4;4;4;4	4;4;4;4;4	4;4;4;4;4	Suppressor of SWI4 1 homo	PPAN;PPAN
Q15526-2;Q15526	Q15526-2;(1;1	1;1	1;1	Surfeit locus protein 1	SURF1
Q5T8U5;O15260-2;O15	Q5T8U5;O12;2;2;1;1	2;2;2;1;1	2;2;2;1;1	Surfeit locus protein 4	SURF4
O75683	O75683	3	3	Surfeit locus protein 6	SURF6
O75940	O75940	2	2	Survival of motor neuron-re	SMNDC1
F8VXC8;Q8TAQ2-2;Q8T	F8VXC8;Q83;3;3;3;1	3;3;3;3;1	3;3;3;3;1	SWI/SNF complex subunit S	SMARCC2
O60264	O60264	9	9	SWI/SNF-related matrix-ass	SMARCA5
J3KMX2;B9EGA3;Q9292	J3KMX2;B92;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	SWI/SNF-related matrix-ass	SMARCD2
K7EMQ8;J3QKS7;B4DGI	K7EMQ8;J32;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	SWI/SNF-related matrix-ass	SMARCE1
E7EMB1;Q9UH65	E7EMB1;Q92;2	2;2	2;2	Switch-associated protein 7	SWAP70
Q99536;K7ERT7;Q9953	Q99536;K79;6;6;3;2;2	9;6;6;3;2;2	9;6;6;3;2;2	Synaptic vesicle membrane	VAT1
O15498-2;O15498;H7C	O15498-2;(2;2;1	2;2;1	2;2;1	Synaptobrevin homolog YK1	YKT6
Q16563-2;Q16563	Q16563-2;(1;1	1;1	1;1	Synaptophysin-like protein	SYPL1
Q9H987-2;Q9H987	Q9H987-2;1;1	1;1	1;1	Synaptopodin 2-like protein	SYNPO2L
O95721	O95721	1	1	Synaptosomal-associated p	SNAP29
H3BV99;H3BP15;H3BQ	H3BV99;H32;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	Synaptosomal-associated p	SNAP23
P18827;E9PHH3;H7C1K	P18827;E9I2;1;1	2;1;1	2;1;1	Syndecan-1	SDC1
P31431-2;P31431	P31431-2;F2;2	2;2	2;2	Syndecan-4	SDC4
O43752	O43752	2	2	Syntaxin-6	STX6
O15400-2;O15400	O15400-2;(2;2	2;2	2;2	Syntaxin-7	STX7
O00560;O00560-3;B4DI	O00560;OC10;8;7;7	10;8;7;7	1;1;0;0	Syntenin-1	SDCBP
O00560-2;G5EA09	O00560-2;(10;9	1;1	1;1	Syntenin-1	SDCBP
Q9Y490;H0YMT1;A0A1	Q9Y49010;1;1;1	10;1;1;1	10;1;1;1	Talin-1	TLN1
A0A0G2JKZ1;A2AB90;A	A0A0G2JKZ2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	Tapasin	TAPBP
Q13148;A0A087WX29;F	Q13148;A06;5;5;5;5;5	6;5;5;5;5;5	6;5;5;5;5;5	TAR DNA-binding protein 4	TARDBP
Q92804-2;Q92804;A0A	Q92804-2;(6;6;5;3;1	6;6;5;3;1	4;4;3;3;1	TATA-binding protein-assoc	TAF15
B8ZZD4;Q86VP1-3;Q86	B8ZZD4;Q86;6;6;6;6;3	6;6;6;6;6;3	6;6;6;6;6;3	Tax1-binding protein 1	TAX1BP1
O14907	O14907	1	1	Tax1-binding protein 3	TAX1BP3
Q8TC07-2;Q8TC07-3;Q	Q8TC07-2;(3;3;3	3;3;3	3;3;3	TBC1 domain family memb	TBC1D15
Q9BYX2-6;Q9BYX2-5;Q	Q9BYX2-6;(1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	TBC1 domain family memb	TBC1D2
P17987;E7EQR6;F5H28	P17987;E7I17;12;11;1	17;12;11;1	17;12;11;1	T-complex protein 1 subuni	TCP1
P78371;F5GWF6;P7837	P78371;F5(17;16;16;1	17;16;16;1	17;16;16;1	T-complex protein 1 subuni	CCT2
P50991-2;P50991	P50991-2;F15;15	15;15	15;15	T-complex protein 1 subuni	CCT4
E7ENZ3;P48643;B7ZAR	E7ENZ3;P411;11;10;1	11;11;10;1	11;11;10;1	T-complex protein 1 subuni	CCT5
Q99832-3;Q99832;Q99	Q99832-3;(10;10;9;8;1	10;10;9;8;1	10;10;9;8;1	T-complex protein 1 subuni	CCT7
P49368;B4DUR8;P4936	P49368;B415;14;14;5	15;14;14;5	15;14;14;5	T-complex protein 1 subuni	CCT3
P50990;P50990-2;P509	P50990;P5(20;19;16;8	20;19;16;8	20;19;16;8	T-complex protein 1 subuni	CCT8
P40227;P40227-2;Q925	P40227;P4(10;9;2;2;1	10;9;2;2;1	10;9;2;2;1	T-complex protein 1 subuni	CCT6A
Q5UIP0-2;Q5UIP0;H7C2	Q5UIP0-2;(3;3;1;1	3;3;1;1	3;3;1;1	Telomere-associated protei	RIF1

Q68CZ2-2;Q68CZ2;E9PC	Q68CZ2-2;(2;2;1	2;2;1	2;2;1	Tensin-3	TNS3
Q9UGI8-2;Q9UGI8;F8W	Q9UGI8-2;(2;2;1;1	2;2;1;1	2;2;1;1	Testin	TES
E9PRJ3;E9PMR4;P4850	E9PRJ3;E9F 3;3;3	3;3;3	3;3;3	Tetraspanin;CD151 antigen	CD151
F8VV56;F8W022;F8VW	F8VV56;F8' 3;3;3;3;3	3;3;3;3;3	3;3;3;3;3	Tetraspanin;CD63 antigen	CD63
E9PJK1;E9PRJ8;HOYDL9	E9PJK1;E9F 3;3;3;3;3	3;3;3;3;3	3;3;3;3;3	Tetraspanin;CD81 antigen	CD81
A6NNI4;G8JLH6;P2192	A6NNI4;G8 2;2;2	2;2;2	2;2;2	Tetraspanin;CD9 antigen	CD9
O60635	O60635	1	1	1 Tetraspanin-1	TSPAN1
O95857	O95857	1	1	1 Tetraspanin-13	TSPAN13
P52888;K7EKB6;K7EP4	P52888;K7I 2;1;1	2;1;1	2;1;1	Thimet oligopeptidase	THOP1
P10599;P10599-2	P10599;P1( 5;4	5;4	5;4	Thioredoxin	TXN
O95881	O95881	2	2	2 Thioredoxin domain-containi	TXNDC12
Q9BRA2;I3L0K2;I3L3M7	Q9BRA2;I3 3;2;2;1	3;2;2;1	3;2;2;1	Thioredoxin domain-containi	TXNDC17
Q8NBS9;Q8NBS9-2	Q8NBS9;Q8 8;7	8;7	8;7	Thioredoxin domain-containi	TXNDC5
E9PIR7;F8W809;A0A08	E9PIR7;F8V 6;6;6;6;6	6;6;6;6;6	5;5;5;5;5;5	Thioredoxin reductase 1, cy	TXNRD1
P30048-2;P30048	P30048-2;F 7;7	7;7	7;7	Thioredoxin-dependent per	PRDX3
O43396;K7ER96;K7EML	O43396;K7 6;5;2;1;1	6;5;2;1;1	6;5;2;1;1	Thioredoxin-like protein 1	TXNL1
Q9H3N1;G3V448	Q9H3N1;G 4;2	4;2	4;2	Thioredoxin-related transm	TMX1
Q9Y320-2;Q9Y320;E9PS	Q9Y320-2;(7;7;2;2;2	7;7;2;2;2	7;7;2;2;2	Thioredoxin-related transm	TMX2
Q16762;B1AH48	Q16762;B1 2;1	2;1	2;1	Thiosulfate sulfurtransferas	TST
A0A0C4DG98;Q8NI27	A0A0C4DG 1;1	1;1	1;1	THO complex subunit 2	THOC2
Q86V81;E9PB61	Q86V81;E9 6;5	6;5	6;5	THO complex subunit 4	ALYREF
Q6I9Y2	Q6I9Y2	1	1	1 THO complex subunit 7 hon	THOC7
P26639;P26639-2;D6RC	P26639;P2( 17;17;3;3;3	17;17;3;3;3	17;17;3;3;3	Threonine--tRNA ligase, cyt	TARS
P07996;P07996-2;CON_	P07996;P0 11;9;8;2	11;9;8;2	11;9;8;2	Thrombospondin-1	THBS1
H3BNW0;Q9NXG2	H3BNW0;C 1;1	1;1	1;1	THUMP domain-containing	THUMPD1
K7ES52;K7ERJ1;K7ERV3	K7ES52;K7I 1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Thymidine kinase;Thymidin	TK1
P62328	P62328	2	2	2 Thymosin beta-4;Hematop	TMSB4X
Q9Y2W1	Q9Y2W1	11	11	11 Thyroid hormone receptor-	THRAP3
Q15654;H7BZE2	Q15654 12;5	12;5	12;5	Thyroid receptor-interactin	TRIP6
A0A1B0GTW1;Q9UDY2	A0A1B0GT 10;10;10;1	10;10;10;1	10;10;10;1	Tight junction protein ZO-2	TJP2
O75663-2;O75663	O75663-2;(1;1	1;1	1;1	TIP41-like protein	TIPRL
Q86XR7-2;A0A0A6YYA0	Q86XR7-2; 7;6;6;6;1;1	7;6;6;6;1;1	7;6;6;6;1;1	TIR domain-containing ada	TICAM2;TM
P13726;P13726-2	P13726;P1 3;2	3;2	3;2	Tissue factor	F3
A0A0A0MRA3;A0A0A0M	A0A0A0MF 1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Titin	TTN
E7EMV7;A0A0A0MRZ4; E7EMV7	A( 5;5;5;5;5;5	5;5;5;5;5;5	5;5;5;5;5;5	TNFAIP3-interacting protei	TNIP1
E9PNS3;F2Z2Y8;Q9H0E	E9PNS3;F2 1;1;1	1;1;1	1;1;1	Toll-interacting protein	TOLLIP
J3KN66;Q5JTV8-3;A0A0	J3KN66;Q5 6;6;5;5;3;2	6;6;5;5;3;2	6;6;5;5;3;2	Torsin-1A-interacting protei	TOR1AIP1
J3KPT4;Q9H4I3	J3KPT4;Q9I 1;1	1;1	1;1	TraB domain-containing prc	TRABD
P37837;F2Z393	P37837;F2 7;5	7;5	7;5	Transaldolase	TALDO1
Q9HBD4;A0A0A0MT49; Q9HBD4	A( 1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Transcription activator BRG	SMARCA4
A0A1W2PPZ5;P23193;B	A0A1W2PP 5;5;4;4;4;2	5;5;4;4;4;2	5;5;4;4;4;2	Transcription elongation fac	TCEA1
E5RHG8;Q15369;Q153	E5RHG8;Q1 3;3;2;1	3;3;2;1	3;3;2;1	Transcription elongation fac	TCEB1
B8ZZU8;I3L0M9;Q1537	B8ZZU8;I3L 4;4;4;4;1	4;4;4;4;1	4;4;4;4;1	Transcription elongation fac	TCEB2
O14776-2;O14776	O14776-2;(2;2	2;2	2;2	Transcription elongation re	TCERG1
Q00059;H7BYN3;Q0005	Q00059;H7 4;3;3	4;3;3	4;3;3	Transcription factor A, mito	TFAM
P20290-2;P20290	P20290-2;F 1;1	1;1	1;1	Transcription factor BTF3	BTF3
Q13263;Q13263-2;M0R	Q13263;Q1 11;10;6;3;2	11;10;6;3;2	11;10;6;3;2	Transcription intermediary	TRIM28
P49711	P49711	3	3	3 Transcriptional repressor C	CTCF
A0A0U1RR30;A0A0U1R	A0A0U1RR 1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Transcriptional repressor p	GATAD2B;(
E9PF19;Q9Y4P3;Q96E4	E9PF19;Q9 3;3;2;1;1	3;3;2;1;1	3;3;2;1;1	Transducin beta-like protei	TBL2

Q12788;J3KNP2;A0A08	Q12788;J3I8;6;2	8;6;2	8;6;2	Transducin beta-like protei	TBL3
P02786;G3V0E5;F8WBE	P02786;G3 23;20;3;3	23;20;3;3	23;20;3;3	Transferrin receptor protei	TFRC
Q13595-2;Q13595-4;Q1	Q13595-2;(1;1;1;1	1;1;1;1	1;1;1;1	Transformer-2 protein hom	TRA2A
P62995;P62995-3;H7C2	P62995;P6 4;3;2;1;1	4;3;2;1;1	4;3;2;1;1	Transformer-2 protein hom	TRA2B
Q15582;H0Y8M8;H0Y8I	Q15582;HC 2;1;1	2;1;1	2;1;1	Transforming growth factor	TGFBI
P61586	P61586	5	1	Transforming protein RhoA	RHOA
P37802;P37802-2;X6RJI	P37802;P3 11;11;10;1	11;11;10;1	11;11;10;1	Transgelin-2	TAGLN2
O43493-6;O43493-4;O4	O43493-6;(2;2;2;2;2	2;2;2;2;2	2;2;2;2;2	Trans-Golgi network integr	TGOLN2
P55072;C9JUP7;C9IZA5	P55072 22;2;2	22;2;2	22;2;2	Transitional endoplasmic re	VCP
P29401;P29401-2;A0A0	P29401;P2 18;18;15;1	18;18;15;1	18;18;15;1	Transketolase	TKT
Q92616	Q92616	9	9	Translational activator GCN	GCN1L1
Q9BSH4	Q9BSH4	2	2	Translational activator of cy	TACO1
Q5W0H4;A0A0B4J2C3;F	Q5W0H4;A 6;6;6;5;4;3	6;6;6;5;4;3	6;6;6;5;4;3	Translationally-controlled ti	TPT1
G3XAN4;Q15629-2;Q15	G3XAN4;Q 3;3;3	3;3;3	3;3;3	Translocating chain-associa	TRAM1
F8WF48;Q99442;F8WC	F8WF48;Q 2;2;1	2;2;1	2;2;1	Translocation protein SEC6	SEC62
Q9UGP8	Q9UGP8	4	4	Translocation protein SEC6	SEC63
B1AH87;P30536	B1AH87;P3 2;2	2;2	2;2	Translocator protein	TSPO
C9J3L8;C9J5W0;E9PAL7	C9J3L8;C9J 3;3;3;3;2	3;3;3;3;2	3;3;3;3;2	Translocon-associated prote	SSR1
P51571;A6NLM8	P51571 3;1	3;1	3;1	Translocon-associated prote	SSR4
C9JA28;Q9UNL2;Q9UNI	C9JA28;Q9 2;2;2;1	2;2;2;1	2;2;2;1	Translocon-associated prote	SSR3
E9PMQ9;E9PSI1;O1532	E9PMQ9;E 3;3;3;3;2;2	3;3;3;3;2;2	3;3;3;3;2;2	Transmembrane 9 superfan	TM9SF1
Q99805	Q99805	6	6	Transmembrane 9 superfan	TM9SF2
Q9HD45;Q5TB53	Q9HD45;Q 3;2	3;2	3;2	Transmembrane 9 superfan	TM9SF3
A0A0C4DFM1;Q92544	A0A0C4DFI 5;5	5;5	5;5	Transmembrane 9 superfan	TM9SF4
J9JIE6;Q9UM00-2;Q9UM	J9JIE6;Q9U 2;2;2;1;1;1	2;2;2;1;1;1	2;2;2;1;1;1	Transmembrane and coiled	TMCO1
Q13445	Q13445	1	1	Transmembrane emp24 doi	TMED1
G3V2K7;P49755	G3V2K7;P4 2;2	2;2	2;2	Transmembrane emp24 doi	TMED10
F5GX39;E7EQ72;Q1536	F5GX39;E7 1;1;1	1;1;1	1;1;1	Transmembrane emp24 doi	TMED2
Q7Z7H5-2;Q7Z7H5;F8W	Q7Z7H5-2; 4;4;3;3	4;4;3;3	3;3;2;2	Transmembrane emp24 doi	TMED4
Q9Y3A6;M0R072;B1AK	Q9Y3A6;M 2;1;1;1	2;1;1;1	2;1;1;1	Transmembrane emp24 doi	TMED5
Q9BVK6	Q9BVK6	3	2	Transmembrane emp24 doi	TMED9
Q14956-2;Q14956	Q14956-2;(3;3	3;3	3;3	Transmembrane glycoprote	GNPMB
Q9BVC6	Q9BVC6	2	2	Transmembrane protein 10	TMEM109
Q9HC07;V9GY93;Q9HCO	Q9HC07;V 3;2;2;1;1	3;2;2;1;1	3;2;2;1;1	Transmembrane protein 16	TMEM165
Q8IY95-2;Q8IY95	Q8IY95-2;C 2;2	2;2	2;2	Transmembrane protein 19	TMEM192
J3KRW7;J3KS81;Q8N51	J3KRW7;J3 1;1;1	1;1;1	1;1;1	Transmembrane protein 19	TMEM199
K7EM09;K7EPR0;K7ELQ	K7EM09;K7 1;1;1;1	1;1;1;1	1;1;1;1	Transmembrane protein 20	TMEM205
Q6NUQ4-2;Q6NUQ4;H7	Q6NUQ4-2 4;4;3;2	4;4;3;2	4;4;3;2	Transmembrane protein 21	TMEM214
K7ENI6;K7ERE1;Q8N2U	K7ENI6;K7 1;1;1	1;1;1	1;1;1	Transmembrane protein 25	TMEM256
D6RAA6;P57088;H0Y8N	D6RAA6;P5 2;2;1	2;2;1	2;2;1	Transmembrane protein 33	TMEM33
Q9BTV4	Q9BTV4	4	4	Transmembrane protein 43	TMEM43
Q9BXS4;Q5T6Z8;Q5T70	Q9BXS4;Q5 5;3;2;1;1	5;3;2;1;1	5;3;2;1;1	Transmembrane protein 59	TMEM59
Q8NBN3-3;Q8NBN3;H3	Q8NBN3-3; 3;3;1;1	3;3;1;1	3;3;1;1	Transmembrane protein 87	TMEM87A
B1ALM5;Q9P0T7;B1ALM	B1ALM5;Q 2;2;1;1;1	2;2;1;1;1	2;2;1;1;1	Transmembrane protein 9	TMEM9
Q92973-2;Q92973;Q92	Q92973-2;(4;4;3;1;1	4;4;3;1;1	4;4;3;1;1	Transportin-1	TNPO1
J3KQ96;E7ETY2;Q1342	J3KQ96;E7I 15;15;15;1	15;15;15;1	15;15;15;1	Treacle protein	TCOF1
P53007;B4DP62	P53007 3;1	3;1	3;1	Tricarboxylate transport prc	SLC25A1
P40939;H0YFD6;P4093	P40939 20;8;1	20;8;1	20;8;1	Trifunctional enzyme subun	HADHA
P55084-2;P55084;F5GZ	P55084-2;F 14;14;12;8	14;14;12;8	14;14;12;8	Trifunctional enzyme subun	HADHB
P22102;P22102-2;C9JZ	P22102;P2 4;3;2;2;2;2	4;3;2;2;2;2	4;3;2;2;2;2	Trifunctional purine biosynt	GART

P60174-1;P60174;P60174	P60174-1;F 15;15;10;7	15;15;10;7	15;15;10;7	Triosephosphate isomerase	TPI1
Q14134-2;Q14134	Q14134-2;(2;2	2;2	2;2	Tripartite motif-containing	TRIM29
Q96LD4-2;Q96LD4	Q96LD4-2;(2;2	2;2	2;2	Tripartite motif-containing	TRIM47
Q08J23-2;Q08J23;Q08J23	Q08J23-2;C 14;14;11;2	14;14;11;2	14;14;11;2	tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2
F5H1S9;G8JLB3;Q9Y606	F5H1S9;G8 3;3;3;1;1	3;3;3;1;1	3;3;3;1;1	tRNA pseudouridine synthase	PUS1
Q9Y310	Q9Y310	8	8	tRNA-splicing ligase	RtcB hcr
Q9NYL9;HOYKU1;HOYNJ	Q9NYL9;HC 4;3;3;1	4;3;3;1	4;3;3;1	Tropomodulin-3	TMOD3
P09493-3;P09493-4;P09493	P09493-3;F 10;9;9;9;8	4;3;3;3;2	1;1;1;1;1	Tropomyosin alpha-1 chain	TPM1
P06753-2;A0A087WWU	P06753-2;A 18;17;17;1	18;17;17;1	12;11;12;1	Tropomyosin alpha-3 chain	TPM3;DKFZ
P67936;K7EPB9;U3KQK	P67936 14;6;1;1;1	2;0;0;0;0	2;0;0;0;0	Tropomyosin alpha-4 chain	TPM4
P67936-2;K7ENT6;K7ER	P67936-2;k 15;11;7;6	6;9;5;1;0	4;2;1;1;0	Tropomyosin alpha-4 chain	TPM4
P23381-2;P23381;HOYJI	P23381-2;F 6;6;3;3;3	2;6;6;3;3;3	2;6;6;3;3;3	Tryptophan--tRNA ligase, cytosine	WARS
Q71U36-2;Q71U36;Q13	Q71U36-2; 18;18;14;1	1;1;1;1;1	1;0;0;0;0	Tubulin alpha-1A chain	TUBA1A;TL
P68363;P68363-2;C9JD	P68363;P6 18;15;5	18;15;5	0;0;0	Tubulin alpha-1B chain	TUBA1B
F5H5D3;Q9BQE3;A0A1	F5H5D3;Q 18;18;12;8	2;2;2;0;0	2;2;2;0;0	Tubulin alpha-1C chain	TUBA1C
P68366-2;P68366;C9JE	P68366-2;F 18;18;6;6	6;4;4;3;3	2;4;4;3;3	Tubulin alpha-4A chain	TUBA4A
Q5JP53;P07437;Q5ST81	Q5JP53;P0 16;16;13;6	4;4;1;0;0	3;3;1;0;0	Tubulin beta chain	TUBB
Q13885;Q9BVA1	Q13885;Q 15;14	3;2	3;2	Tubulin beta-2A chain	TUBB2A;TL
A0A0B4J269;Q13509;Q13509	A0A0B4J26 11;11;9;2	2;2;2;1;1	1;1;1;0;1	Tubulin beta-3 chain	TUBB3
P68371;P04350;M0R2D	P68371;P0 17;12;5;2	2;17;12;5;2	2;2;1;1;1	Tubulin beta-4B chain	TUBB4B;TL
Q9BUF5;K7ESM5;K7ESC	Q9BUF5;K7 9;8;2;2	2;3;2;2;2	2;3;2;2;2	Tubulin beta-6 chain	TUBB6
Q3ZCM7;A0A075B736;Q3ZCM7	A0A075B736;Q 9;8;8	2;2;2	2;2;2	Tubulin beta-8 chain	TUBB8
K7EKE5;Q9NRH3;P2325	K7EKE5;Q9 1;1;1	1;1;1	1;1;1	Tubulin gamma-2 chain	TUBG1;TUBG2
E5RIW3;E5RJD8;O7534	E5RIW3;E5 3;3;3;2	2;3;3;3;2	2;3;3;3;2	Tubulin-specific chaperone	TBCA
Q14166	Q14166	4	4	Tubulin--tyrosine ligase-like	TLL12
Q03169	Q03169	1	1	Tumor necrosis factor alpha	TNFAIP2
O14763-2;O14763	O14763-2;(1;1	1;1	1;1	Tumor necrosis factor receptor	TNFRSF10B
Q9H3D4-10;Q9H3D4-12	Q9H3D4-1(2;2;2;2;2	2;2;2;2;2	2;2;2;2;2	Tumor protein 63	TP63
P55327-2;P55327-4;P55327	P55327-2;F 4;4;4;4;4	4;4;4;4;4	4;4;4;4;4	Tumor protein D52	TPD52
A0A087WYR3;O43399-1	A0A087WY 5;5;5;5;5	5;5;5;5;5	5;5;5;5;5	Tumor protein D54	TPD52L2
Q5T0D9;Q5T0D9-2	Q5T0D9;Q 3;2	3;2	3;2	Tumor protein p63-regulator	TPRG1L
Q12888;Q12888-3;Q12888	Q12888;Q11;1;1	1;1;1	1;1;1	Tumor suppressor p53-binding protein	TP53BP1
P09758	P09758	8	8	Tumor-associated calcium signaling	TACSTD2
Q12792;F8VRG3;F8VS8	Q12792;F8 2;1;1;1;1	2;1;1;1;1	2;1;1;1;1	Twinfilin-1	TWF1
D6RG15;HOY858;Q6IBS	D6RG15;HC 1;1;1	1;1;1	1;1;1	Twinfilin-2	TWF2
Q6RW13-2;Q6RW13	Q6RW13-2 1;1	1;1	1;1	Type-1 angiotensin II receptor	AGTRAP
Q9UIG0-2;Q9UIG0	Q9UIG0-2;(11;11	11;11	11;11	Tyrosine-protein kinase BAZ	BAZ1B
P07948-2;P07948;HOY3	P07948-2;F 5;4;1;1;1	1;5;4;1;1	1;5;4;1;1	Tyrosine-protein kinase Lyn	LYN
P18031;B4DSN5	P18031;B4 8;5	8;5	8;5	Tyrosine-protein phosphatase	PTPN1
P54577;A0A0C4DGZ5	P54577;A0 3;2	3;2	3;2	Tyrosine--tRNA ligase, cytosine	YARS
HOYHS6;Q9Y224	HOYHS6;Q 3;3	3;3	3;3	Tyrosine--tRNA ligase	YARS2
P08621;P08621-2;P08621	P08621;P0 6;5;3;3;2	1;6;5;3;3	1;6;5;3;3	U1 small nuclear ribonucleoprotein	SNRNP70
M0R221;M0R2B8;M0QX	M0R221;M 2;2;2	1;1;1;1	1;1;1;1	U1 small nuclear ribonucleoprotein	SNRPA
A0A0A0MRR7;P09234	A0A0A0MF 2;2	2;2	2;2	U1 small nuclear ribonucleoprotein	SNRPC
P09661;HOYLR3;HOYMA	P09661;H0 4;3;3;1	4;3;3;1	4;3;3;1	U2 small nuclear ribonucleoprotein	SNRPA1
P08579;M0ROG9;M0QX	P08579;MC 2;1;1;1	2;1;1;1	1;0;0;0	U2 small nuclear ribonucleoprotein	SNRPB2;SNRPB
O15042-2;O15042;E7ET	O15042-2;(4;4;3;2;2	2;4;4;3;2	2;4;4;3;2	U2 snRNP-associated SURP	U2SURP
Q9NV31	Q9NV31	2	2	U3 small nucleolar ribonucleoprotein	IMP3
O00566	O00566	1	1	U3 small nucleolar ribonucleoprotein	IMP3
Q9BVJ6-3;Q9BVJ6;Q9BVJ6	Q9BVJ6-3;(5;5;3;2	5;5;3;2	5;5;3;2	U3 small nucleolar RNA-associated	UTP14A



Q9Y5J1;J3QR85;J3KSR7	Q9Y5J1;J3C 2;1;1	2;1;1	2;1;1	U3 small nucleolar RNA-ass	UTP18	
Q9NYH9	Q9NYH9	2	2	2	U3 small nucleolar RNA-ass	UTP6
O43818	O43818	3	3	3	U3 small nucleolar RNA-inte	RRP9
O43172-2;O43172	O43172-2;(1;1	1;1	1;1	U4/U6 small nuclear ribonu	PRPF4	
A0A087X1B2;B9A018;Q A0A087X1E	2;2;2;2;1	2;2;2;2;1	2;2;2;2;1	U4/U6.U5 tri-snRNP-associ	USP39	
O75643;O75643-2;B4EC O75643	17;6;2	17;6;2	17;6;2	U5 small nuclear ribonuclec	SNRNP200	
Q96DI7;Q96DI7-2;Q9N9	Q96DI7;Q9 3;3;1	3;3;1	3;3;1	U5 small nuclear ribonuclec	SNRNP40	
Q9Y333	Q9Y333	1	1	1	U6 snRNA-associated Sm-lik	LSM2
F2Z2Y6;C9JIZ0;C9JNV3;(F2Z2Y6;C9J 1;1;1;1	1;1;1;1	1;1;1;1	1;1;1;1	U6 snRNA-associated Sm-lik	LSM8	
Q9UMX0-2;Q9UMX0;Q9 Q9UMX0-2	5;5;2;1;1;1	5;5;2;1;1;1	3;3;2;1;0;1	Ubiquilin-1	UBQLN1	
H3BPW3;H3BVA5;H3BP H3BPW3;H 1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Ubiquinone biosynthesis pr	COQ9	
H3BQP1;Q14694;Q1469 H3BQP1;Q 1;1;1;1	1;1;1;1	1;1;1;1	1;1;1;1	Ubiquitin carboxyl-terminal	USP10	
P45974-2;P45974;F5H5 P45974-2;F 2;2;1	2;2;1	2;2;1	2;2;1	Ubiquitin carboxyl-terminal	USP5	
P15374;A0A087WTB8;C P15374;A0. 6;5;4	6;5;4	6;5;4	6;5;4	Ubiquitin carboxyl-terminal	UCHL3	
A6NJA2;P54578-2;P545 A6NJA2;P5 8;8;8;8;1;1	8;8;8;8;1;1	8;8;8;8;1;1	8;8;8;8;1;1	Ubiquitin carboxyl-terminal	USP14	
H0Y6Y4;Q5LJB0;Q5LJA5 H0Y6Y4;Q5 2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	Ubiquitin carboxyl-terminal	UCHL5	
Q92890;Q92890-1;C9J6 Q92890;Q9 2;2;1;1	2;2;1;1	2;2;1;1	2;2;1;1	Ubiquitin fusion degradatio	UFD1L	
F5GYN4;J3KR44;Q96FW F5GYN4;J3I 4;4;4;3;3;3	4;4;4;3;3;3	4;4;4;3;3;3	4;4;4;3;3;3	Ubiquitin thioesterase OTU	OTUB1	
P62979;J3QS39;J3QTR3 P62979;J3C 7;5;5;5;5;5	7;5;5;5;5;5	7;5;5;5;5;5	7;5;5;5;5;5	Ubiquitin-40S ribosomal pr	RPS27A;UB	
F8W726;Q14157-4;Q14 F8W726;Q 4;4;4;4;4;4	4;4;4;4;4;4	4;4;4;4;4;4	4;4;4;4;4;4	Ubiquitin-associated protei	UBAP2L	
O00762-2;O00762-3;OC O00762-2;(2;2;2	2;2;2	2;2;2	2;2;2	Ubiquitin-conjugating enzyr	UBE2C	
P61086;D6RDM7;P6108 P61086;D6 3;2;2;1	3;2;2;1	3;2;2;1	3;2;2;1	Ubiquitin-conjugating enzyr	UBE2K	
A0A1B0GUS4;P68036-2 A0A1B0GU 1;1;1;1	1;1;1;1	1;1;1;1	1;1;1;1	Ubiquitin-conjugating enzyr	UBE2L3	
P61088;F8VZ29;F8VSD4 P61088;F8 4;3;3;3;3;1	4;3;3;3;3;1	4;3;3;3;3;1	4;3;3;3;3;1	Ubiquitin-conjugating enzyr	UBE2N;UBI	
I3L0A0;Q13404;Q13404 I3L0A0;Q1 4;3;3;3;3;2	4;3;3;3;3;2	4;3;3;3;3;2	2;1;1;1;1;0	Ubiquitin-conjugating enzyr	TMEM189-	
Q15819	Q15819	4	2	2	Ubiquitin-conjugating enzyr	UBE2V2
H0Y614;P61960	H0Y614;P6 1;1	1;1	1;1	Ubiquitin-fold modifier 1	UFM1	
P22314-2;P22314;Q5JR P22314-2;F 21;21;8;5;5	21;21;8;5;5	21;21;8;5;5	21;21;8;5;5	Ubiquitin-like modifier-acti	UBA1	
Q9BZL1;K7EQ43	Q9BZL1;K7 2;1	2;1	2;1	Ubiquitin-like protein 5	UBL5	
A0A087WTZ5;E9PJ81;E9 A0A087WT 1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	UBX domain-containing pro	UBXN1	
Q92575	Q92575	3	3	3	UBX domain-containing pro	UBXN4
O60701;O60701-2;O607 O60701;O6 9;8;6;3;3;3	9;8;6;3;3;3	9;8;6;3;3;3	9;8;6;3;3;3	UDP-glucose 6-dehydrogen	UGDH	
Q9NYU2-2;Q9NYU2;H7I Q9NYU2-2; 10;10;2;1	10;10;2;1	10;10;2;1	10;10;2;1	UDP-glucose:glycoprotein g	UGGT1	
P19224-3;P19224;C9JMP19224-3;F 4;4;2;1;1;1	4;4;2;1;1;1	4;4;2;1;1;1	4;4;2;1;1;1	UDP-glucuronosyltransfera	UGT1A6	
P30085;Q5T0D2;P3008 P30085;Q5 5;4;3	5;4;3	5;4;3	5;4;3	UMP-CMP kinase	CMPK1	
Q8N999-3;Q8N999	Q8N999-3; 1;1	1;1	1;1	Uncharacterized protein C1	C12orf29	
Q8WWC4	Q8WWC4	1	1	1	Uncharacterized protein C2	C2orf47
C9JQV0;Q9BRJ6;H7COT C9JQV0;Q9 2;2;1;1	2;2;1;1	2;2;1;1	2;2;1;1	Uncharacterized protein C7	C7orf50	
E9PDF6;O43795-2;O437 E9PDF6;O4 20;20;20;9	20;20;20;9	20;20;20;9	20;20;20;9	Unconventional myosin-Ib	MYO1B	
F5H6E2;O00159-3;O001 F5H6E2;O0 12;12;12;1	12;12;12;1	12;12;12;1	12;12;12;1	Unconventional myosin-Ic	MYO1C	
Q12965;H0YLE5;M0QX Q12965;H0 3;2;1;1	3;2;1;1	3;2;1;1	3;2;1;1	Unconventional myosin-Ie	MYO1E	
A0A0A0MRM8;A0A0D9 A0A0A0MF 2;2;2;2;2	2;2;2;2;2	2;2;2;2;2	2;2;2;2;2	Unconventional myosin-VI	MYO6	
Q9H7E9;Q9H7E9-2	Q9H7E9;Q9 1;1	1;1	1;1	UPF0488 protein C8orf33	C8orf33	
H0YJB9;G3V4C6;Q9Y22 H0YJB9;G3 1;1;1	1;1;1	1;1;1	1;1;1	UPF0568 protein C14orf166	C14orf166	
H0YF29;Q6P1X6-2;Q6P H0YF29;Q6 1;1;1	1;1;1	1;1;1	1;1;1	UPF0598 protein C8orf82	C8orf82	
Q96IX5	Q96IX5	2	2	2	Up-regulated during skeleta	USMG5
P11172-3;P11172;E9PFI P11172-3;F 3;3;2;2;1	3;3;2;2;1	3;3;2;2;1	3;3;2;2;1	Uridine 5-monophosphate s	UMPS	
C9J486;C9JIP2;B4DND0 C9J486;C9J 3;3;3;3;1	3;3;3;3;1	3;3;3;3;1	3;3;3;3;1	Uridine phosphorylase 1	UPP1	
G3V170;Q9HA47-2;Q9H G3V170;Q9 1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Uridine-cytidine kinase 1	UCK1	
Q5T446;H0Y5R6;A0A1B Q5T446;H0 1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Uroporphyrinogen decarbo	UROD	

Q5H8X8;O95399;O9539	Q5H8X8;O9539	1;1;1	1;1;1	1;1;1	Urotensin-2	UTS2
A0A087WYS1;E7EUC7;C	A0A087WY3;3;3;2;2	3;3;3;2;2	3;3;3;2;2	3;3;3;2;2	UTP--glucose-1-phosphate	UGP2
P54727;P54727-2;H0Y5	P54727;P54727-2;H0Y5	8;5;3;3;1;1	8;5;3;3;1;1	8;5;3;3;1;1	UV excision repair protein	RAD23B
Q3ZAQ7	Q3ZAQ7	1	1	1	Vacuolar ATPase assembly	VMA21
O75436;S4R3Q6;O7543	O75436;S4R3Q6;O7543	3;2;2	3;2;2	3;2;2	Vacuolar protein sorting-as	VPS26A
E9PLM9;E9PR04;E9PQR	E9PLM9;E9PR04;E9PQR	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Vacuolar protein sorting-as	VPS28
Q96QK1;I3L4S0;A0A1W	Q96QK1	6;1;1;1	6;1;1;1	6;1;1;1	Vacuolar protein sorting-as	VPS35
O75351;I3L4J1;Q9UN37	O75351;I3L4J1;Q9UN37	2;1;1;1;1	2;1;1;1;1	2;1;1;1;1	Vacuolar protein sorting-as	VPS4B;VPS
A0A087WY55;Q9NP79;A	A0A087WY2;2;1;1	2;2;1;1	2;2;1;1	2;2;1;1	Vacuolar protein sorting-as	VTA1
A0A140T936;P26640;P2	A0A140T936;P26640;P2	5;5;2;1;1;1	5;5;2;1;1;1	5;5;2;1;1;1	Valine--tRNA ligase	VARS
Q8TAA9-2;Q8TAA9	Q8TAA9-2;Q8TAA9	1;1	1;1	1;1	Vang-like protein 1	VANGL1
P49748;P49748-3;P497	P49748;P49748-3;P497	21;21;20;7	21;21;20;7	21;21;20;7	Very long-chain specific acy	ACADVL
Q6Y1H2	Q6Y1H2	1	1	1	Very-long-chain (3R)-3-hydr	HACD2
Q9P035;H3BS72;H3BPZ	Q9P035;H3BS72;H3BPZ	7;6;5;5;3;2	7;6;5;5;3;2	7;6;5;5;3;2	Very-long-chain (3R)-3-hydr	HACD3
A0A1B0GV93;Q53GQ0;A	A0A1B0GV3;3;1;1	3;3;1;1	3;3;1;1	3;3;1;1	Very-long-chain 3-oxoacyl-C	HSD17B12
Q9NZ01;M0QXM3;M0R	Q9NZ01;M0QXM3;M0R	3;2;1;1	3;2;1;1	3;2;1;1	Very-long-chain enoyl-CoA	TECR
Q5TIH2;O95562	Q5TIH2;O95562	1;1	1;1	1;1	Vesicle transport protein	SFT2D2
Q15836;K7ENK9;K7EKX	Q15836;K7ENK9;K7EKX	4;2;2;2;2;2	4;2;2;2;2;2	4;2;2;2;2;2	Vesicle-associated membra	VAMP3;VA
Q9BV40;B8ZZT4;C9JXZ5	Q9BV40;B8ZZT4;C9JXZ5	3;2;1	3;2;1	3;2;1	Vesicle-associated membra	VAMP8
Q9P0L0	Q9P0L0	2	1	1	Vesicle-associated membra	VAPA
O95292;E5RK64;O9529	O95292	5;2;2;1	5;2;2;1	4;1;1;0	Vesicle-associated membra	VAPB
I3L0N3;P46459-2;P4645	I3L0N3;P46459-2;P4645	1;1;1	1;1;1	1;1;1	Vesicle-fusing ATPase	NSF
F8WAU7;C9JR77;C9J46	F8WAU7;C9JR77;C9J46	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Vesicle-trafficking protein	SEC22A
O75396;A0A087X1A9	O75396	3;1	3;1	3;1	Vesicle-trafficking protein	SEC22B
Q12907;D6RIU4;D6RBV	Q12907;D6RIU4;D6RBV	5;4;4;3;1	5;4;4;3;1	5;4;4;3;1	Vesicular integral-membran	LMAN2
A0A024R4E5;Q00341;Q	A0A024R4E5;Q00341;Q	8;8;7;4;4;2	8;8;7;4;4;2	8;8;7;4;4;2	Vigilin	HDLBP
P18206-2;P18206;P182	P18206-2;P18206;P182	22;22;3	22;22;3	22;22;3	Vinculin	VCL
CON__Q3MHN5;CON__	CON__Q3MHN5;CON__	2;2;1;1;1;1	2;2;1;1;1;1	2;2;1;1;1;1	Vitamin D-binding protein	GC
Q8N0U8;Q8N0U8-2	Q8N0U8;Q8N0U8-2	1;1	1;1	1;1	Vitamin K epoxide reductas	VKORC1L1
P21796;C9JH87	P21796;C9JH87	17;10	17;10	17;10	Voltage-dependent anion-s	VDAC1
P45880;A0A0A0MR02;F	P45880;A0A0A0MR02;F	17;16;15;1	17;16;15;1	17;16;15;1	Voltage-dependent anion-s	VDAC2
Q9Y277;Q9Y277-2;E5R	Q9Y277;Q9Y277-2;E5R	8;7;4;4;3	8;7;4;4;3	8;7;4;4;3	Voltage-dependent anion-s	VDAC3
Q8IWT6	Q8IWT6	2	2	2	Volume-regulated anion ch	LRRC8A
P27449	P27449	1	1	1	V-type proton ATPase 16 k	ATP6VOC
P38606-2;P38606;C9JA	P38606-2;P38606;C9JA	7;7;1;1	7;7;1;1	7;7;1;1	V-type proton ATPase catal	ATP6V1A
K7EQW2;K7ELZ6;K7EM	K7EQW2;K7ELZ6;K7EM	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	V-type proton ATPase subu	ATP6VOA1
P21281;C9JL73;P15313	P21281;C9JL73;P15313	8;4;4;3;2;2	8;4;4;3;2;2	8;4;4;3;2;2	V-type proton ATPase subu	ATP6V1B2;
H0YJ55;H0YJS0;G3V559	H0YJ55;H0YJS0;G3V559	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	V-type proton ATPase subu	ATP6V1D
F5GYQ1;P61421;J3QL14	F5GYQ1;P61421;J3QL14	3;3;2;2;1;1	3;3;2;2;1;1	3;3;2;2;1;1	V-type proton ATPase subu	ATP6V0D1
P36543;P36543-3;P365	P36543;P36543-3;P365	4;3;3;2;1	4;3;3;2;1	4;3;3;2;1	V-type proton ATPase subu	ATP6V1E1
O75348;F2Z307;O9567	O75348	3;1;1;1	3;1;1;1	3;1;1;1	V-type proton ATPase subu	ATP6V1G1
G3V126;Q9UI12-2;Q9U	G3V126;Q9UI12-2;Q9U	5;5;5;1;1	5;5;5;1;1	5;5;5;1;1	V-type proton ATPase subu	ATP6V1H
O75083;D6RD66;O7508	O75083;D6RD66;O7508	7;4;4	7;4;4	7;4;4	WD repeat-containing prote	WDR1
U3KQC1;A0A0A0MQU0	U3KQC1;A0A0A0MQU0	5;5;5;3;2;1	5;5;5;3;2;1	5;5;5;3;2;1	WD repeat-containing prote	WDR18
A0A0A0MTB8;Q8NI36	A0A0A0MTB8;Q8NI36	3;3	3;3	3;3	WD repeat-containing prote	WDR36
Q15061;C9JEE7;C9IZK7	Q15061	3;1;1	3;1;1	3;1;1	WD repeat-containing prote	WDR43
O15213;H0Y6G3	O15213;H0Y6G3	4;3	4;3	1;0	WD repeat-containing prote	WDR46
P61964	P61964	1	1	1	WD repeat-containing prote	WDR5
H0YMF6;H0YMF9;H0YN	H0YMF6;H0YMF9;H0YN	1;1;1;1	1;1;1;1	1;1;1;1	WD repeat-containing prote	WDR61
E9PS41;Q6RFH5;H0YFP	E9PS41;Q6RFH5;H0YFP	2;2;1;1	2;2;1;1	2;2;1;1	WD repeat-containing prote	WDR74

Q8IWA0;F8WE20;F8WC	Q8IWA0;F8	2;1;1	2;1;1	2;1;1	WD repeat-containing prote	WDR75
Q9UBH6-2;Q9UBH6	Q9UBH6-2;1;1	1;1	1;1	1;1	Xenotropic and polytropic r	XPR1
P13010;C9JZ81;H7C0H9	P13010	16;2;1	16;2;1	16;2;1	X-ray repair cross-complem	XRCC5
P12956;B1AHC9;P12956	P12956;B1	13;12;12	13;12;12	13;12;12	X-ray repair cross-complem	XRCC6
P16989-2;P16989-3;P16	P16989-2;F	6;6;6;3	3;3;3;1	3;3;3;1	Y-box-binding protein 3	YBX3
Q9Y5A9-2;Q9Y5A9;A0A	Q9Y5A9-2;1	2;2;1;1;1;1	2;2;1;1;1;1	2;2;1;1;1;1	YTH domain-containing fam	YTHDF2;YT
E9PQ61;O75152	E9PQ61;O7	2;2	2;2	2;2	Zinc finger CCCH domain-co	ZC3H11A
Q8WU90-2;Q8WU90	Q8WU90-2	1;1	1;1	1;1	Zinc finger CCCH domain-co	ZC3H15
C9J6P4;Q7Z2W4-3;Q7Z	C9J6P4;Q7	5;5;5;5	5;5;5;5	5;5;5;5	Zinc finger CCCH-type antivi	ZC3HAV1
O95159;H0YCU8;E9PM	O95159;H0	2;1;1;1;1;1	2;1;1;1;1;1	2;1;1;1;1;1	Zinc finger protein-like 1	ZFPL1
Q96KR1	Q96KR1	2	2	2	Zinc finger RNA-binding pro	ZFR
Q9BQ52-4;Q9BQ52;V9C	Q9BQ52-4;3	3;3;2;2;1;1	3;3;2;2;1;1	3;3;2;2;1;1	Zinc phosphodiesterase ELA	ELAC2
H0Y362;Q8NEW0	H0Y362;Q8	2;2	2;2	2;2	Zinc transporter 7	SLC30A7
Q5T4K2;Q5T4K4;Q5T4K	Q5T4K2;Q5	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	Zinc transporter ZIP1	SLC39A1
E5RIP4;Q15043-2;Q150	E5RIP4;Q1	1;1;1;1	1;1;1;1	1;1;1;1	Zinc transporter ZIP14	SLC39A14
Q8N4Q0	Q8N4Q0	2	2	2	Zinc-binding alcohol dehydr	ZADH2
H0Y2Y8;Q15942;Q1594	H0Y2Y8;Q1	3;3;2;1	3;3;2;1	3;3;2;1	Zyxin	ZYX

Fasta header	Number of Peptides	Razor + unique peptides	Unique peptides	Peptides 1	Peptides 2	Peptides 3	Peptides 4
sp P61604	4	8	8	8	8	7	7
sp Q15029	6	10	9	9	7	8	5
sp Q9NRX4	2	1	1	1	1	1	1
sp P31946	6	8	4	4	8	8	7
sp P62258	7	15	12	12	12	11	12
sp Q04917	4	12	9	9	8	8	10
sp P61981	1	10	7	7	7	6	8
sp P31947	2	17	17	14	14	15	14
sp P27348	2	12	8	8	11	11	10
sp P63104	11	14	11	10	11	10	10
sp Q9C0C2	2	3	3	3	1	0	1
sp Q9NUUQ	1	2	2	2	2	2	2
sp P09543	2	1	1	1	1	1	0
sp Q16698	7	7	7	7	6	7	7
sp Q9Y6K5	3	4	4	4	3	2	0
tr A0A087V	6	7	7	7	7	7	5
sp P62191	3	5	5	5	4	4	2
tr E9PM69	6	5	5	5	4	4	4
sp P43686	2	4	4	4	4	4	2
sp P35998	4	10	10	10	8	7	6
tr J3QQM1	9	5	5	4	4	3	2
tr A0A087V	6	6	6	6	3	4	1
tr B1AJY5	5	2	2	2	1	1	0
sp O00231	4	10	10	10	6	4	3
sp O00232	4	6	6	6	2	4	1
tr J3KNQ3	9	6	6	6	2	2	3
sp O00487	1	1	1	1	1	1	1
sp Q13200	7	12	12	12	8	12	6
sp O43242	2	5	5	5	5	4	5
tr Q5VWC4	5	2	2	2	0	0	0
sp Q15008	7	4	4	4	0	0	0
tr H3BNT7	4	3	3	3	1	2	1
tr F5H5V4	7	2	2	2	1	1	1
sp Q13442	1	5	5	5	0	0	2
sp P82912	2	1	1	1	1	1	1
tr A6ND22	3	1	1	1	1	1	1
tr E9PE17	3	2	2	2	1	2	2
sp Q9Y676	2	4	4	4	3	4	4
sp Q9Y399	2	3	3	3	3	3	3
sp P82921	1	1	1	1	1	1	1
tr G5E9W7	7	4	4	4	3	2	3
tr J3QLR8	2	2	2	2	1	1	2
sp P82663	4	3	3	3	3	3	1
tr D6RH20	5	2	2	2	2	2	2
sp Q9Y2Q5	7	2	2	2	2	0	2
sp P82909	2	2	2	2	2	2	2
sp P82675	1	1	1	1	1	1	1
sp P82932	1	1	1	1	1	1	1



tr J3QQS1	5	3	3	3	3	3	3	3
sp P82933	1	2	2	2	1	2	1	1
tr E9PDF2	11	18	18	18	14	16	17	16
tr H0Y8N7	2	1	1	1	1	1	1	1
sp Q9Y3B7	5	3	3	3	2	2	3	3
tr B4DLN1	2	6	6	3	4	3	4	3
tr H0YAX3	3	2	2	2	2	2	2	1
sp Q9H0U0	1	3	3	3	2	2	2	3
tr C9IY40	2	1	1	1	1	0	1	1
tr E7ESL0	5	2	2	2	2	2	2	2
sp Q96A35	1	2	2	2	1	2	1	1
tr H0Y4J2	4	1	1	1	1	1	1	1
sp Q96DV4	2	2	2	2	2	1	2	2
tr C9JG87	3	1	1	1	0	1	0	1
tr K7EKI4	7	1	1	1	1	1	1	1
tr H0YBU8	9	2	2	2	2	2	2	2
sp Q9H9J2	1	1	1	1	1	1	1	1
tr E9PI78	3	1	1	1	1	1	1	1
sp Q8N5N	2	2	2	2	1	2	1	1
sp Q96EL3	1	2	2	2	1	1	1	1
sp Q9BYD2	1	1	1	1	1	1	1	1
sp Q15125	3	3	3	3	3	3	2	1
sp Q99714	3	9	9	9	5	6	6	8
sp P31937	2	2	2	2	2	2	2	2
tr K7ERC8	2	1	1	1	1	1	1	1
sp P51857	2	1	1	1	1	0	1	1
sp P46783	5	5	5	5	2	2	1	3
sp P62280	4	10	10	10	8	8	9	8
sp P25398	1	7	7	7	7	7	7	6
sp P62277	3	6	6	6	6	5	5	3
sp P62263	3	7	7	7	6	7	6	5
tr I3L3P7 I	3	7	7	2	5	4	4	4
sp P62249	6	6	6	6	5	4	4	4
sp P08708	5	7	7	7	7	5	5	4
sp P62269	4	6	6	6	6	6	6	6
sp P39019	6	8	8	8	7	5	6	6
sp P15880	7	9	9	9	7	8	8	7
sp P60866	5	3	3	3	3	3	3	3
tr Q8WVC:	3	5	5	5	3	2	3	2
sp P62266	5	4	4	4	4	4	3	4
tr E7ETK0	6	3	3	3	2	2	2	2
sp P62851	1	3	3	3	2	2	2	2
sp P62854	2	3	3	3	3	3	3	2
sp P42677	6	4	4	4	4	4	3	3
sp P62857	1	2	2	2	1	2	2	2
sp P62273	3	2	2	2	1	1	1	1
sp P23396	15	13	13	13	12	12	11	9
tr E9PR30	2	1	1	1	1	1	1	1
sp P61247	12	12	12	12	10	12	10	9
sp P62701	4	12	12	12	8	10	6	6

tr M0R0F0	4	7	7	7	7	7	7	4
sp P62753	3	6	6	6	5	6	4	5
sp P62081	2	4	4	4	3	4	3	2
sp P62241	2	10	10	10	10	10	10	9
tr A0A024I	6	9	9	9	8	8	7	7
tr C9J9K3	4	8	8	8	8	8	7	7
sp P08195	12	25	25	25	24	22	23	22
sp Q9H0D6	2	2	2	2	2	2	2	2
sp P21589	5	2	2	2	2	1	2	2
sp P10809	7	28	28	28	25	26	26	25
tr F8VU65	13	9	9	9	5	8	8	9
sp P05386	1	2	1	1	2	2	2	2
sp P05387	3	7	7	6	7	7	6	6
tr X1WI28	4	8	8	2	7	8	6	5
sp P62906	1	8	8	8	7	7	6	7
sp P62913	3	4	4	1	4	4	3	4
sp P62913	1	4	1	1	4	4	3	4
sp P30050	2	6	6	6	5	6	5	5
sp P26373	5	7	7	7	5	6	5	5
sp P40429	6	8	8	8	6	7	6	6
tr E7EPB3	2	4	4	4	4	4	4	4
sp P61313	6	6	6	6	6	6	6	6
tr A0A087A	14	7	7	7	4	4	4	2
tr G3V203	8	4	4	4	4	4	4	4
tr M0R3D6	5	5	5	5	5	4	5	5
tr G3V1B3	3	2	2	2	2	1	2	1
tr K7EJT5	7	2	2	2	2	2	2	2
sp P62829	5	4	4	4	4	4	4	4
tr H7BY10	6	4	4	4	3	4	3	4
tr C9JXB8	3	6	6	6	4	5	5	5
sp P61254	11	6	6	6	4	6	4	3
sp P61353	4	4	4	4	3	4	3	2
tr E9PLL6	4	4	4	4	3	3	3	3
tr H0YMF4	8	5	5	5	4	4	4	4
sp P47914	1	2	2	2	0	2	2	2
sp P39023	7	16	16	16	15	16	12	11
sp P62888	5	5	5	5	4	5	5	4
tr H7C2W5	8	4	4	4	4	4	3	3
tr D3YTB1	3	5	5	5	4	4	4	4
sp P49207	1	6	6	6	5	6	6	6
tr F2Z388	2	2	2	2	2	2	2	1
tr C9K025	4	5	5	5	4	4	4	4
sp Q9Y3U8	3	3	3	3	3	3	3	3
tr H0Y5B4	6	2	2	2	2	2	2	2
tr C9J4Z3	8	4	4	4	2	3	3	1
tr J3KT73	3	1	1	1	1	1	1	1
sp P36578	4	15	15	15	14	14	13	11
sp P46777	2	9	9	9	7	9	8	6
sp Q02878	7	13	13	13	12	12	12	10
tr A8MUD9	4	6	6	6	6	6	6	6

sp P62424	3	14	14	14	12	13	13	13
tr R4GMU	3	1	1	1	1	1	1	1
sp P62917	5	5	5	5	3	3	3	3
sp P32969	5	5	5	5	5	4	4	3
tr J3QLW7	3	2	2	2	0	1	0	0
sp P52209	5	10	10	10	3	4	5	4
tr M0R0U3	4	2	2	2	0	0	0	1
sp P36639	4	2	2	2	0	1	1	2
sp P11021	1	30	30	29	27	28	25	24
sp Q9UBM	8	6	6	6	5	5	5	6
sp Q7L2J0	1	1	1	1	1	0	0	0
tr A0A0J9Y	4	3	3	3	1	1	3	2
tr M0R026	2	1	1	1	0	1	1	0
sp Q9BWD	2	2	2	2	1	1	1	0
sp P24752	5	6	6	6	6	6	6	6
sp O00763	7	1	1	1	1	1	1	0
tr H0YN26	4	4	4	3	1	0	2	1
sp Q92688	2	2	1	1	1	0	1	1
tr A2A274	2	9	9	9	6	8	6	6
sp P60709	14	19	1	1	19	19	19	18
sp P63261	7	19	19	1	19	19	19	18
sp P63267	10	10	1	1	10	10	10	10
sp O96019	5	6	6	6	4	4	4	4
sp P61160	5	5	5	5	0	2	1	2
sp O15143	16	4	4	4	3	2	2	2
sp O15144	4	4	4	4	1	2	2	1
tr F8VR50	3	1	1	1	0	0	0	0
tr F8WDD7	11	4	4	4	3	3	2	2
tr B1ALC0	3	1	1	1	1	1	1	1
sp Q9BPXE	1	1	1	1	0	1	1	1
sp P61158	7	7	7	7	6	4	6	6
sp P53999	1	3	3	3	3	3	3	3
sp O95433	7	8	8	8	1	2	2	3
sp Q86WX	1	1	1	1	0	0	0	0
sp O14561	3	2	2	2	2	2	1	1
tr C9JIF9 C	2	2	2	2	1	1	2	2
sp Q9H84E	2	5	5	5	5	5	5	5
sp O00767	1	2	2	2	2	2	2	2
tr B8ZWD1	8	3	3	3	1	2	2	2
sp Q9NPJ3	2	1	1	1	1	1	1	1
tr H7C5A7	4	2	2	2	2	2	2	2
sp Q9Y305	5	5	5	5	5	5	5	5
tr A0A087	7	3	3	3	1	2	3	3
tr Q5QPQC	2	2	2	2	2	2	2	1
sp Q6P587	3	1	1	1	1	1	1	0
tr H3BSW3	6	3	3	3	2	3	1	0
sp Q8TB61	5	2	2	2	1	1	1	0
sp P55263	4	1	1	1	1	0	0	0
sp P23526	2	15	15	15	10	11	11	9
tr F8W1A4	11	6	6	6	5	3	3	3

sp P27144	2	2	2	2	1	1	2	2
tr Q5T9B7	4	5	5	5	2	3	3	2
tr A0A096I	9	2	2	2	0	0	0	0
sp P30520	1	5	5	5	0	0	2	3
sp Q01518	18	11	11	11	6	7	9	9
sp Q9HDC9	3	6	6	6	5	6	5	5
sp Q15847	1	1	1	1	0	0	0	1
sp P05141	2	15	15	6	14	14	13	15
sp P12236	1	13	4	2	13	13	13	13
sp Q9BRR6	8	3	3	3	2	3	3	3
sp P84077	6	6	6	3	4	4	5	4
tr C9JPM4	3	3	1	1	3	3	3	3
tr C9J1Z8	5	5	2	2	3	3	2	3
sp P62330	1	3	3	3	3	3	3	3
sp Q9NVJ2	1	2	2	1	2	2	2	2
tr A6NCQ0	6	3	3	3	0	0	2	1
sp Q9Y4W	1	2	2	2	1	2	2	2
tr A0A087V	9	5	5	5	4	4	4	4
sp O00170	1	1	1	1	0	1	1	1
tr H0YK84	5	1	1	1	0	0	1	0
tr H3BU82	5	2	2	2	2	2	2	2
sp P49588	3	7	7	7	6	6	5	3
sp P14550	4	4	4	4	0	0	1	3
sp P11766	3	4	4	4	1	2	2	2
sp P47895	10	18	18	16	14	13	12	9
sp P30837	1	4	2	2	2	2	2	3
sp Q04828	2	11	11	0	7	9	6	5
tr B4DK69	4	10	2	2	6	8	6	5
tr A0A0A0	7	8	2	2	4	6	3	2
sp P15121	5	5	5	5	2	2	2	3
sp O00116	3	10	10	10	10	10	10	9
sp Q9H553	2	1	1	1	1	1	1	1
tr E9PK47	6	1	1	1	0	0	0	1
sp P30533	1	2	2	2	2	1	1	1
sp P12814	18	36	36	23	13	16	19	19
sp Q43707	14	35	22	22	11	15	18	18
tr A0A1B0I	16	5	5	5	4	2	4	3
tr R4GMTC	2	1	1	1	1	1	0	0
tr A0A1W2	11	1	1	1	0	0	1	0
sp P06733	15	23	23	23	12	14	16	14
sp Q16706	1	2	2	2	2	1	2	2
tr H0YKM7	7	1	1	1	0	0	0	0
tr M0R0Y2	10	6	6	6	3	4	5	4
sp P40222	1	1	1	1	1	1	0	1
sp P21397	4	4	4	4	4	4	4	4
sp Q12904	3	4	4	4	4	4	2	2
sp Q13155	3	3	3	3	2	3	2	2
tr A6NKB8	5	6	6	6	3	2	4	4
sp Q86SJ2	1	2	2	2	2	2	2	2
tr E9PG40	14	8	8	7	6	7	7	8



sp Q06481	8	7	6	6	5	6	7	6
sp Q9Y679	3	1	1	1	1	0	1	1
tr A0A1W2	15	1	1	1	1	1	1	0
sp P04083	3	23	23	23	22	21	22	22
sp Q9UJ72	1	1	1	1	1	1	1	0
sp P50995	6	7	7	7	5	5	5	4
sp P07355	25	25	25	25	25	25	24	24
sp P12429	6	12	12	12	8	7	11	10
sp P09525	4	11	11	11	6	11	10	10
sp P08758	5	11	11	11	9	8	8	8
sp P20073	2	11	11	11	7	10	6	8
sp P13928	10	10	10	10	8	8	7	8
sp P46013	2	15	15	15	5	9	12	11
tr A0A140	2	2	2	2	1	1	1	2
sp Q10567	5	7	7	3	2	2	4	4
tr H7C1E4	3	2	2	2	1	0	1	1
sp O95782	7	4	4	4	0	3	2	3
tr A0A087	9	6	2	2	2	3	3	3
tr A0A087	10	3	3	3	2	2	3	2
sp O14617	5	1	1	1	0	1	0	0
sp Q9Y2T2	1	1	1	1	0	1	0	0
sp Q92572	2	2	2	2	1	2	1	1
sp P04114	1	7	5	5	6	6	5	7
tr B0YIW2	2	1	1	1	1	1	1	1
tr J3KQL8	3	2	2	2	2	2	2	2
tr G3V1B6	4	2	2	2	2	0	2	2
sp Q9BZZ5	9	4	4	4	0	0	1	0
sp Q07812	8	3	3	3	1	1	1	1
sp O95831	7	9	9	9	9	9	9	8
tr S4R3H4	9	8	8	8	6	7	7	6
tr A0A087	4	1	1	1	0	0	0	1
sp P54136	4	8	8	8	5	5	4	3
sp P08243	8	5	5	5	4	5	3	4
sp O43776	7	6	6	6	3	4	4	4
sp P17174	2	4	4	4	0	0	1	1
sp P00505	2	13	13	13	11	12	12	11
sp P14868	7	20	20	20	15	12	11	13
sp Q6PI48	1	2	2	2	2	2	2	0
sp Q12797	17	4	4	4	4	4	4	4
tr B1AKZ5	3	1	1	1	1	1	1	1
sp Q8WWI	9	2	2	2	1	0	1	2
tr B5MCNC	7	3	3	3	3	2	2	3
tr F5H6I7	3	2	2	2	2	2	0	1
tr Q5QNZ2	2	7	7	7	6	6	6	5
sp P00846	1	1	1	1	1	1	1	1
sp P25705	9	24	24	24	22	21	16	18
sp P06576	5	22	22	22	21	21	16	17
sp O75947	3	8	8	8	8	6	7	6
sp P30049	1	2	2	2	2	2	2	2
sp P56385	1	2	2	2	2	2	2	2

sp P56134	7	2	2	2	1	2	2	1
tr E9PN17	2	3	3	3	2	3	2	3
sp P36542	2	10	10	10	10	10	8	9
sp P48047	4	7	7	7	5	7	6	4
sp P18859	3	4	4	4	4	4	4	4
sp Q9NVI7	10	6	6	6	5	5	5	5
tr E9PJR8	6	1	1	1	1	1	1	1
sp P28288	3	2	2	2	2	2	2	2
sp P61221	4	4	4	4	2	1	1	1
tr H0YGW:	3	2	2	2	2	2	0	1
sp Q9UG6:	2	1	1	1	1	1	1	1
sp Q9NUQ	2	1	1	1	1	1	0	0
sp P53396	5	22	22	22	7	9	13	13
sp P17858	2	4	2	2	4	4	3	3
sp P08237	4	4	3	3	4	3	0	0
sp Q01813	8	13	13	11	12	11	10	9
sp O76031	3	5	5	5	5	4	4	3
tr M0R208	3	3	3	3	3	3	3	3
sp P46063	1	3	3	3	1	2	1	2
sp Q08211	2	26	26	26	19	19	18	16
tr F1T0B3	5	10	10	10	2	5	4	3
sp Q9NVP:	2	9	9	9	5	6	6	7
tr I3L0H8	13	2	2	2	1	1	0	1
tr G3V529	6	6	6	6	2	3	5	4
sp O00148	19	8	1	1	6	7	3	3
tr A0A0D9	21	14	13	13	10	12	7	9
tr A0A0A0	3	1	1	1	0	0	0	0
sp Q8TDD:	3	6	6	6	4	3	4	4
sp Q8IYB8	1	2	2	2	2	2	2	2
tr J3KRJ2 J	10	1	1	1	0	0	1	1
sp O95816	1	1	1	1	1	0	1	1
sp O95817	1	3	3	3	2	2	2	1
tr A0A0C4	11	2	2	2	1	1	0	0
sp O75531	1	1	1	1	1	1	1	1
sp P98160	1	1	1	1	0	1	0	0
sp Q7L1Q6	6	4	4	4	1	1	1	1
tr Q75MG:	11	3	3	3	0	0	1	1
sp P35613	9	8	8	8	7	7	7	7
sp P51572	6	6	6	6	3	3	4	4
sp Q16611	2	1	1	1	1	1	0	1
tr E9PJA7	11	4	4	4	4	4	4	4
tr A0A087^	4	3	3	3	3	2	3	3
sp P61769	3	3	3	3	3	3	2	2
sp Q13425	1	1	1	1	1	1	1	1
sp P42025	1	1	1	1	0	1	0	0
sp Q53H82	1	3	3	3	2	2	2	1
sp P55957	4	3	3	3	0	0	2	0
sp Q13057	6	3	3	3	2	3	2	1
sp P07814	3	22	22	22	20	17	17	11
sp P13995	3	2	2	2	2	1	1	0

sp P31939	5	13	13	13	6	8	7	7
sp Q8NFC6	1	1	1	1	1	1	1	1
tr A0A087A	7	2	2	2	1	0	1	2
tr F5GXW6	2	1	1	1	1	1	1	1
sp Q9UHR4	1	4	4	4	3	3	4	4
sp P54687	5	1	1	1	0	0	0	0
sp Q9P287	4	2	2	2	1	2	1	0
sp Q8WY2	1	2	2	2	1	2	2	2
sp Q9NRL2	2	2	2	2	0	1	0	0
sp Q96CX2	1	4	4	4	1	0	0	1
tr H3BSS5	2	1	1	1	1	1	0	1
tr J3QRS9	12	4	4	4	1	1	1	3
tr F5H2F4	3	15	15	15	14	13	12	11
sp O75844	1	4	4	4	4	4	4	4
tr E9PKA7	3	1	1	1	1	1	1	1
tr F8VPD4	5	20	20	20	14	18	12	11
tr A0A087A	3	2	2	2	1	0	1	2
sp P22223	2	4	4	4	4	4	4	4
sp Q99653	5	3	3	3	2	2	2	3
sp Q8IU85	2	1	1	1	1	0	0	1
sp Q9UJS0	5	17	17	17	14	15	14	13
sp Q6NUK0	2	6	6	6	5	6	5	5
tr B4E2Q0	14	7	7	7	6	6	7	6
sp Q9HB71	2	6	6	6	5	5	4	3
sp P27824	13	21	21	21	21	20	16	17
tr K7EM73	9	4	4	4	3	3	4	3
sp P07384	11	8	8	8	2	5	4	5
sp P17655	2	6	6	6	5	6	4	3
tr E7EQ12	24	5	5	5	0	0	0	1
tr B4DDF4	13	8	8	8	2	1	3	3
sp P27797	3	15	15	15	15	15	13	14
sp O43852	16	3	3	3	1	0	2	2
sp P10644	4	3	3	3	3	1	2	3
tr H7C1L0	3	1	1	1	1	1	1	1
tr G3V153	4	4	4	4	2	2	2	3
sp P00918	3	4	4	4	2	3	3	4
sp P16152	5	12	12	12	2	2	5	5
sp O75976	3	8	8	8	6	5	7	4
sp P50416	6	9	9	9	8	9	9	9
sp P23786	6	6	6	6	5	4	5	4
tr D6REM4	10	3	3	3	2	3	2	1
tr E7EU96	5	2	2	2	1	1	1	0
tr Q5SRQ3	7	2	2	2	2	2	1	1
tr F5GX99	9	2	2	2	2	1	1	1
sp Q9BXW	2	2	2	2	1	1	0	1
sp P04040	1	9	9	9	5	6	5	7
sp P21964	6	6	6	6	3	3	3	1
sp P35221	30	21	21	21	13	12	12	15
tr B4DGU4	2	7	5	5	4	5	6	6
tr C9JZR2	36	14	14	14	11	13	11	11

tr A0A1B0	13	6	6	6	3	3	5	4
sp P20645	7	3	3	3	3	3	3	2
sp P11717	1	8	8	8	5	4	6	6
sp Q03135	5	8	8	8	8	8	8	8
sp Q03701	1	2	2	2	1	1	2	2
sp Q6YHK3	4	3	3	3	3	3	3	3
tr H7C543	5	3	3	3	3	2	3	2
tr A0A0C4	10	2	2	2	2	2	2	2
tr H0YD13	29	6	6	6	5	6	4	4
tr E9PNW4	4	3	3	3	3	3	2	3
sp P27701	3	3	3	3	3	2	3	3
sp P48960	3	3	3	3	3	2	3	3
tr I3L1N9	2	2	2	2	2	2	2	2
tr B3KY94	4	2	2	2	1	1	1	1
sp Q8N163	6	4	4	4	3	3	2	1
sp P60953	3	5	4	4	2	4	4	4
sp Q99459	1	4	4	4	2	1	0	2
sp Q9NX58	2	2	2	2	1	1	2	2
sp P62633	6	5	5	1	1	2	3	2
tr Q5JVD3	3	1	1	1	0	0	0	0
sp Q7Z7K6	3	2	2	2	1	2	1	2
tr A0A1B0	13	2	2	2	2	2	2	2
tr M0R1L7	3	1	1	1	1	1	1	1
sp Q9H444	2	5	5	5	5	5	5	5
sp O00299	1	9	9	9	4	7	6	6
sp Q8WWI	3	3	3	3	2	2	3	3
sp Q8IWA5	3	1	1	1	0	0	0	1
tr A0A0C4	2	1	1	1	1	1	1	1
tr H7BZN1	9	1	1	1	1	1	1	1
tr A0A087	5	1	1	1	1	1	1	1
sp Q13185	8	6	6	6	3	3	3	4
tr F5GWXE	7	2	2	2	2	2	1	1
tr B4DJV2	20	9	9	8	8	9	9	9
tr A0A087	9	46	46	35	30	32	30	26
sp P09496	7	3	3	3	2	1	2	2
sp P09497	2	2	2	2	1	1	2	2
tr K7EP40	7	2	2	2	2	2	2	1
sp O95832	1	3	3	3	3	3	2	3
sp P56749	1	1	1	1	1	1	1	1
sp O14493	4	2	2	2	2	2	2	2
sp O43809	3	3	3	3	1	3	3	2
tr F8WJN3	5	4	4	4	4	3	2	2
tr J3QT54	7	1	1	1	0	1	0	0
tr A0A0A0	5	1	1	1	0	1	1	1
sp O96005	5	5	5	5	4	1	3	5
tr G5E9Z2	3	3	3	3	2	3	3	3
tr I3L2B0 I	3	3	3	3	0	1	0	1
sp Q14019	2	5	5	5	2	2	3	4
tr Q9NQPE	3	1	1	1	1	1	1	1
sp P53621	2	10	10	10	7	5	7	4



sp P53618	2	5	5	5	2	2	2	2
sp P35606	7	10	10	10	9	7	6	6
sp P48444	5	7	7	7	4	5	4	4
tr M0QXB4	5	3	3	3	3	3	1	1
sp Q9Y678	2	4	4	4	1	1	1	0
sp P23528	9	14	14	13	11	10	8	8
tr Q68DW1	3	1	1	1	0	0	1	0
sp Q96A33	2	5	5	5	5	5	3	3
sp Q96ER9	2	1	1	1	1	1	1	1
tr C9JQ41	3	1	1	1	1	1	1	1
tr H0YG79	2	1	1	1	0	1	0	1
sp Q9Y6H1	2	3	3	3	3	2	3	3
sp O75534	7	5	5	5	3	3	3	3
sp Q9UMC	3	11	11	11	6	9	9	8
sp Q07021	3	8	8	8	7	6	6	4
sp Q15021	1	1	1	1	0	0	0	0
tr E9PHA2	6	4	4	4	1	2	1	2
sp Q9BPX3	2	3	3	3	1	1	1	1
sp Q96JB2	2	1	1	1	1	0	0	1
sp Q9NZB2	7	8	8	8	5	7	6	6
tr C9JFE4	17	2	2	2	1	0	1	1
tr D6RAX7	5	2	2	2	0	0	0	1
tr E9PGT6	4	2	2	2	1	1	1	1
sp O75131	7	10	10	9	10	10	8	8
tr E7ENV7	8	2	1	1	2	2	2	2
sp O75367	5	10	10	9	7	7	8	8
tr I3L1U7	6	1	1	1	1	1	1	1
sp Q9BR76	1	2	2	2	1	0	1	2
sp Q9ULV4	11	6	6	6	3	4	5	4
sp Q92828	1	1	1	1	1	1	1	1
tr Q5SZC9	2	1	1	1	0	0	0	0
sp P78310	5	4	4	4	3	3	3	3
sp P12532	10	3	3	3	0	2	1	0
sp P46109	1	2	2	2	0	0	1	2
tr X6RI56	2	1	1	1	0	0	1	0
tr Q5SQP8	4	2	2	2	2	2	1	0
sp P17812	2	5	5	5	4	5	3	3
sp Q9H5V8	3	3	3	3	2	2	1	2
tr G5EA30	7	1	1	1	0	1	0	0
tr K4DI93	4	1	1	1	0	0	0	0
sp Q86VP6	5	7	7	7	0	0	2	3
tr A0A0240	52	5	4	4	3	4	3	3
sp Q00534	1	6	6	5	4	3	4	3
sp P01040	1	1	1	1	0	0	0	0
sp P04080	2	3	3	3	2	1	2	2
sp P01034	1	1	1	1	1	1	1	0
sp P21291	4	6	6	6	2	3	3	4
sp Q9UHD	6	2	2	2	2	1	2	2
sp Q9H1C7	1	1	1	1	1	1	1	1
sp Q9NZV1	3	3	3	3	3	2	2	3

tr H0YFA4	3	1	1	1	0	0	1	0
sp Q6UXH:	4	1	1	1	1	1	1	1
sp P00167	3	1	1	1	1	1	1	1
tr H3BUX2	4	2	2	2	2	2	2	1
sp P31930	1	14	14	13	12	13	10	8
sp P22695	7	13	13	13	10	9	10	10
sp P07919	2	3	3	3	3	1	2	2
sp P14927	4	2	2	2	2	2	2	2
sp Q9UDW	1	1	1	1	1	1	1	1
sp P47985	2	5	5	5	3	4	3	4
tr C9JFR7	3	2	2	2	2	2	1	1
sp Q9Y2R0	2	3	3	3	3	3	3	2
sp Q7KZNC	2	1	1	1	1	1	1	1
tr C9J8T6	2	1	1	1	1	1	1	1
sp P00403	1	3	3	3	3	3	3	3
sp P13073	6	4	4	4	4	3	4	4
tr H3BNX8	4	2	2	2	2	2	2	2
sp P10606	1	5	5	5	5	5	4	5
sp P14854	1	4	4	4	4	3	3	2
sp P09669	1	3	3	3	3	3	1	1
tr D6RIE3	5	2	2	2	2	2	2	2
sp O14548	3	2	2	2	2	1	1	2
tr D6R9Z7	2	2	2	2	2	2	2	2
sp O00483	1	2	2	2	2	2	2	2
sp P08574	1	2	2	2	2	2	1	1
sp P53701	1	4	4	4	4	4	4	3
sp Q14204	2	41	41	41	28	27	22	19
sp Q13409	18	3	3	3	0	0	0	0
tr J3KRI4 J	4	3	3	3	2	2	2	1
sp Q7L576	14	4	4	4	2	1	1	2
sp Q07065	1	22	22	22	19	19	19	19
sp P28838	3	3	3	3	1	1	1	1
sp O00154	8	2	2	2	0	1	0	0
sp Q96KP4	4	5	5	5	2	1	4	3
tr Q5JUV6	3	2	2	2	0	0	0	0
tr A0A286'	14	10	10	10	9	9	7	8
tr K7EQ02	5	3	3	3	2	2	2	1
sp Q5BKZ1	4	2	2	2	2	2	2	2
sp Q9H773	1	2	2	2	0	0	0	1
tr A0A087'	3	2	2	2	1	1	2	2
sp P30046	6	4	4	4	1	4	3	3
tr A0A0A0	3	2	2	2	1	1	2	2
sp Q9Y394	5	3	3	3	3	3	2	2
tr Q3LIE7	4	5	5	5	5	5	5	5
sp Q13011	3	4	4	3	4	3	2	3
sp P30038	4	2	2	2	2	1	1	1
sp P54886	2	15	15	15	13	12	13	12
sp O43583	1	1	1	1	0	0	0	0
tr J3KP30	3	3	3	3	1	3	3	3
tr G3V158	3	1	1	1	0	0	0	0

tr A0A0C4I	9	5	5	5	1	0	2	2
tr E5RGY0	4	1	1	1	1	1	1	1
tr I3L1T3 I	2	1	1	1	1	0	1	0
sp Q02487	2	1	1	1	0	0	0	1
sp Q14574	3	4	4	4	2	4	3	3
sp Q14126	1	12	12	12	9	11	11	10
sp P32926	1	12	12	12	11	10	11	11
sp P15924	3	46	46	46	37	38	35	37
sp P60981	3	8	7	7	3	3	3	3
sp Q9Y295	1	2	2	2	1	1	2	2
sp P09622	7	5	5	5	5	3	3	5
sp P10515	3	5	5	5	4	4	4	4
sp P36957	6	8	8	8	6	8	8	8
tr G3V1D3	4	1	1	1	0	0	0	0
sp O14672	1	2	2	2	1	1	2	2
tr F8WC54	4	5	5	5	4	4	4	4
tr Q05BS2	3	1	1	1	1	1	1	1
sp Q16531	7	9	9	9	6	5	4	4
sp Q6UX6E	1	1	1	1	1	0	0	0
tr B0QYD3	6	5	5	5	3	3	1	1
tr B1AHB1	4	5	5	5	2	4	2	0
tr E9PHA6	4	3	3	3	3	3	2	0
sp P52701	6	4	4	4	3	3	2	1
tr E5RFF9	2	1	1	1	0	0	1	0
tr H0Y8E6	2	12	12	12	5	3	1	1
sp P25205	4	8	8	8	6	5	3	4
sp P33991	3	11	11	11	8	10	6	4
sp Q14566	1	8	8	8	5	5	5	4
sp P33993	4	16	16	16	12	14	9	4
sp P11387	4	14	14	14	8	12	12	12
sp P11388	8	14	14	14	11	11	12	12
tr G3V5Q1	9	5	5	5	0	2	1	2
sp P78527	2	56	56	56	37	39	30	32
sp O95602	2	2	2	2	1	1	2	2
sp O15446	2	2	2	2	0	2	2	2
sp P24928	2	1	1	1	0	0	0	0
tr K7EMH3	2	1	1	1	1	1	1	1
tr C9J2Y9	4	2	2	2	2	2	2	1
sp O15160	5	2	2	2	0	0	1	1
tr A0A087A	3	1	1	1	0	0	1	1
sp P31689	2	3	3	3	1	2	2	1
sp O60884	3	4	4	4	4	3	3	3
sp Q96EY1	3	3	3	3	2	3	2	3
sp P25685	9	4	4	4	1	3	2	2
sp Q9UBS4	2	4	4	4	4	3	4	4
tr V9GY70	5	1	1	1	1	0	1	1
sp Q9NVH	3	4	4	4	2	2	2	2
tr H0YA63	2	1	1	1	0	0	0	0
tr X6R9L0	2	3	3	3	1	3	3	3
sp Q9H3Z4	1	1	1	1	1	1	1	1

sp Q99615	13	4	4	4	2	2	3	2
sp Q8WXX	1	1	1	1	0	0	0	0
tr Q5QPK2	4	3	3	3	3	3	3	3
sp Q9P2X0	2	2	2	2	2	1	2	2
tr A0A0C4I	5	8	8	8	7	7	5	5
sp P04843	3	24	24	24	20	22	19	19
sp P04844	6	11	11	11	10	10	10	8
tr F5GXX5	4	4	4	4	4	3	4	4
sp P46977	5	5	5	5	4	5	4	4
sp Q8TCJ2	1	2	2	2	2	2	1	2
sp Q9Y673	2	1	1	1	1	0	0	1
tr A0A087V	5	2	2	2	1	2	2	2
tr H0YCK3	6	3	3	3	2	2	1	1
tr A8MY26	4	1	1	1	1	1	1	1
tr H0Y5J4	8	3	3	3	3	3	3	3
sp Q02750	2	1	1	1	0	0	0	0
sp P36507	1	1	1	1	0	0	0	0
sp P46734	6	3	3	3	1	3	1	1
tr E7EX90	9	2	2	2	2	1	2	2
tr G8JLD5	13	3	3	3	0	0	1	1
tr E5KLJ9 I	8	3	3	3	3	3	2	0
tr A0A075I	3	1	1	1	1	1	1	1
sp P63167	4	3	1	1	2	2	1	1
sp Q96FJ2	1	3	3	1	2	2	1	1
sp Q9NP97	8	3	3	3	0	0	0	0
tr Q6P0N6	11	1	1	1	0	0	0	0
sp Q14118	1	2	2	2	2	2	2	2
sp P49792	16	22	22	21	19	21	20	20
sp Q14258	1	7	7	7	2	2	2	2
tr H3BUD0	4	1	1	1	1	1	1	1
sp Q7Z6Z7	4	5	5	5	1	2	3	2
tr F8WCDC	2	3	3	3	1	3	3	3
tr Q5JVVY0	2	1	1	1	1	1	1	1
sp Q9C037	3	2	2	2	2	2	1	1
tr A0A087V	5	3	3	3	2	2	1	1
sp Q96C19	5	7	7	7	3	6	6	6
sp O43854	2	2	2	2	2	1	2	2
tr C9J2Z4	3	2	2	1	0	1	2	2
sp Q9H223	2	6	6	5	5	3	4	2
sp Q15717	4	7	7	7	6	3	5	4
tr H0YKF0	8	6	6	6	5	5	5	6
sp P38117	3	10	10	10	7	8	9	8
sp Q05639	1	9	1	1	8	8	8	7
sp P24534	4	5	5	5	5	4	5	4
tr E9PK01	22	8	8	1	6	6	4	7
sp P29692	3	8	1	1	5	5	3	7
sp P26641	2	16	16	16	10	12	11	11
sp P13639	1	34	34	33	30	28	23	22
tr C9IZ01 I	4	5	5	5	5	4	4	3
sp P43897	7	3	3	3	3	2	2	3

sp P49411	2	19	19	19	15	16	14	15
sp Q9BW6	1	1	1	1	1	1	1	1
tr A0A0A0	4	1	1	1	1	1	1	1
tr F5H2T0	2	1	1	1	1	1	1	1
sp P50402	2	5	5	5	5	5	3	4
sp O94919	1	3	3	3	3	3	3	3
tr M0QYEC	4	1	1	1	0	0	0	0
sp Q9NZ08	4	7	7	7	6	5	7	7
tr E7ER77	4	4	4	4	4	4	4	4
sp P30040	3	7	7	6	6	6	6	6
sp Q9BS26	1	6	6	6	5	5	5	6
tr H0Y621	8	3	3	3	3	3	3	2
sp P14625	7	28	26	26	26	25	23	22
sp O60869	3	2	2	2	0	0	0	0
sp P84090	2	3	3	3	1	3	3	3
sp P42126	4	5	5	5	4	5	5	5
tr A0A0C4	7	4	4	4	3	3	3	2
sp P30084	1	8	8	8	7	8	7	7
sp P98172	1	1	1	1	1	1	1	1
sp P00533	23	30	30	30	26	25	27	25
tr G3V2V8	8	3	3	3	2	3	3	2
tr B5MCA4	3	6	6	6	5	5	5	5
tr H0YBR2	8	2	2	2	2	1	0	1
sp P07099	1	6	6	6	5	5	5	4
sp Q99808	2	1	1	1	1	0	1	1
tr M0R1Y2	5	2	2	2	2	2	1	2
sp Q8N766	4	3	3	3	2	0	1	0
sp Q15006	2	3	3	3	2	2	3	2
tr S4R3U9	3	1	1	1	0	0	1	0
sp O43402	3	2	2	2	2	1	1	1
sp O75477	4	5	2	2	5	5	4	5
tr E5RHW4	3	6	6	3	5	6	5	6
sp Q96HE7	7	12	12	12	6	11	11	11
tr A0A096	12	2	2	2	2	2	2	0
sp Q9H501	1	1	1	1	0	1	1	1
sp Q92506	1	1	1	1	1	1	1	1
sp P60842	24	20	20	16	10	19	13	11
sp P38919	2	8	4	4	4	5	4	6
sp P15170	6	7	7	7	3	5	4	3
tr B7Z7P8	6	6	6	6	0	0	1	2
tr D6RBD7	6	2	2	2	2	2	1	1
tr K7EM18	4	2	2	2	0	0	0	0
sp P47813	4	3	3	3	0	0	1	2
sp P05198	3	5	5	5	2	2	4	3
sp P20042	1	7	7	7	3	5	4	4
sp P41091	5	8	8	8	3	4	4	4
tr C9IZE1	7	2	2	2	0	0	1	0
sp Q14152	2	11	11	11	2	3	2	4
sp P55884	4	8	8	8	4	4	3	2
sp Q99613	5	7	7	7	4	2	3	3



sp O15371	7	9	9	9	5	5	4	3
sp P60228	6	7	7	7	6	6	6	5
sp O00303	2	3	3	3	2	2	2	2
tr K7EL20	5	4	4	4	2	0	0	1
tr A0A087A	9	4	4	4	3	3	3	2
sp Q13347	2	10	10	10	6	6	6	5
tr H0YGJ7	5	2	2	2	0	1	2	2
tr K7ES31	4	1	1	1	0	1	1	1
tr B0QY89	7	7	7	7	2	1	4	4
tr E9PRY0	5	1	1	1	0	0	1	0
sp Q04637	28	16	16	16	9	10	7	10
tr H0YCH5	6	2	2	2	1	0	1	0
tr E7EX17	4	4	4	4	0	0	2	3
sp Q15056	2	6	6	6	1	3	3	4
sp P55010	5	2	2	2	1	0	0	1
tr I3L397 I	9	8	8	8	6	5	5	4
tr A0A087A	2	5	5	5	2	3	2	1
sp P56537	7	5	5	5	4	4	2	2
tr R4GNH9	6	1	1	1	1	1	1	1
sp Q5RKV6	1	4	4	4	3	3	1	3
sp Q13868	2	1	1	1	0	0	0	1
sp Q15024	1	2	2	2	1	2	1	1
tr F2Z2C0	4	2	2	2	2	1	0	0
sp O14980	10	9	9	9	2	1	3	1
sp P55060	4	12	12	12	5	4	6	7
sp Q9HAV4	3	2	2	2	2	2	1	1
sp Q9BSJ8	2	11	11	11	8	10	9	8
tr E7EQR4	8	14	9	9	6	6	9	7
sp Q9Y5B9	4	10	10	10	5	6	5	5
sp Q08945	4	10	10	10	9	8	8	7
sp P52907	1	7	7	6	6	7	7	6
sp P47755	5	6	5	5	3	3	3	3
sp P47756	5	10	10	10	6	5	7	7
sp Q96AE4	4	12	11	11	0	1	3	4
tr A0A087A	8	14	14	13	5	5	4	6
sp Q96I24	2	8	7	7	5	6	4	2
sp P14324	6	3	3	3	1	1	1	2
sp Q96CS3	1	6	6	6	6	5	6	4
sp Q16658	4	19	19	19	13	13	13	12
tr A0A0U1	5	49	49	49	36	31	31	28
sp Q01469	3	4	4	4	0	0	2	2
tr E9PNW8	2	3	3	3	3	3	3	3
tr J3QRD1	22	7	7	7	4	5	6	4
tr G3V1L6	5	4	4	4	3	2	2	3
sp P02794	9	6	6	6	6	5	6	6
sp Q4ZHG4	2	1	1	1	0	0	0	0
sp P21333	8	88	88	80	69	69	66	69
sp O75369	13	48	43	41	30	32	35	37
sp Q8WUP	3	2	2	2	1	0	1	0
sp P39748	4	6	6	6	4	5	5	3

sp P30043	3	5	5	5	0	1	2	2
sp O75955	13	5	5	5	5	5	5	5
tr J3QLD9	4	6	6	6	5	5	5	5
tr J3KNW4	3	2	2	2	2	0	2	2
tr B4DXZ6	20	6	6	6	4	4	4	3
tr H7C585	5	2	2	2	2	2	2	2
sp O60353	2	1	1	1	1	1	1	1
sp P04075	10	23	23	17	13	14	17	15
sp P09972	6	8	2	2	4	3	7	4
sp P07954	2	11	11	11	9	9	9	9
tr S4R445	4	1	1	1	1	1	1	1
tr E9PN19	9	5	5	5	4	4	4	4
sp P09382	2	8	8	8	7	8	8	7
sp P17931	2	2	2	2	0	1	0	0
sp Q08380	5	4	4	4	4	3	4	2
sp P60520	8	2	2	2	2	2	2	2
sp O75223	7	3	3	3	0	1	2	3
sp Q16666	16	9	9	9	7	7	8	7
sp Q9H488	2	2	2	2	2	2	2	2
;tr A0A0AC	10	12	12	12	11	12	9	5
sp Q12789	2	1	1	1	1	1	0	0
sp P78347	5	8	8	8	7	7	4	5
sp O60763	2	2	2	2	0	0	1	2
tr G3V4P8	2	1	1	1	0	0	0	0
sp Q9NZM	1	2	2	2	0	0	1	1
tr G3V5E4	3	1	1	1	0	0	0	0
tr D6RAY7	10	5	5	5	0	1	1	2
sp P11413	6	15	15	15	8	8	6	6
tr A0A0A0	17	10	10	10	4	4	5	5
tr K7ELL7	7	16	16	16	16	15	15	15
sp P00367	4	18	18	18	18	18	15	16
tr E1CEI4	4	2	2	2	0	0	0	0
sp P48507	2	1	1	1	0	0	0	0
sp Q9BQ67	2	3	3	3	0	0	0	0
sp O94925	7	10	10	10	9	10	8	8
sp Q06210	2	4	4	4	4	4	3	4
sp P47897	10	6	6	2	5	5	4	3
sp O76003	1	2	2	2	0	0	1	1
sp Q86SX6	1	1	1	1	0	1	1	1
sp P00390	7	4	4	4	1	2	3	3
tr E9PFN5	5	3	3	3	1	1	1	1
sp P78417	5	6	6	6	0	1	3	2
sp P09211	4	9	9	9	3	4	5	5
sp P04406	4	15	15	15	12	12	12	11
sp Q53EU6	1	1	1	1	1	1	1	1
sp P43304	3	8	8	8	7	8	7	7
tr A0A1W2	3	2	2	2	2	1	2	2
sp P41250	3	5	5	5	3	2	2	4
sp P49841	2	1	1	1	1	1	1	1
tr G5E9W8	5	1	1	1	0	0	0	1

tr F6TLX2	6	3	3	3	0	0	3	2
tr U3KQ56	2	1	1	1	0	1	1	1
sp P35052	7	7	7	7	5	6	7	6
sp P49915	2	7	7	7	4	4	3	4
sp Q92896	6	6	6	6	5	5	4	4
tr F8W785	2	3	3	3	3	2	1	1
sp Q9H4A6	2	2	2	2	1	1	1	1
sp Q9H8Y8	3	4	4	4	2	2	3	4
sp Q9H3P7	1	1	1	1	1	1	1	0
tr F6RU00	5	1	1	1	1	1	1	1
sp Q08379	3	4	4	4	2	3	4	3
sp Q7Z5G4	2	1	1	1	1	1	1	1
tr D6R9J9	9	1	1	1	0	0	0	1
sp Q9Y653	7	2	2	2	2	1	0	1
tr H0Y8R1	5	2	2	2	2	2	2	2
sp Q9H3K2	1	2	2	2	1	1	0	0
sp Q9HAV7	1	5	5	5	4	5	3	3
sp Q9UIJ7-	3	1	1	1	1	1	1	1
sp P01116	7	2	2	2	2	1	2	2
tr B5MDF5	7	7	7	7	5	4	6	6
tr C9J931	2	1	1	1	1	1	1	0
tr H0Y5E8	3	1	1	1	1	1	1	1
sp P52735	3	2	2	2	1	2	1	1
sp P63096	4	8	4	4	5	6	5	3
sp P04899	6	8	4	4	6	6	6	5
sp Q9UBI6	1	5	5	5	5	4	3	4
sp P62873	12	7	4	4	6	5	5	6
sp P62879	9	9	9	6	7	6	7	7
sp P08754	18	8	8	4	6	6	6	4
sp P50148	2	2	2	1	2	2	2	2
sp P63092	10	4	3	3	4	4	4	4
sp P29992	2	2	1	1	2	2	2	2
sp Q14344	2	1	1	1	1	0	0	1
sp P63244	22	14	14	14	10	12	11	7
sp Q9BVP2	2	2	2	2	1	2	2	2
tr H0Y2M6	3	1	1	1	0	0	0	1
sp Q9NY12	2	2	2	2	2	2	2	2
sp Q9NX24	4	4	4	4	3	3	3	2
sp O60832	7	6	6	6	4	6	5	5
tr Q5T3Q7	3	10	10	10	8	9	9	7
sp Q0VDF9	1	1	1	1	1	1	1	1
tr A0A0G2	5	29	29	15	18	18	19	18
sp P34932	4	19	18	18	6	10	11	13
sp P17066	2	10	1	1	9	9	9	9
sp P11142	15	28	24	18	22	21	20	22
sp O75506	1	1	1	1	1	1	1	1
sp Q92598	10	21	21	20	9	13	13	12
sp Q12931	4	13	13	13	11	10	9	9
sp P04792	3	14	14	14	12	13	13	13
sp P07900	6	34	19	19	23	25	27	25

sp P08238	2	39	39	19	31	30	34	31
sp P54652	1	11	1	1	8	9	9	10
tr J3KT51	5	4	4	4	0	0	2	2
tr H3BMTC	10	2	2	2	0	0	0	0
sp P30519	9	4	4	4	3	3	1	2
tr Q5THN1	2	1	1	1	0	0	1	1
;tr G3V1N2	4	5	5	5	5	5	3	3
sp P68871	2	3	2	2	1	1	1	3
;tr D6RAR4	3	3	3	3	3	3	2	2
tr I3L1P5 I	3	1	1	1	1	1	1	1
sp P51858	3	5	5	5	0	0	1	2
tr B0QZK4	6	6	6	6	3	2	4	3
tr D6R9P3	7	4	4	4	1	2	3	3
sp Q13151	1	5	5	5	5	4	4	3
tr F8W6I7	10	11	10	10	2	4	4	5
sp P51991	3	8	8	8	6	4	3	4
tr H0YA96	10	7	7	7	2	1	2	3
tr A0A087A	4	3	3	3	1	2	1	1
sp P52597	2	11	11	9	9	9	8	8
tr E9PCY7	23	10	8	4	10	10	9	9
sp P55795	1	9	4	4	8	8	8	8
sp P31942	6	7	7	7	7	7	4	4
sp P61978	6	17	17	17	10	12	7	6
sp P14866	14	14	14	8	10	8	3	4
sp P52272	12	23	23	23	19	19	18	15
sp O60506	7	16	16	11	10	10	9	8
sp O43390	5	14	9	9	12	13	10	12
sp Q00839	16	24	24	24	18	21	16	16
tr M0R3F1	9	3	3	3	2	2	2	3
sp Q1KMD	2	15	15	15	12	10	8	10
sp P22626	3	16	16	15	7	7	10	12
tr G3V4WC	30	15	15	15	10	12	14	12
tr E9PB90	2	9	8	8	7	7	7	8
sp P19367	8	14	14	13	12	14	14	12
sp P30825	1	2	2	2	2	2	2	2
tr Q5T7C4	3	5	5	4	3	3	3	1
tr D6R9A6	2	2	1	1	0	1	0	1
tr E9PES6	4	1	1	1	0	0	0	0
sp P17096	4	4	4	4	2	3	3	3
tr F5H2U8	9	1	1	1	0	0	1	0
sp P49773	5	4	4	4	2	2	1	2
tr D6RJE6	8	2	2	2	1	1	1	1
sp O14929	2	1	1	1	0	0	1	0
sp Q92769	2	4	4	2	2	3	3	3
sp P07305	2	4	4	4	2	3	4	4
sp P16403	1	10	10	3	7	9	9	9
sp P10412	4	9	2	2	8	8	8	8
sp P16401	1	7	6	6	6	7	7	7
sp Q92522	1	2	2	2	1	1	1	1
tr A0A0U1	11	5	5	1	5	5	5	5

sp Q71UI9	7	4	2	2	4	4	4	4
tr Q5SQT3	2	2	1	1	1	1	1	1
sp P16104	11	4	1	1	4	4	4	4
sp Q99880	2	8	1	0	8	7	8	7
sp Q16778	6	7	1	0	6	7	7	6
sp Q8N257	1	7	1	1	7	5	7	5
tr U3KQK0	10	8	8	0	7	8	8	7
tr Q5TEC6	1	5	5	1	5	4	5	5
sp P62805	1	8	8	8	8	8	8	8
sp Q09028	15	9	9	5	4	3	5	5
sp Q16576	4	6	2	2	3	3	3	2
sp P16189	19	12	2	0	12	10	10	10
sp P30453	10	12	12	0	12	10	10	10
tr Q8MH48	6	2	1	1	2	2	2	2
sp P30479	7	8	2	0	8	8	7	7
sp P30508	40	9	5	0	9	8	7	7
sp Q95604	1	8	2	0	7	7	6	6
sp P50502	7	7	7	7	5	5	6	6
sp Q16543	5	8	8	8	4	4	4	5
tr H3BRH5	3	1	1	1	1	1	1	1
tr A0A0D9	13	5	5	5	5	5	5	4
sp P35914	1	2	2	2	1	2	2	2
sp Q01581	2	8	8	8	4	2	4	7
sp Q6YN16	2	5	5	5	5	5	5	5
sp P00492	1	5	5	5	1	0	2	5
tr A0A087	13	8	8	8	7	7	8	6
tr A0A1W2	2	1	1	1	1	1	1	1
sp P52292	4	9	9	9	6	7	6	6
sp O00629	2	5	5	4	4	3	4	3
sp O00505	1	2	1	1	1	1	2	1
sp P52294	8	2	2	2	1	2	1	1
sp Q14974	7	15	15	15	10	12	10	10
tr H0Y8C6	12	10	10	10	1	0	3	1
sp O95373	1	4	4	4	1	1	1	1
sp Q96P70	1	2	2	2	1	0	0	0
sp Q13308	9	2	2	2	1	2	2	2
sp Q70UQI	2	2	1	1	2	2	2	2
sp Q70UQI	1	2	2	1	2	2	2	2
sp Q9NQS7	2	2	2	2	1	1	2	2
sp Q9Y2U8	1	2	2	2	0	1	2	2
sp Q15181	2	9	9	9	5	5	4	6
sp Q9BY32	3	2	2	2	1	0	0	1
tr H0Y4R1	4	12	12	11	10	12	10	8
sp Q14573	11	6	6	6	6	6	5	5
sp O00425	11	4	4	4	4	4	3	1
sp Q9Y287	2	4	4	4	3	3	3	3
tr J3QRY6	8	1	1	1	1	1	1	1
sp P17301	5	15	15	15	13	13	13	12
sp P26006	4	5	5	5	5	4	4	4
sp P23229	10	22	22	22	20	20	19	15



sp P06756	4	5	5	5	5	5	4	5
tr A0A0871	4	2	2	2	2	2	2	2
sp P05556	15	14	14	14	13	14	13	14
sp P16144	8	36	36	36	29	32	31	33
sp P05362	2	2	2	2	2	2	2	2
sp P15260	4	3	3	3	2	2	2	2
tr B1AJU4	3	3	3	3	0	0	1	1
tr H7BYV1	6	1	1	1	0	0	1	1
sp P19525	4	5	5	5	4	5	5	3
tr B4DY09	4	8	8	8	3	6	6	5
sp Q12906	20	20	20	20	7	9	11	11
sp Q27J81	2	1	1	1	0	1	1	0
tr D6RGE2	2	1	1	1	0	0	0	0
tr H0YL72	9	8	8	8	6	6	5	6
sp P51553	7	3	3	3	2	2	3	2
sp O75874	6	13	13	13	6	6	6	8
sp P41252	5	12	12	12	9	9	6	5
sp Q9NSE4	1	7	7	7	6	7	7	7
tr C9JD53	4	1	1	1	1	1	1	1
sp P14923	7	20	20	18	15	17	17	17
sp Q9Y624	3	9	9	9	8	5	6	9
tr K7EM02	4	1	1	1	1	1	1	1
;sp P13645	9	7	4	4	4	6	5	4
;sp P13646	10	27	25	11	27	27	27	24
;sp P19012	5	16	7	5	16	15	14	15
sp P05783	7	25	24	18	23	22	21	21
;sp P08727	6	33	33	22	30	32	31	30
sp P35527	3	5	4	4	1	1	3	3
;sp P04264	2	8	4	2	4	5	5	6
;sp P35908	3	7	1	1	5	5	5	5
;sp P13647	21	28	24	5	24	25	24	23
;sp P02538	9	23	12	2	16	21	20	20
sp P04259	1	20	1	0	13	17	17	17
;sp P08729	2	37	37	3	34	32	32	31
;sp P05787	52	36	33	29	33	34	33	31
sp Q07666	3	3	3	3	2	2	1	1
sp Q86UP2	7	5	5	5	0	0	1	1
sp P33176	5	6	6	6	5	6	3	3
sp Q15058	1	1	1	1	1	1	1	1
tr H7BYN4	6	5	5	5	3	5	5	5
sp Q13601	2	1	1	1	1	1	0	1
tr K7EM91	6	4	4	3	4	4	4	3
sp Q16719	1	1	1	1	0	0	0	0
sp Q04760	2	2	2	2	1	1	2	0
tr E9PDI4	6	7	7	7	4	6	6	6
sp P42166	2	11	4	4	10	10	10	8
sp P42167	4	13	13	6	11	11	11	11
sp Q14739	3	4	4	4	2	4	4	3
sp P20700	4	32	31	30	25	29	28	27
sp Q03252	1	27	25	25	26	25	24	24

tr K7EIP4	8	1	1	1	1	1	1	1
sp O15230	2	3	3	3	2	3	1	1
sp Q13751	2	7	7	7	6	6	6	6
sp P11047	1	5	5	5	5	5	5	4
sp Q13753	2	7	7	7	7	5	7	7
tr F8WDS9	3	1	1	1	0	0	1	1
tr A0A0C4I	4	6	6	6	3	6	4	3
sp P48449	5	3	3	3	3	3	3	3
sp Q01650	1	5	5	5	4	4	4	3
tr A0A0G2	13	3	3	3	0	0	0	0
sp Q14696	1	2	2	2	2	2	2	1
sp Q8NC56	5	2	2	2	2	2	2	1
sp O95202	1	5	5	5	5	5	5	4
sp P42704	9	33	33	33	25	27	27	25
sp Q32MZ	9	5	5	5	2	1	1	2
sp O75473	3	1	1	1	1	1	1	1
sp Q8N1G	1	3	3	3	1	1	1	1
sp Q96AG	2	8	8	8	7	7	7	7
sp Q9P2J5	3	5	5	5	4	3	2	3
sp Q9UIQ6	3	3	3	3	1	2	3	2
sp P30740	2	4	4	4	1	0	2	2
sp Q08722	4	3	3	3	3	3	3	3
sp P09960	5	6	6	6	1	1	4	5
sp Q14847	7	8	8	8	4	4	5	5
tr F8VQE1	8	12	12	12	5	3	7	9
tr S4R3V8	9	3	3	3	2	2	2	2
sp P00338	22	13	13	12	7	9	8	7
sp P07195	4	9	8	8	4	2	5	6
tr K7EJE8	7	6	6	6	6	5	6	6
sp Q6P1M	2	4	4	4	4	4	4	2
sp O95573	2	12	12	10	11	11	10	10
sp O60488	3	5	3	3	5	4	4	4
sp P24666	7	3	3	3	1	2	0	1
tr J3KMZ9	9	5	5	5	4	3	4	5
sp Q7Z4F1	1	1	1	1	1	0	1	1
tr J3KPP4	5	3	3	3	1	2	1	1
sp P05455	3	4	4	4	0	0	1	1
tr C9JY28	5	1	1	1	0	1	1	1
sp Q15046	5	8	8	8	5	5	6	6
sp Q6UWP	10	3	3	3	3	3	3	3
tr A0A0G2	3	2	2	2	1	2	2	2
sp Q7L5N7	3	3	3	3	1	3	1	1
sp Q6P1A2	2	1	1	1	1	1	1	1
sp Q96N66	3	4	4	4	3	4	3	3
tr D6RDG0	12	1	1	1	1	1	1	1
sp P11279	2	4	4	4	4	3	4	4
sp P13473	3	2	2	2	2	2	2	2
tr H0YAR1	2	2	2	2	2	2	2	1
sp P14174	1	2	2	2	2	1	2	2
sp P40121	4	4	4	4	1	1	2	4

tr A0A087	3	3	3	3	3	3	3	3
sp P07199	1	4	4	4	3	2	2	2
tr D6RIZ4	4	1	1	1	0	1	1	1
sp Q95460	3	1	1	1	1	1	1	1
tr A2A2V1	3	2	2	2	2	1	2	2
sp Q14764	10	11	11	11	8	7	10	11
tr B9A041	7	6	6	6	1	2	3	4
sp P40926	3	18	18	18	18	18	17	17
sp Q14165	4	4	4	4	4	4	3	4
sp Q9ULC4	3	1	1	1	0	0	0	0
sp Q9Y5P6	2	1	1	1	0	0	0	0
tr J3KSI4 J	14	2	2	2	1	1	1	1
sp Q13724	4	6	6	6	4	4	4	2
sp Q8NDCI	1	1	1	1	0	0	0	0
sp P49006	1	2	2	2	0	0	0	1
tr A0A0R4.	21	17	17	17	14	15	11	9
sp P50281	2	4	4	4	4	2	3	3
sp Q14676	5	8	8	8	3	5	6	7
tr E9PGW7	6	1	1	1	0	0	0	0
tr B7Z9I1	6	2	2	2	1	2	2	1
sp P08582	1	3	3	3	0	1	2	1
sp Q8N4V:	2	1	1	1	1	1	1	1
sp O00264	2	4	3	3	4	4	4	4
sp O15173	3	4	4	3	4	4	4	4
tr I3L1H7	10	1	1	1	1	1	1	0
tr A8K878	3	4	4	4	3	4	4	4
tr B8ZZX6	5	2	2	2	2	1	1	1
sp P80297	10	2	2	2	1	1	1	1
sp O94776	2	4	4	4	3	2	4	4
sp Q13505	4	4	4	4	4	3	3	4
tr C9JAZ1	4	2	2	2	2	2	2	2
tr H7C0X7	5	1	1	1	0	0	1	1
sp P53582	3	3	3	3	3	3	3	3
tr G3V1U3	9	2	2	2	0	0	1	1
sp P56192	8	6	6	6	3	4	3	3
tr X6RBL6	3	1	1	1	0	1	1	0
sp Q9HCCC	5	3	3	3	3	2	3	3
tr G5E9X5	5	1	1	1	1	1	1	1
sp Q9BQA:	2	1	1	1	0	1	1	1
tr E9PMI6	3	1	1	1	1	1	1	1
tr F5H8H2	4	2	2	2	1	2	1	2
tr A0A087	5	2	2	2	1	2	2	2
tr C9JRZ6	4	6	6	6	5	4	4	4
tr J3QTB2	3	1	1	1	1	1	1	1
sp Q16891	9	16	16	16	15	15	13	13
sp Q99735	2	1	1	1	1	1	1	1
tr Q5VV89	3	2	2	2	1	2	1	2
sp P11137	2	1	1	1	0	0	0	0
sp Q15691	1	8	8	8	0	1	2	2
tr H0Y2V1	10	3	3	3	0	1	1	1

tr E9PPJ5	4	2	2	2	2	2	2	2
sp Q9BTE3	2	1	1	1	1	0	0	1
sp Q8TCT9	6	3	3	3	2	2	2	2
sp Q8N4C8	5	1	1	1	1	1	1	1
tr I3L1P8 I	3	5	5	5	5	5	5	5
sp Q7Z434	2	3	3	3	2	2	2	2
tr H0Y8C3	4	4	4	4	4	4	4	4
sp Q9Y6C9	2	6	6	6	2	4	4	3
sp Q9UBX3	3	4	1	1	3	3	3	2
sp Q9Y3D6	1	2	2	2	1	2	1	1
tr E9PJH7	16	2	2	2	1	2	2	2
sp Q9Y5L4	1	2	2	2	2	2	0	0
sp O43615	3	6	6	6	5	4	6	6
tr M0R047	3	1	1	1	1	1	1	1
sp O60220	1	2	2	2	2	2	2	2
tr G3V2F3	5	1	1	1	1	1	1	1
sp Q9NS69	1	5	5	5	5	5	5	5
sp Q15785	1	4	4	4	3	2	1	3
sp O96008	4	9	9	9	9	7	7	9
sp O94826	1	8	8	8	7	8	7	7
tr C9JC63	7	1	1	1	0	1	0	0
sp Q99797	1	1	1	1	1	1	1	1
tr C9JVB6	2	3	3	3	3	3	3	3
sp Q10713	3	6	6	6	3	3	5	5
sp O75439	5	4	3	3	3	3	3	1
sp P28482	2	2	2	2	0	0	0	0
tr J3QT28	4	5	5	5	5	4	5	5
sp Q8IVT2	1	2	2	2	1	1	1	1
sp Q9BYG3	4	3	3	3	3	3	3	3
sp P26038	2	21	21	16	7	5	10	11
sp P53985	1	2	2	2	2	2	2	2
tr A0A087A	7	3	3	3	3	3	3	2
tr H3BVD1	19	2	2	2	1	1	1	1
tr E9PPG9	4	5	5	5	4	4	4	5
sp Q9UKD3	1	3	3	3	2	2	3	3
tr F8WCY8	3	1	1	1	0	1	1	1
tr F5GYQ2	4	1	1	1	1	1	1	1
tr E9PBS1	4	8	8	8	5	3	3	4
tr C9JP00	15	2	2	2	2	2	0	1
sp Q9BQG1	5	15	15	15	9	13	13	12
sp Q9NUJ1	3	2	2	2	2	2	2	1
sp O95297	6	4	4	4	3	3	4	2
sp O60487	1	1	1	1	1	1	1	1
tr C9JJV6 I	5	2	2	2	2	2	2	2
sp Q9NZM	24	49	49	49	44	46	44	43
sp P05976	3	1	1	1	1	1	0	1
tr F8W1R7	14	9	9	7	8	7	6	7
tr J3KSW8	6	2	2	2	1	2	2	1
tr J3QRS3	6	8	8	8	7	8	6	6
sp P35580	5	13	1	1	13	13	10	8

sp P35749	4	11	1	1	10	11	9	9
sp Q7Z406	7	9	2	2	9	9	6	6
sp P35579	20	104	104	88	99	94	75	68
tr C9JL85	2	2	2	2	0	0	1	2
sp P29966	1	8	8	8	5	5	6	7
sp O14745	3	2	2	2	0	0	0	0
sp Q86SF2	4	2	2	2	2	2	2	2
sp Q9H0A0	5	13	13	13	12	11	10	12
tr A0A0G2	23	4	4	4	4	3	2	1
sp Q13423	4	4	4	4	2	2	1	2
tr B4DLR8	6	4	4	4	3	2	2	3
tr A0A1W2	13	4	4	4	4	4	4	3
sp Q9BU61	1	1	1	1	1	1	1	1
tr F8WAS3	6	1	1	1	1	1	1	1
tr F5H0J3	2	1	1	1	1	1	0	0
tr H3BPJ9	4	2	2	2	1	1	1	1
tr E7EPT4	2	2	2	2	2	2	2	2
sp O75306	2	2	2	2	0	1	2	2
sp O75489	1	1	1	1	1	1	1	1
tr H7C0R7	2	1	1	1	1	1	1	1
sp P00387	4	6	6	6	5	5	5	5
sp P48163	2	1	1	1	0	0	0	0
tr A0A0A0	14	3	3	3	2	1	3	3
sp P16435	3	4	4	4	4	3	3	3
tr E7EQ69	9	2	2	2	1	0	1	1
tr F8VZJ2	8	2	2	2	2	2	2	2
sp Q9Y2A7	2	1	1	1	0	0	0	1
sp Q9BT67	1	1	1	1	1	0	0	0
tr H7C5F7	4	2	2	2	2	2	1	2
sp P61081	3	3	3	3	0	0	0	0
sp Q9UMX	1	2	2	2	2	1	2	2
sp Q09666	7	138	138	138	101	107	120	120
tr H0YAK4	3	1	1	1	1	0	1	0
sp Q9Y639	8	3	3	3	2	3	3	2
sp Q14697	2	26	26	1	25	25	20	17
sp Q14697	4	26	1	1	25	25	20	17
sp P43007	2	2	2	2	2	2	2	2
sp Q15758	6	9	9	9	8	8	8	8
tr A0A0R4	6	4	4	4	4	4	4	3
tr X6R8F3	3	4	4	4	4	4	4	4
tr B7Z5R6	3	1	1	1	1	1	1	1
tr B1AHD1	2	3	3	3	2	3	3	3
sp Q96TA1	2	3	3	3	1	0	0	2
sp Q969V3	4	4	4	4	3	3	3	2
sp P43490	4	8	8	8	3	3	4	4
sp Q6XQN	2	1	1	1	0	0	0	1
tr K7EQ23	3	1	1	1	1	1	1	1
tr J3KN36	11	6	6	6	6	6	6	6
sp P05204	4	3	3	3	0	0	0	0
sp Q15233	6	13	12	12	8	10	9	6



sp P22307	7	4	4	4	4	3	4	4
tr J3QRU1	7	3	3	3	1	1	1	1
sp Q9UNZ:	8	6	6	6	0	0	3	4
sp Q9BV86	2	1	1	1	1	1	1	1
tr H0YDS9	8	3	3	3	0	0	0	1
sp Q09161	1	4	4	4	2	2	1	2
tr F8WE41	3	1	1	1	0	0	1	1
tr D6RH30	3	1	1	1	0	1	1	0
sp Q7Z417	1	3	3	3	2	3	3	1
sp Q9Y266	3	5	5	5	2	3	3	3
sp Q14980	16	46	46	46	33	30	38	36
sp P57740	5	6	6	6	5	4	5	5
sp Q8WUN	1	6	6	6	5	4	4	4
sp P49790	3	6	6	6	3	4	4	4
tr E9PF10	4	13	13	13	10	9	10	10
tr G3V198	6	7	7	7	5	5	5	5
sp Q92621	2	9	9	9	7	5	7	5
tr A0A0A0	10	5	5	5	2	4	4	4
sp Q9UKX:	2	1	1	1	1	1	1	1
tr J3QL54	9	2	2	2	2	2	2	2
tr J3KMX1	4	5	5	5	5	5	5	5
tr H3BVG0	12	7	7	7	7	7	5	6
sp P52948	10	6	6	6	5	4	5	4
sp P37198	2	3	3	3	2	2	2	3
sp Q8TEM	2	4	4	4	3	4	3	2
sp Q8TAT6	2	1	1	1	0	0	0	0
sp Q13772	6	6	6	6	6	4	4	5
sp P61970	2	5	5	5	1	3	3	2
sp Q9H1E3	2	3	3	3	0	0	1	0
sp O15381	5	1	1	1	1	1	1	1
sp P67809	4	10	10	7	5	6	9	8
sp Q02818	2	3	3	3	2	2	0	1
tr A0A0A0	7	5	5	5	2	1	4	2
sp Q9Y3T9	1	4	4	4	1	2	3	4
sp Q8WTT	1	1	1	1	0	0	0	0
sp Q9BZE4	4	10	10	10	6	8	8	7
sp O60287	1	1	1	1	0	0	1	1
sp Q9H8H6	4	2	2	2	2	2	2	2
tr E9PFK5	3	1	1	1	0	1	1	1
tr D6RC60	7	1	1	1	0	1	1	1
sp O00567	4	10	10	10	8	9	10	10
sp Q9Y2X3	3	10	10	10	9	10	10	9
sp Q9H6R4	6	2	2	2	2	2	1	2
sp Q9NR36	3	18	18	17	15	15	15	16
tr E9PKP7	4	3	3	3	2	2	3	3
sp P19338	6	23	23	23	17	17	16	17
tr F8WE16	7	1	1	1	0	0	0	0
sp P06748	5	12	12	12	9	10	10	10
tr F8VTY2	2	1	1	1	1	1	1	1
sp Q8NFH:	2	3	3	3	3	3	2	3

sp Q8NFH!	8	5	5	5	4	4	5	4
sp Q7Z3B4	3	3	3	3	2	2	3	3
sp Q96EE3	6	5	5	5	4	4	2	3
sp P12270	2	14	14	14	9	8	9	8
tr A0A0G2	2	1	1	1	0	1	0	1
sp P15531	4	5	1	1	1	3	2	2
tr Q32Q12	7	8	8	4	3	5	3	4
tr H0YHC3	18	3	3	3	3	3	3	2
tr C9JZI7 C	14	4	4	4	3	1	3	4
sp Q96RS6	3	2	2	2	0	0	0	0
tr E5RFP0	2	1	1	1	1	1	1	1
tr C9JTK6	4	1	1	1	1	0	1	1
sp Q56VL3	4	3	3	3	3	3	3	3
tr A0A087^	3	1	1	1	1	1	1	1
sp Q9NQR-	3	7	7	7	6	6	6	6
sp Q99650	2	1	1	1	1	1	1	1
tr F6WST4	4	1	1	1	1	1	0	0
tr J3QRM9	3	1	1	1	1	1	1	1
sp P04181	2	10	10	10	10	9	9	9
sp Q92882	1	1	1	1	0	0	1	0
sp P36551	3	5	5	5	5	5	4	3
sp Q9NWT	1	1	1	1	0	0	1	1
sp Q15645	3	3	3	3	3	3	3	1
tr E9PSE5	6	1	1	1	1	1	1	1
tr B4DRN8	2	1	1	1	1	1	1	1
sp Q8WXF	3	3	3	3	1	0	0	1
sp O00151	1	10	10	10	2	2	6	7
sp O14908	5	2	2	2	1	1	1	1
sp Q96EY7	2	2	2	2	2	1	2	2
sp P62937	1	8	1	1	8	8	8	7
sp P62937	12	11	11	4	10	10	9	8
sp P23284	1	10	10	10	9	9	7	9
sp P45877	1	1	1	1	1	1	1	1
sp P30405	9	4	3	3	0	0	1	1
sp P62942	7	3	3	3	0	1	1	1
sp P26885	2	2	2	2	1	1	2	2
sp Q00688	1	3	3	3	0	0	1	1
sp Q02790	4	12	12	12	5	8	6	9
tr M0R2K9	3	1	1	1	1	1	1	1
sp Q9Y3C6	1	2	2	2	1	0	0	1
sp Q8WUA^	1	1	1	1	0	0	0	0
tr J3KQ48	2	2	2	2	2	2	2	2
tr E5RGQ4	8	2	2	2	1	0	0	1
sp O60664	7	8	8	8	2	3	7	6
sp Q15269	3	3	3	3	3	2	2	1
sp Q06830	3	15	15	11	11	11	10	11
sp P32119	3	9	8	8	4	4	5	4
sp Q13162	4	12	9	9	10	10	8	5
sp P30044	4	6	6	6	6	6	6	6
sp P30041	1	9	9	9	6	7	8	7

tr I3L2U4	5	1	1	1	1	1	1	1
sp Q92968	1	1	1	1	0	1	1	0
sp O75381	2	2	2	2	1	2	1	2
sp P51659	8	17	17	17	15	14	16	15
tr M0QXB5	2	1	1	1	1	1	1	1
tr B5MCF9	5	8	8	8	1	3	3	3
tr C9JZE2	10	1	1	1	1	1	1	1
sp Q7RTVC	1	2	2	2	2	2	2	1
tr K7ER00	5	3	3	3	1	2	2	1
sp Q9NSD9	2	10	10	10	3	3	2	2
sp Q8WW0	1	2	2	2	0	1	2	2
sp Q00325	6	8	8	8	7	7	6	6
sp O95674	1	1	1	1	1	1	1	1
sp P30086	1	6	6	6	0	0	2	1
tr C9J3E3	5	1	1	1	1	1	1	0
tr A0A0A0	15	4	4	4	1	1	1	1
sp Q13492	24	4	4	4	2	2	2	3
sp P48651	3	1	1	1	1	1	0	1
sp Q16822	9	4	4	4	3	3	3	3
sp P36871	3	8	8	8	0	0	2	2
sp Q96G03	2	1	1	1	0	0	1	1
sp P00558	3	15	15	15	10	13	13	12
sp P18669	3	11	11	11	5	4	5	5
sp Q8IV08	2	2	2	2	1	1	1	1
tr C9J7K9	7	2	2	2	1	1	2	2
tr C9JDU5	9	1	1	1	0	1	1	0
sp Q9Y617	2	8	8	8	2	2	3	4
tr C9JBI3 C	2	1	1	1	0	0	0	1
sp Q9H307	1	3	3	3	3	3	3	3
sp O00625	1	1	1	1	0	0	0	0
sp Q13835	2	2	2	2	1	2	2	1
sp Q99959	3	2	2	2	1	1	1	1
sp Q9Y446	7	9	9	9	4	8	8	8
sp P20020	32	3	3	3	3	3	3	3
sp Q8NC51	4	11	11	11	3	3	6	7
sp P05120	6	6	6	6	3	3	2	4
sp P13796	4	19	19	13	7	7	10	12
tr A0A0A0	8	16	10	10	5	5	5	7
sp P43034	3	5	5	5	2	3	4	5
sp P68402	4	1	1	1	0	0	0	0
tr R4GND3	2	1	1	1	1	1	1	1
sp Q15149	14	102	102	102	86	88	87	79
sp O43660	3	2	2	2	1	0	2	2
sp O75051	1	1	1	1	1	1	1	1
sp O15031	4	6	6	6	6	5	6	5
sp P09874	3	17	17	17	13	14	12	11
sp Q9NVV4	2	1	1	1	1	1	1	1
sp Q15365	2	9	9	7	6	7	5	6
sp Q15366	23	8	6	6	5	6	5	6
tr A0A0J9Y	18	8	8	8	2	2	7	7

sp P11940	26	18	18	14	14	16	12	12
sp Q86U42	6	2	2	2	1	1	1	2
tr B1ANR0	8	7	3	3	4	5	3	4
tr D6REB4	4	2	2	2	0	0	0	0
tr B4DEM9	2	1	1	1	1	1	1	1
tr F6VRR5	7	2	2	2	2	1	1	1
sp Q6NZI2	3	10	10	10	7	8	8	7
sp Q10471	5	9	9	9	8	8	8	8
tr E7EUL0	3	3	3	3	3	2	3	3
tr A6NLN1	12	10	10	8	6	7	7	6
sp O95758	8	8	6	6	7	7	5	3
sp Q8TCS8	4	3	3	3	3	2	2	1
tr A6NP52	2	1	1	1	1	1	1	1
tr E5RGS4	2	1	1	1	0	0	0	1
sp Q9UHV9	1	1	1	1	0	0	0	0
tr E9PQY2	2	1	1	1	0	0	0	0
sp P02545	10	39	39	38	32	35	33	33
sp Q9UMS	5	10	10	10	6	7	7	7
sp O75400	3	2	2	2	2	2	1	1
sp O94906	2	9	9	9	4	7	4	5
sp Q6P2Q9	3	16	16	16	9	10	9	8
sp Q8NAV9	1	1	1	1	0	1	1	0
sp O43143	1	6	6	6	5	5	5	5
sp Q9ULRC	3	1	1	1	1	0	0	0
sp Q9UHG	5	2	2	2	1	1	1	1
sp Q8IY81	1	7	7	7	4	5	6	7
sp Q2NL82	2	4	4	4	4	4	1	0
sp Q5JRX3	6	6	6	6	6	5	5	5
sp Q96IZ0	1	1	1	1	1	0	1	1
sp P46087	10	14	14	14	10	8	13	14
tr F5GYY1	14	1	1	1	1	1	1	1
tr A0A1X79	6	18	18	11	15	16	13	12
tr B7Z6D5	4	7	7	7	3	4	7	6
tr F8WAJ0	4	2	2	2	1	2	1	2
tr A0A0C4I	3	7	7	7	7	6	4	2
sp Q9H0S4	2	2	2	2	2	2	2	2
tr J3KTA4	10	17	10	10	15	14	10	12
tr F8WDT8	5	1	1	1	0	1	1	1
sp P26196	2	2	2	2	2	1	2	2
sp Q9HA75	3	2	2	2	1	1	2	1
tr A0A0A0	4	3	2	2	2	3	2	1
sp Q96K78	1	1	1	1	0	0	0	0
tr H3BMQ9	2	1	1	1	1	1	1	1
sp Q9Y4C8	1	2	2	2	2	1	2	2
tr H7C2Q8	2	7	7	7	3	4	4	5
sp Q8NBJS	3	9	9	9	8	8	7	8
sp Q02809	2	4	4	4	3	2	3	4
tr E7ETU9	4	2	2	2	2	2	2	2
sp O60568	4	7	7	7	7	6	6	6
sp P07737	4	10	10	10	7	7	7	8

sp Q8WUN	7	7	7	7	4	5	5	5
sp Q53EL6	2	1	1	1	0	0	0	0
tr A0A0240	3	2	2	2	0	2	1	0
sp P35232	7	13	13	13	12	11	11	12
sp Q99623	9	17	17	17	12	14	13	13
sp P12004	1	7	7	7	4	2	7	5
sp Q9UQ80	6	16	16	16	7	7	6	7
sp P13674	3	6	6	6	6	5	5	5
sp O15460	2	3	3	3	2	2	1	1
sp P48147	1	3	3	3	2	1	2	1
tr C9JIZ6 C	6	8	8	8	4	4	4	3
sp O14684	1	2	2	2	2	2	2	2
tr X6RJ95	3	3	3	3	3	3	3	3
tr A0A0870	6	5	5	5	4	3	0	1
sp Q9P2B2	1	2	2	2	1	2	2	1
sp Q14914	4	6	6	6	1	0	4	1
sp Q16186	2	2	2	2	2	2	2	1
sp Q06323	4	5	5	5	0	0	4	3
tr H0YM7C	4	2	2	2	1	0	1	2
tr K7ENH2	12	3	3	3	0	0	0	0
tr H0Y555	4	1	1	1	0	1	1	1
tr C9JCK5	3	2	2	2	0	1	2	0
tr H0YMZ1	12	5	5	5	4	3	3	3
tr G3V295	9	7	7	7	2	4	6	5
sp P25786	4	11	11	11	3	5	5	4
sp P25788	5	3	3	3	0	0	1	1
sp P28066	2	8	8	8	4	5	3	2
sp O14818	9	9	9	9	6	5	6	5
tr X5D2R7	5	3	3	3	0	0	1	1
tr A2ACR0	6	1	1	1	0	0	1	1
sp P20618	1	5	5	5	4	4	5	4
sp P49721	2	2	2	2	0	0	0	0
tr A0A0870	4	2	2	2	1	2	2	2
sp P28070	1	2	2	2	0	0	1	1
sp P28074	4	7	7	7	3	2	2	3
sp P28072	3	3	3	3	3	2	3	3
sp Q99436	3	2	2	2	1	1	1	1
tr J3KN16	4	2	2	2	0	0	0	0
sp Q9NY61	3	3	3	3	1	0	2	1
sp Q99873	10	7	7	7	4	5	5	4
tr H0YJX6	10	2	2	2	2	2	2	2
sp Q8TD16	2	1	1	1	0	0	0	0
sp P41223	3	2	2	2	1	0	1	1
tr F8W031	9	5	4	4	4	3	3	4
tr A0A0J9Y	2	2	2	2	2	1	2	2
sp Q9UKY7	8	3	3	3	0	0	2	3
tr A6NLH6	2	1	1	1	1	1	1	1
tr C9IZG4	4	1	1	1	0	0	1	1
sp Q99497	3	6	6	6	3	3	3	4
sp P35659	7	5	5	5	4	4	5	5

tr A0A140	7	9	9	9	0	1	1	1
sp P07237	12	22	22	22	21	21	18	19
sp P30101	1	22	22	17	21	21	19	19
sp P13667	1	14	14	14	12	12	12	13
sp Q15084	5	13	13	13	12	9	11	9
tr H3BPB3	4	1	1	1	1	0	1	1
sp Q8WYP	4	4	4	4	2	2	4	4
sp P49257	1	9	9	9	8	8	7	8
tr H7C3D5	2	1	1	1	1	0	1	1
sp Q49AJ0	5	2	2	2	1	1	1	2
tr F8W7Q4	3	3	3	3	3	3	2	2
tr K7ELZ8	5	1	1	1	1	1	0	1
sp Q92520	3	6	6	6	3	5	4	3
sp Q9NUUQ	12	3	3	3	0	1	3	0
sp Q6ZRV2	2	22	22	22	19	20	18	18
sp Q8NCA!	2	1	1	1	1	1	0	0
sp Q52LJ0	2	3	3	3	2	2	1	2
sp Q13045	6	2	2	2	2	1	2	1
tr G5E994	3	1	1	1	0	0	1	1
tr M0R2E1	5	1	1	1	1	0	0	0
sp P78504	4	2	2	2	2	2	2	2
tr A0A0U1	6	2	2	2	1	0	0	0
tr E9PIE3	2	2	2	2	1	2	2	2
sp P41743	1	1	1	1	1	1	1	1
tr C9JEN3	8	2	2	2	2	2	2	2
tr G3V1D4	6	2	2	2	0	0	0	1
sp Q9C0E8	4	2	2	2	1	2	2	2
sp Q86UE4	3	5	5	5	3	4	5	5
tr F5H6P7	6	2	2	2	2	2	1	1
tr H0YBV6	2	1	1	1	1	0	0	0
sp Q969L2	1	1	1	1	1	1	1	1
sp Q92597	14	9	9	9	3	4	4	4
sp Q9BZQ8	1	4	4	4	0	1	1	2
sp Q9BPW	3	2	2	2	0	2	1	1
sp Q9UFN(	1	1	1	1	1	1	1	1
sp Q96C9C	1	2	2	2	1	0	2	2
tr B5MBZ8	9	1	1	1	0	0	0	0
sp O15355	1	5	5	5	1	1	1	1
sp P29590	16	12	12	12	10	10	9	10
tr E7EPN9	9	2	2	2	1	0	1	0
sp Q9P258	1	7	7	7	5	4	4	4
tr Q5T092	4	1	1	1	1	1	1	1
sp Q14690	1	6	6	6	4	4	3	5
tr R4GN98	2	2	2	2	1	1	1	2
sp P60903	1	3	3	3	2	3	2	2
sp P31949	1	4	4	4	4	4	4	4
sp Q99584	1	1	1	1	0	0	0	1
sp Q9HCY8	1	5	5	5	4	5	5	3
sp Q96FQ6	1	2	2	2	1	2	2	2
sp P29034	3	5	5	5	5	4	3	3



sp O43819	1	2	2	2	2	2	2	2
sp P55735	5	4	4	4	4	3	3	4
sp Q01105	7	8	8	8	1	0	2	4
sp P18583	11	4	4	4	3	3	3	4
tr H3BT44	8	1	1	1	1	1	1	1
tr H7C4R5	3	2	2	2	1	2	2	1
sp Q92734	7	4	4	4	3	2	3	3
tr G5EA31	3	2	2	2	2	1	2	2
tr D6RHZ5	13	1	1	1	0	1	1	0
tr B4DR61	15	4	4	4	4	4	4	4
sp P60468	2	3	3	3	3	3	3	3
sp P60059	1	1	1	1	1	1	1	1
tr A0A1W2	3	1	1	1	1	1	0	0
tr E9PS11	3	1	1	1	1	1	1	1
sp Q969M	2	1	1	1	0	1	0	0
tr A0A0A0	6	5	5	5	3	3	3	4
tr Q5TG12	9	3	3	3	3	3	2	2
tr B8ZZQ6	6	5	5	5	0	0	2	4
sp Q08174	5	7	7	7	7	4	4	7
sp O60245	4	3	3	3	3	3	3	2
sp P00491	4	7	7	7	0	0	1	2
tr J3QSB7	11	4	4	4	2	1	2	1
tr E9PLK3	11	8	8	8	2	2	5	5
sp O43865	7	2	2	2	1	1	1	0
sp Q4W5N	1	1	1	1	0	0	0	0
tr H7BXY3	4	1	1	1	1	1	1	1
sp Q5VTE0	7	19	19	11	18	18	16	16
sp Q58FF8	1	10	1	1	7	9	9	9
sp Q58FF6	1	6	1	1	3	4	4	4
tr Q5JR04	3	3	3	3	2	2	1	1
sp Q5T280	2	2	2	2	2	2	2	1
tr K7EMM5	6	1	1	1	0	0	1	1
tr A0A087^	5	2	2	2	1	0	0	0
sp Q96HJ9	10	3	3	3	1	2	2	2
sp Q5T440	1	1	1	1	1	1	1	1
sp A6NIL9	1	1	1	1	1	1	0	0
tr A0A087^	9	2	2	2	2	2	1	1
sp P11498	4	8	8	8	7	5	7	6
sp P08559	8	3	3	3	3	3	3	3
sp P11177	5	5	5	5	5	3	4	5
sp O00330	2	1	1	1	0	0	1	1
sp P14618	11	39	39	4	29	32	29	28
sp P14618	4	36	1	1	26	29	26	25
sp P50395	10	13	13	13	6	5	9	8
sp Q9H0H5	4	3	3	3	3	3	3	3
sp Q6IAA8	5	4	4	4	4	4	4	3
tr R4GMU8	4	1	1	1	1	1	1	1
sp P46060	5	12	12	12	6	6	7	8
sp P43487	7	3	3	3	2	2	2	3
sp Q13283	8	9	9	9	0	4	3	4

sp P46940	9	36	36	35	19	19	21	24
sp Q15404	2	2	2	2	0	0	1	1
sp P63000	3	9	9	3	5	7	5	7
sp P15153	13	8	2	2	5	7	3	7
sp Q9HB9C	3	2	2	2	1	1	0	0
sp P61026	3	6	5	5	5	5	6	6
sp Q15907	8	11	11	10	9	9	10	9
sp P61106	2	13	13	13	13	12	12	5
sp Q9NP72	6	7	7	7	6	6	7	5
sp P62820	11	11	11	4	11	10	11	11
sp Q9H0U4	3	11	4	3	9	9	9	9
sp Q9UL25	1	4	4	4	4	4	4	3
sp P57735	1	2	1	1	2	2	2	2
tr H3BU81	7	1	1	1	1	1	1	1
sp P61019	10	7	7	7	7	7	6	5
sp Q13637	3	5	5	4	4	5	5	5
tr F5H157	3	2	2	2	2	2	1	1
sp Q86YS6	1	1	1	1	1	0	1	1
sp P51148	19	7	7	7	7	7	7	6
sp P20340	14	5	5	5	3	5	4	4
sp P51149	7	16	16	16	12	16	13	12
sp O14966	4	3	2	2	2	2	2	2
sp P61006	2	3	1	1	2	2	3	2
sp P51151	3	3	3	3	2	3	3	3
tr H7C3P7	2	4	4	3	3	3	4	3
sp P61224	23	6	6	2	5	5	5	5
sp P61225	1	4	4	2	3	4	3	3
sp P10301	1	3	1	1	3	3	3	3
sp P62070	7	4	4	2	4	4	4	4
sp P60602	2	1	1	1	1	1	1	1
sp Q00765	6	3	3	3	3	3	3	3
tr Q96L35	3	2	2	2	2	1	2	2
sp P10586	7	4	4	4	3	2	2	2
sp Q9BRX8	2	4	4	4	4	4	4	4
sp P18754	7	8	8	8	5	7	7	6
sp Q96DB5	10	3	3	3	3	2	2	2
tr H0YNE5	3	1	1	1	1	1	1	1
sp Q92900	2	1	1	1	1	1	1	1
sp Q8WUF	2	2	2	2	2	2	2	2
sp P35250	9	3	3	3	2	2	2	2
sp P40938	3	5	5	5	5	5	4	3
tr C9JZI1 C	8	2	2	2	2	2	0	1
sp P40937	5	2	2	2	1	1	1	1
tr B5MC59	2	3	3	3	0	2	1	1
sp P15927	5	2	2	2	0	0	0	1
sp P27694	2	2	2	2	1	0	1	1
sp Q15293	2	9	9	9	6	8	5	5
tr H0YL43	3	3	3	3	2	2	2	2
sp Q9NQC	9	7	7	7	4	6	5	6
sp P06400	1	1	1	1	1	1	0	0

sp Q8NFJ5	2	2	2	2	2	2	2	2
sp Q8IZV5	2	3	3	3	3	2	2	3
sp Q8TC12	8	5	5	5	5	5	5	5
sp Q9HBH!	1	2	2	2	1	2	2	1
tr J3KRE2	7	3	3	3	2	3	2	2
tr F5H2R5	5	2	2	2	1	1	2	2
sp Q07960	3	5	5	5	1	2	2	3
tr R4GNI4	7	1	1	1	0	0	0	0
tr Q5JR08	13	5	5	1	5	5	5	4
sp P84095	1	6	5	5	4	5	5	5
sp P13489	10	10	10	10	6	5	6	6
sp P23921	4	3	3	3	0	0	1	0
tr C9JXC1	9	4	4	4	1	2	2	1
sp P60891	4	3	2	2	1	2	1	1
sp P11908	8	4	4	3	2	2	1	1
sp Q9Y4W	3	1	1	1	0	0	0	0
sp O76021	6	16	16	16	10	10	12	13
tr J3QR09	4	4	4	4	3	3	4	3
sp P56182	2	5	5	5	4	4	4	4
sp Q92979	4	3	3	3	2	2	3	3
sp Q9Y3A4	1	1	1	1	0	1	1	1
sp Q14692	1	5	5	5	4	2	4	4
sp Q14137	3	7	7	7	5	5	5	4
sp Q8TDN6	1	6	6	6	1	4	1	1
tr A0A0A0	3	3	3	3	3	3	3	2
sp Q9GZL7	1	4	4	4	4	3	3	4
sp Q15050	1	2	2	2	2	2	2	2
tr F8WE72	3	2	2	2	0	0	1	2
tr Q5VXN0	4	4	4	4	2	3	2	2
tr A0A0A0	21	17	17	17	3	5	12	13
sp Q96E11	9	5	5	5	4	5	5	5
tr D6RAL1	6	1	1	1	1	1	0	0
sp P38159	12	11	11	11	4	4	9	9
sp Q96PK6	2	10	10	8	9	9	9	9
sp Q96PK6	7	4	2	0	4	4	4	4
sp P49756	6	3	3	3	3	3	2	3
tr U3KPZ7	2	1	1	1	0	0	0	1
sp Q9NW1	4	5	5	5	4	5	5	5
tr Q5TCT4	4	2	2	2	0	1	2	2
tr A0A0U1	15	7	7	7	5	6	5	4
sp Q9Y5S9	3	3	3	3	1	2	3	3
tr B0QYK0	10	6	6	6	1	1	3	2
tr H3BPE7	3	5	3	3	1	2	5	5
tr H3BUR4	2	1	1	1	1	1	1	1
sp Q9NRX:	2	2	2	2	1	2	2	2
tr Q5QPL9	6	5	5	5	3	4	4	4
tr H3BV80	8	2	2	2	2	2	1	1
sp Q5TZA2	3	2	2	2	1	2	2	2
tr M0R299	8	5	5	5	5	5	5	5
sp Q6IN84	1	1	1	1	1	1	1	1

sp A6NHQ	1	1	1	1	1	1	1	1
tr G3V2ME	4	1	1	1	1	1	1	1
sp Q5JTH9	4	4	4	4	0	2	2	2
sp Q9Y3B9	1	3	3	3	1	2	2	2
sp Q9Y265	6	12	12	12	8	8	8	8
sp Q9Y230	5	13	13	13	7	10	8	6
sp P31153	2	5	5	5	2	4	2	3
tr F8VZQ9	3	2	2	2	0	0	0	0
sp P16615	18	22	22	22	21	20	20	20
sp Q15424	5	9	9	4	5	8	8	7
sp Q14151	2	8	3	3	4	5	7	6
tr B7ZKQ9	7	1	1	1	1	1	1	1
sp Q08AF3	1	1	1	1	1	1	1	0
sp Q8WVN	9	4	4	4	0	0	4	4
sp Q12765	6	3	3	3	0	1	1	3
tr A0A087	3	1	1	1	1	1	1	1
sp O15127	1	1	1	1	1	1	1	1
sp O14828	2	4	4	4	4	3	3	4
sp Q969E2	2	1	1	1	0	0	0	0
sp P35270	1	1	1	1	0	0	0	0
tr D6RDP1	12	1	1	1	0	0	1	1
sp Q13501	8	14	14	14	13	14	14	12
sp P83111	2	2	2	2	1	2	1	1
sp P34897	17	15	15	14	15	14	13	14
sp Q9NRX5	1	4	4	4	2	1	3	2
sp O15269	2	7	7	7	7	6	7	5
sp O15270	2	2	2	2	1	2	2	2
tr M0R088	5	1	1	1	0	0	0	0
sp Q9UQ3	9	13	13	13	9	8	10	9
tr J3KTL2	7	7	7	7	6	7	7	7
tr Q5JRI1	8	2	2	2	2	2	1	1
tr Q5T760	3	1	1	1	1	1	1	1
tr J3KP15	6	5	5	5	5	4	5	5
tr A0A087	3	4	3	3	3	3	3	3
sp Q13243	6	3	2	2	3	3	3	3
sp Q13247	5	5	5	4	4	4	4	5
tr A0A0B4	7	6	6	5	4	6	5	4
sp Q13242	3	7	7	7	5	6	5	7
tr H0Y630	6	2	2	1	1	2	2	1
tr E7ETY4	18	2	2	2	1	2	2	2
tr C9JIG9	2	1	1	1	1	0	0	0
sp Q13177	12	5	5	5	0	1	2	4
tr H0YJF7	2	1	1	1	1	0	1	1
sp P63151	7	2	2	2	2	2	2	2
sp P30153	13	11	11	11	5	6	7	8
tr A6PVN9	19	3	3	3	0	0	0	0
sp P67775	10	7	7	6	5	6	4	5
sp Q96HS1	3	5	5	5	4	5	4	4
sp P62136	4	8	2	2	4	5	5	3
sp P62140	6	9	9	3	7	8	6	4

tr E7ETC2	13	2	2	2	1	1	1	1
tr H3BV22	6	4	3	3	2	1	1	1
tr F8VYE8	6	8	2	2	5	6	6	4
sp Q9Y3F4	3	5	5	5	3	4	2	3
tr Q5T5C7	2	4	4	4	2	2	2	1
tr M0QWZ	7	2	2	2	2	2	2	2
tr F8WE70	5	4	4	4	1	1	1	1
sp P36952	3	14	14	14	5	8	8	8
tr A0A0240	9	6	6	6	0	1	3	3
sp P50454	13	13	13	13	12	12	12	11
sp Q9BXP5	6	3	3	3	2	1	2	1
tr J3QT77	6	1	1	1	1	1	1	1
tr U3KQT1	4	1	1	1	0	0	1	0
tr Q5T123	2	2	2	2	0	1	2	2
sp Q9NR45	1	2	2	2	0	0	2	2
tr A0A0A0	4	6	6	6	3	3	5	5
sp Q9H9B4	5	6	6	6	6	5	5	4
tr H0YNG3	8	2	2	2	1	2	2	1
sp Q9Y6A9	3	3	3	3	2	2	2	1
tr E9PL01	5	4	4	4	4	2	4	4
sp P61009	1	3	3	3	3	3	2	2
tr H0YLA2	2	4	4	4	1	2	1	2
tr A0A0871	3	2	2	2	0	0	0	1
sp P49458	3	4	4	4	1	1	3	2
sp Q9Y5M1	2	6	6	6	5	5	5	5
sp Q9UHB1	4	3	3	3	3	2	1	1
sp O76094	3	3	3	3	2	1	1	1
tr J3KPM9	8	5	5	5	3	3	4	4
sp Q92783	2	1	1	1	0	1	1	0
sp O75886	2	1	1	1	0	1	1	1
sp Q04837	4	4	4	4	4	4	4	4
tr G3V1B8	3	1	1	1	1	1	1	1
tr K7EMD6	2	2	2	2	0	1	1	1
sp P62306	1	2	2	2	1	1	1	1
sp P62314	3	2	2	2	1	1	0	0
sp P62316	3	3	3	3	0	1	1	1
sp P62318	3	4	4	4	4	4	3	3
tr J3QLE5	8	5	5	5	4	3	2	3
sp O75691	1	3	3	3	1	2	2	1
tr B8ZZN6	6	3	3	3	2	2	3	2
sp P61956	7	2	2	2	0	0	2	2
tr G3V5R3	3	1	1	1	0	0	0	0
sp P05023	19	28	28	27	25	28	27	23
sp P05026	3	4	4	4	4	4	4	4
sp P54709	5	3	3	3	3	2	2	2
tr F8VX04	2	2	2	2	1	1	1	2
sp Q96QD1	4	3	3	3	2	2	3	2
sp Q8WUX	8	4	4	4	3	3	3	3
tr H7BZK4	2	1	1	1	1	1	1	1
tr G3XAL9	3	2	2	2	0	2	2	2

sp P11166	1	3	3	3	3	3	3	3
sp Q9NQZ:	1	1	1	1	1	1	1	1
sp Q00796	4	8	8	8	3	3	3	5
tr C9J0K6	5	5	5	5	2	5	2	3
sp Q9Y512	1	2	2	2	1	1	1	1
sp Q9UMY	4	2	2	2	0	0	1	1
sp O60493	4	2	2	2	2	1	1	1
sp Q9NUQ	16	10	10	10	6	10	9	8
sp Q9BW0	2	2	2	2	0	1	2	2
tr A0A0D9	8	29	29	29	7	8	19	21
tr A0A087^	5	17	17	17	3	4	12	9
tr E5RJR5	6	3	3	3	2	3	3	2
tr H7BXF4	7	2	2	2	0	1	1	2
tr H0Y3V8	3	2	2	2	2	2	2	2
sp Q13838	17	9	9	2	5	6	2	3
sp Q15637	9	4	4	4	2	1	2	2
sp Q15459	3	3	3	3	0	0	2	1
sp Q12874	1	4	4	4	0	0	4	2
sp O75533	5	9	9	9	3	8	7	9
sp Q13435	7	6	6	6	1	3	4	4
sp Q15393	6	10	10	10	5	5	5	6
sp Q9Y3B4	1	2	2	2	1	2	2	2
sp P0DN76	11	4	4	4	4	4	3	3
tr K7ENG2	3	6	6	6	4	4	4	3
sp P23246	4	17	17	16	7	4	9	7
sp Q8WW!	1	3	3	3	3	3	3	3
tr E9PNM1	12	11	11	11	6	9	6	5
tr F8VV04	3	1	1	1	0	0	0	0
tr A0A087^	8	3	3	3	2	3	2	3
sp Q14247	5	17	17	17	9	8	11	11
sp Q7KZF4	2	16	16	16	11	11	9	9
sp P16949	3	5	5	5	0	0	0	1
tr E5RGX5	3	1	1	1	0	0	0	0
sp Q5K651	2	2	2	2	1	2	1	0
tr A0A087^	4	1	1	1	1	1	1	1
sp Q15738	2	6	6	6	5	5	4	6
tr A0A087^	4	8	8	8	6	6	5	7
sp Q8WXE	2	1	1	1	1	1	1	1
sp P38646	5	33	33	32	29	31	32	30
sp P31948	6	16	16	16	9	9	10	10
sp Q9HCN:	1	2	2	2	1	2	2	1
tr H0YDB2	5	1	1	1	1	1	1	1
sp O95347	4	6	6	6	3	3	3	3
sp Q9UQE`	1	5	5	5	1	0	2	2
tr G8JLG1	4	4	4	4	1	0	2	2
tr E9PD53	7	6	6	6	6	4	3	3
sp P31040	6	8	8	8	8	8	7	7
sp P53597	2	4	4	4	3	2	2	3
sp Q9P2R7	7	5	5	5	4	4	5	5
sp Q96I99	4	4	4	4	4	4	4	4



sp P55809	3	6	6	6	5	6	6	5
tr A8MXB5	17	3	3	3	3	2	2	3
sp Q9Y6NE	6	12	12	12	12	11	12	9
tr M0QX6E	6	1	1	1	0	0	0	0
tr H3BPC4	4	3	3	3	2	1	1	1
tr H7C2K3	9	1	1	1	1	1	1	1
sp P42285	2	2	2	2	1	1	1	1
sp P00441	2	3	3	3	1	1	1	2
sp P04179	10	5	5	5	4	5	4	4
sp Q9Y2Z0	2	4	4	4	2	1	3	1
sp Q9BRV8	2	1	1	1	0	0	0	0
tr A8MV53	9	4	4	4	1	1	3	3
sp Q15526	2	1	1	1	1	1	1	1
tr Q5T8U5	5	2	2	2	2	1	1	2
sp O75683	1	3	3	3	1	2	1	1
sp O75940	1	2	2	2	0	1	0	1
tr F8VXC8	5	3	3	3	1	1	2	3
sp O60264	1	9	9	8	6	8	9	7
tr J3KMX2	6	2	2	2	1	0	1	1
tr K7EMQ8	10	2	2	2	1	0	1	1
tr E7EMB1	2	2	2	2	0	0	0	0
sp Q99536	9	9	9	9	4	3	7	7
sp O15498	3	2	2	2	0	1	1	2
sp Q16563	2	1	1	1	1	1	1	1
sp Q9H987	2	1	1	1	1	1	1	1
sp O95721	1	1	1	1	0	0	0	0
tr H3BV99	10	2	2	2	2	2	2	2
sp P18827	3	2	2	2	1	2	2	2
sp P31431	2	2	2	2	2	2	1	2
sp O43752	1	2	2	2	0	1	1	1
sp O15400	2	2	2	2	2	2	2	2
sp O00560	4	10	10	1	8	9	9	8
sp O00560	2	10	1	1	8	9	9	8
sp Q9Y490	4	10	10	10	4	4	6	4
tr A0A0G2	11	2	2	2	2	2	2	2
sp Q13148	19	6	6	6	5	6	4	2
sp Q92804	5	6	6	4	1	2	5	4
tr B8ZZD4	6	6	6	6	6	6	6	6
sp O14907	1	1	1	1	1	1	1	1
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sp P78371	4	17	17	17	9	6	6	7
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sp P50990	5	20	20	20	13	9	12	13
sp P40227	6	10	10	10	3	5	6	5
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sp O43396	5	6	6	6	3	5	6	6
sp Q9H3N1	2	4	4	4	2	4	4	3
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sp Q16762	2	2	2	2	2	2	2	1
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sp Q6I9Y2	1	1	1	1	0	0	0	0
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sp P07996	4	11	11	11	9	10	10	11
tr H3BNW1	2	1	1	1	0	0	0	0
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sp P62328	1	2	2	2	0	0	1	1
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tr A0A1B0I	10	10	10	10	5	7	8	7
sp O75663	2	1	1	1	0	0	0	1
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tr A0A0A0	14	1	1	1	1	1	1	0
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tr E9PNS3	3	1	1	1	1	0	1	1
tr J3KN66	8	6	6	6	5	5	5	5
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tr Q9HBD4	7	1	1	1	1	1	1	1
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tr B8ZZU8	5	4	4	4	2	2	2	2
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sp Q9Y3A6	4	2	2	2	2	2	2	2
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sp Q9NYL9	4	4	4	4	3	3	0	1
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sp P06753	16	18	18	12	14	13	13	15
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sp P23381	22	6	6	6	1	0	2	1
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sp P68363	3	18	18	0	15	16	16	14
tr F5H5D3	15	18	2	2	15	16	16	12
sp P68366	6	18	4	4	15	15	16	15
tr Q5JP53	7	16	4	3	16	15	14	13
sp Q13885	2	15	3	3	14	15	13	11
tr A0A0B4	7	11	2	1	11	11	9	9
sp P68371	13	17	17	2	16	17	15	15
sp Q9BUFE	10	9	3	3	8	8	6	6
sp Q3ZCM	3	9	2	2	9	9	8	7
tr K7EKE5	3	1	1	1	1	1	1	0
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sp Q14166	1	4	4	4	3	3	1	1
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tr H0Y6Y4	9	2	2	2	1	0	1	1
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tr F5GYN4	7	4	4	4	3	3	4	3
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tr F8W726	13	4	4	4	1	0	1	2
sp O00762	3	2	2	2	1	1	1	0
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sp Q15819	1	4	2	2	2	1	3	3
tr H0Y614	2	1	1	1	1	1	1	1
sp P22314	8	21	21	21	9	12	13	12
sp Q9BZL1	2	2	2	2	0	1	2	0
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tr F5H6E2	10	12	12	12	11	11	10	9
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sp Q9H7E5	2	1	1	1	0	1	0	1
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tr U3KQC1	7	5	5	5	4	3	3	3
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tr H0Y362	2	2	2	2	2	2	2	2
tr Q5T4K2	5	1	1	1	1	1	1	1
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2	2	2	2	1	1	1	0	2
9	8	8	6	10	9	8	8	9
2	2	2	0	1	2	2	2	2
24	26	25	7	8	19	21	20	24
14	15	14	3	4	12	9	10	14
3	3	3	2	3	3	2	2	3
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7	8	7	0	0	0	0	0	1
4	3	3	2	1	2	2	2	4
3	2	2	0	0	2	1	0	3
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8	9	7	3	8	7	9	8	8
6	5	6	1	3	4	4	2	6
6	7	6	5	5	5	6	6	6
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3	4	3	4	4	3	3	2	3
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13	14	14	6	4	9	7	7	12
2	3	1	3	3	3	3	2	2
9	9	9	6	9	6	5	3	9
0	0	1	0	0	0	0	0	0
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12	14	14	9	8	11	11	14	12
15	15	13	11	11	9	9	11	15
4	5	3	0	0	0	1	2	4
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7	4	6	6	6	5	7	6	7
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8	7	7	8	8	7	7	7	8
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9	9	7	4	3	7	7	6	9
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9	16	14	9	6	6	7	4	9
13	14	15	10	12	8	8	7	13
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7	8	8	6	5	6	7	7	7
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2	3	3	1	1	2	2	2	2
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4	2	3	2	4	4	3	3	4
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6	5	6	0	0	3	2	3	6
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10	9	11	9	10	10	11	9	10
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9	12	10	8	9	5	5	5	9
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2	2	0	2	2	2	2	2	2
18	20	20	16	15	18	18	16	18
16	17	18	9	12	9	12	10	16
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5	2	3	4	4	5	4	5	5
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12	13	9	9	11	9	11	13	12
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17	17	15	18	18	20	17	14	17
11	11	12	13	12	13	12	11	11
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11	12	11	14	12	10	9	7	11
3	2	2	2	2	1	1	2	3
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4	4	4	1	1	1	1	1	1
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2	2	1	2	2	2	2	2	2
8	8	7	1	1	1	1	1	1
5	5	5	1	0	2	1	1	5
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16	18	17	0	0	0	0	0	0
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3	4	3	3	3	3	3	3	3
3	3	4	3	2	2	2	2	2
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3	3	2	0	0	1	1	2	3
3	4	3	3	3	1	1	1	3
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3	3	3	0	0	1	2	0	3
5	5	5	0	1	4	4	1	5
3	3	3	2	2	2	2	1	3
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9	4	6	8	6	9	8	11	9
4	3	4	5	4	5	5	4	4
8	7	8	5	4	4	6	5	8
3	3	3	3	3	2	2	2	3
3	3	3	3	3	3	2	1	3
5	5	6	3	2	3	4	3	5
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2	2	2	0	0	1	2	1	2
3	2	4	0	2	3	2	0	3
1	2	2	0	0	0	0	1	1
2	3	3	2	2	1	2	1	2
1	2	0	2	2	1	2	2	1
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13	15	14	11	12	9	10	6	13
2	3	3	2	1	2	2	1	2
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2	1	2	0	0	1	0	0	2
6	6	6	2	2	4	5	5	6
6	8	7	0	1	2	1	0	6
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4	3	3	1	1	2	2	2	2
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7	7	9	7	7	5	6	6	7
8	6	5	9	9	10	9	8	8
2	3	2	3	4	3	2	2	2
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13	16	16	16	16	13	14	10	13
10	11	11	11	11	10	9	8	10
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7	8	8	4	3	4	6	4	7
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17	18	16	18	19	18	17	10	17
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13	16	15	11	12	10	7	7	13
10	13	12	6	7	7	9	8	10
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1	1	1	1	1	1	1	1	1
1	0	0	0	1	1	2	2	1
3	3	3	0	0	1	3	3	3



Unique pe	Unique pe	Sequence c	Unique + r	Unique seq	Mol. weigh	Sequence l	Sequence l	Q-value
7	8	68.6	68.6	68.6	10.932	102	102;101;47	0
7	7	13.7	12.6	12.6	105.38	937	937;972;96	0
1	1	9.7	9.7	9.7	13.671	124	124;125	0
4	4	36.9	23	23	27.85	244	244;246;74	0
12	11	61.2	51.4	51.4	29.174	255	255;233;94	0
7	7	48	41.1	41.1	28.218	246	246;162;39	0
5	4	35.6	25.5	25.5	28.302	247	247	0
13	14	71.3	71.3	59.7	24.336	216	216;248	0
7	8	45.7	31.8	31.8	27.764	245	245;149	0
7	7	52.7	42.4	38.8	27.745	245	245;246;13	0
2	2	3.1	3.1	3.1	181.79	1729	1729;778	0
2	0	6.3	6.3	6.3	42.072	364	364	0
0	0	6.5	6.5	6.5	45.098	401	401;421	0
5	6	26.4	26.4	26.4	34.994	326	326;335;15	0
3	3	5.1	5.1	5.1	121.17	1087	1087;177;2	0
6	6	26.8	26.8	26.8	45.796	403	403;389;26	0
5	5	20.2	20.2	20.2	41.167	367	367;440;84	0
5	4	18.4	18.4	18.4	44.323	397	397;423;43	0
2	3	18.9	18.9	18.9	43.507	387	387;418	0
10	10	31.6	31.6	31.6	48.633	433	433;400;29	0
4	4	23.6	23.6	19	29.347	263	263;398;40	0
4	6	10.7	10.7	10.7	105.85	953	953;922;95	0
2	2	17.3	17.3	17.3	20.217	185	185;193;22	0
10	9	28.9	28.9	28.9	47.463	422	422;423;18	0
6	4	14	14	14	50.578	436	436;456;38	0
5	6	22.3	22.3	22.3	39.829	349	349;376;37	0
1	1	4.2	4.2	4.2	34.577	310	310	0.001542
9	9	15.5	15.5	15.5	100.2	908	908;778;74	0
5	5	14.9	14.9	14.9	41.183	356	356;534	0
0	2	4.7	4.7	4.7	41.079	380	380;377;19	0
3	3	13.1	13.1	13.1	41.181	350	350;351;38	0
3	3	23.2	23.2	23.2	20.064	177	177;198;32	0
1	2	17.6	17.6	17.6	16.913	153	153;179;22	0
5	4	22.1	22.1	22.1	20.63	181	181	0
1	1	15	15	15	20.459	193	193;194	0
1	1	18.2	18.2	18.2	11.15	99	99;123;137	0
1	2	29.5	29.5	29.5	14.374	129	129;225;13	0
4	2	23.6	23.6	23.6	29.395	258	258;215	0
3	3	9.8	9.8	9.8	33.249	296	296;270	0
1	0	16.1	16.1	16.1	10.688	87	87	0.001534
2	1	15.4	15.4	15.4	36.805	319	319;359;36	0
1	1	13.2	13.2	13.2	17.517	152	152;190	0
2	1	24.3	24.3	24.3	20.116	173	173;110;12	0
0	1	12	12	12	34.458	299	299;358;41	0
1	0	10.2	10.2	10.2	20.843	187	187;86;103	0
1	0	29.1	29.1	29.1	11.466	103	103;38	0
1	1	3.3	3.3	3.3	48.006	430	430	0
1	1	10.4	10.4	10.4	14.226	125	125	0.004801

2	1	19.8	19.8	19.8	19.903	172 172;271;24	0
1	2	6.8	6.8	6.8	45.834	396 396	0
12	9	22.5	22.5	22.5	117.24	1034 1034;1038;	0
1	1	5.2	5.2	5.2	26.614	231 231;325	0.007601
1	3	23.5	23.5	23.5	18.205	166 166;192;18	0
2	2	20.6	20.6	12.7	48.099	442 442;198	0
0	0	53.2	53.2	53.2	5.7685	47 47;147;178	0
0	1	15	15	15	20.576	180 180	0
1	1	11.1	11.1	11.1	24.43	225 225;305	0
1	1	11.8	11.8	11.8	24.325	212 212;232;12	0
0	0	17.1	17.1	17.1	24.915	216 216	0
1	1	6.1	6.1	6.1	29.485	264 264;292;48	0.001525
1	1	8.4	8.4	8.4	44.596	380 380;196	0
0	0	5.1	5.1	5.1	34.032	297 297;338;35	0.007608
1	0	15	15	15	14.056	127 127;163;22	0
1	1	14.9	14.9	14.9	16.567	148 148;169;18	0
0	0	5.7	5.7	5.7	37.535	332 332	0
1	1	13.1	13.1	13.1	11.348	99 99;140;166	0
1	0	23	23	23	15.524	135 135;158	0
1	1	20.5	20.5	20.5	12.107	112 112	0
1	1	3.7	3.7	3.7	30.243	267 267	0.00294
2	3	16.5	16.5	16.5	26.352	230 230;145;16	0
9	5	54	54	54	26.923	261 261;252;16	0
1	2	8.6	8.6	8.6	35.329	336 336;206	0
0	1	5.4	5.4	5.4	22.62	203 203;332	0
1	1	3.1	3.1	3.1	32.747	290 290;326	0.00892
3	5	27.9	27.9	27.9	18.898	165 165;176;17	0
9	8	53.2	53.2	53.2	18.431	158 158;118;79	0
7	7	53.8	53.8	53.8	14.515	132 132	0
5	5	43	43	43	17.222	151 151;148;11	0
5	7	38.4	38.4	38.4	16.273	151 151;120;13	0
1	1	61	61	16	11.477	100 100;130;58	0
6	5	39	39	39	16.445	146 146;100;12	0
5	4	51.9	51.9	51.9	15.55	135 135;136;19	0
6	6	32.9	32.9	32.9	17.718	152 152;82;33;	0
6	7	43.4	43.4	43.4	16.06	145 145;71;76;	0
9	9	31.7	31.7	31.7	31.324	293 293;195;23	0
3	3	22.7	22.7	22.7	13.373	119 119;142;46	0
4	4	46.9	46.9	46.9	8.85	81 81;83;90	0
4	4	28.7	28.7	28.7	15.807	143 143;134;55	0
3	3	26.7	26.7	26.7	15.197	131 131;132;13	0
2	3	22.4	22.4	22.4	13.742	125 125	0
3	2	31.3	31.3	31.3	13.015	115 115;115	0
4	4	39.3	39.3	39.3	9.461	84 84;66;100;	0
2	2	33.3	33.3	33.3	7.8409	69 69	0
2	0	32.1	32.1	32.1	6.6767	56 56;67;53	0
11	11	54.7	54.7	54.7	26.688	243 243;259;23	0
1	1	10.2	10.2	10.2	10.905	98 98;59	0.000531
11	12	47.3	47.3	47.3	29.945	264 264;223;22	0
11	10	44.1	44.1	44.1	29.597	263 263;262;26	0

6	6	35	35	35	22.391	200 200;204;22	0
4	6	26.1	26.1	26.1	28.68	249 249;218;91	0
4	3	24.2	24.2	24.2	22.127	194 194;187	0
9	10	50	50	50	24.205	208 208;188	0
8	9	38.7	38.7	38.7	22.591	194 194;194;13	0
8	7	40.7	40.7	40.7	29.404	263 263;300;29	0
23	23	50.5	50.5	50.5	57.944	529 529;599;63	0
2	1	2.7	2.7	2.7	99.96	874 874;950	0
1	1	4.4	4.4	4.4	57.948	524 524;574;17	0
27	26	59.7	59.7	59.7	61.054	573 573;234;22	0
9	8	41.7	41.7	41.7	27.187	247 247;317;15	0
1	1	28.9	14	14	11.514	114 114	0
6	5	79.1	79.1	64.3	11.665	115 115;92;89	0
2	2	40.5	40.5	14.5	22.975	200 200;214;10	0
7	7	37.3	37.3	37.3	24.831	217 217	0
1	0	23	23	6.7	20.252	178 178;174;13	0
1	0	22.6	6.2	6.2	20.124	177 177 0.009786	
6	6	54.5	54.5	54.5	17.818	165 165;132	0
5	6	34.1	34.1	34.1	24.261	211 211;164;12	0
7	6	37.4	37.4	37.4	23.577	203 203;210;14	0
4	4	36.3	36.3	36.3	14.558	124 124;215	0
6	6	25	25	25	24.146	204 204;133;17	0
5	6	50.3	50.3	50.3	19.586	169 169;171;17	0
4	4	27.4	27.4	27.4	18.756	164 164;167;19	0
5	5	37.6	37.6	37.6	16.714	141 141;147;15	0
2	2	29.9	29.9	29.9	9.8864	87 87;122;160	0
2	2	51.1	51.1	51.1	5.0827	47 47;48;53;7!	0
4	4	37.9	37.9	37.9	14.865	140 140;81;91;	0
4	4	26.6	26.6	26.6	17.692	158 158;170;17	0
5	4	36.4	36.4	36.4	14.369	121 121;150;15	0
5	6	29	29	29	17.258	145 145;96;107	0
4	4	36	36	36	15.798	136 136;144;80	0
3	4	38	38	38	12.201	108 108;148;91	0
4	5	42	42	42	12.39	112 112;170;69	0
2	2	14.5	14.5	14.5	17.752	159 159	0
15	14	39.7	39.7	39.7	46.108	403 403;351;30	0
5	4	59.1	59.1	59.1	12.784	115 115;114;51	0
3	4	44.4	44.4	44.4	12.701	108 108;115;12	0
4	5	38.3	38.3	38.3	15.616	133 133;153;13	0
6	5	36.8	36.8	36.8	13.293	117 117	0
2	2	24	24	24	10.645	96 96;123	0
5	4	44.7	44.7	44.7	10.645	94 94;110;55;!	0
3	3	28.6	28.6	28.6	12.254	105 105;94;68	0
2	2	15.2	15.2	15.2	13.228	112 112;118;14	0
3	3	69.1	69.1	69.1	7.624	68 68;92;60;7.	0
1	1	15.6	15.6	15.6	7.5649	64 64;67;70 0.009772	
13	13	35.1	35.1	35.1	47.697	427 427;333;17	0
9	9	38	38	38	34.362	297 297;130	0
13	12	29.5	29.5	29.5	32.728	288 288;159;16	0
5	6	33.2	33.2	33.2	24.433	208 208;248;88	0

12	12	44.4	44.4	44.4	29.995	266 266;151;19	0
1	1	5.1	5.1	5.1	22.874	198 198;153;24	0.003887
5	4	25.3	25.3	25.3	28.024	257 257;205;23	0
5	5	35.4	35.4	35.4	21.863	192 192;166;18	0
1	2	17.3	17.3	17.3	12.453	110 110;133;18	0.00155
9	10	30.9	30.9	30.9	51.872	470 470;483;20	0
1	1	17.3	17.3	17.3	18.912	179 179;216;25	0.001549
1	2	16	16	16	17.951	156 156;171;17	0
27	27	47.7	47.7	47.7	72.332	654 654	0
4	3	14.3	14.3	14.3	54.489	475 475;164;25	0
1	1	3.5	3.5	3.5	74.354	689 689	0.001535
3	2	1.9	1.9	1.9	231.71	2131 2131;1723;	0
1	0	4	4	4	56.732	525 525;632	0.001563
2	1	11.8	11.8	11.8	41.35	397 397;426	0
6	6	21.1	21.1	21.1	45.199	427 427;136;16	0
1	1	1	1	1	255.09	2256 2256;2268;	0
3	3	27.7	27.7	18.6	19.997	177 177;249;23	0
1	1	13.8	5.6	5.6	22.276	195 195;251	0.000536
8	9	15	15	15	87.819	805 805;780	0
1	1	69.6	4.5	4.5	41.736	375 375;125;16	0.008523
1	1	69.6	69.6	4.5	41.792	375 375;214;21	0
1	1	26.6	4.3	4.3	41.876	376 376;377;37	0
5	5	22.1	22.1	22.1	47.46	429 429;387;16	0
4	4	17.5	17.5	17.5	44.76	394 394;399;33	0
4	3	16.4	16.4	16.4	40.949	372 372;128;13	0
4	3	14	14	14	34.333	300 300;38;89;'	0
1	0	13.1	13.1	13.1	9.7261	84 84;99;178	0.002956
4	4	37.2	37.2	37.2	13.057	113 113;181;62	0
1	1	25.9	25.9	25.9	14.807	135 135;151;15	0
1	1	7.8	7.8	7.8	16.941	153 153	0
7	7	23.2	23.2	23.2	47.371	418 418;367;84	0
3	3	26	26	26	14.395	127 127	0
7	6	35.8	35.8	35.8	32.339	288 288;338;21	0
0	0	9.6	9.6	9.6	15.434	136 136	0.001557
2	1	14.7	14.7	14.7	17.417	156 156;70;111	0
2	2	2.8	2.8	2.8	81.673	737 737;732	0
5	5	11.3	11.3	11.3	68.76	621 621;384	0
2	2	10.6	10.6	10.6	41.522	359 359	0
3	2	45.4	45.4	45.4	11.15	97 97;143;87;'	0
0	0	10.3	10.3	10.3	12.366	117 117;140	0
1	1	18.7	18.7	18.7	23.333	209 209;319;17	0
5	5	19	19	19	43.206	379 379;406;43	0
2	2	19.3	19.3	19.3	17.981	166 166;197;21	0
2	2	15.9	15.9	15.9	17.659	164 164;231	0
0	1	13.8	13.8	13.8	24.843	224 224;226;24	0.002006
3	3	58.7	58.7	58.7	6.9189	63 63;148;153	0
1	1	7.7	7.7	7.7	32.663	299 299;339;38	0
1	1	9.8	9.8	9.8	34.084	305 305;327;34	0
14	14	39.6	39.6	39.6	47.716	432 432;404	0
4	4	30.2	30.2	30.2	25.63	232 232;224;23	0

2	0	9	9	9	25.268	223 223;171	0
5	5	32.4	32.4	32.4	23.411	210 210;194;13	0
1	2	8.9	8.9	8.9	40.826	360 360;480;48	0.002947
5	4	15.4	15.4	15.4	50.097	456 456	0
10	11	26.4	26.4	26.4	51.83	474 474;475;17	0
4	5	29.4	29.4	29.4	32.161	289 289;416;40	0
1	1	18.4	18.4	18.4	7.8547	76 76	0
5	4	43	43	16.4	32.852	298 298;315	0
2	2	42.3	15.8	7.4	32.866	298 298	0
3	2	10.9	10.9	10.9	53.96	496 496;497;22	0
3	3	43.6	43.6	20.4	20.697	181 181;181;21	0
1	1	33.1	7.9	7.9	14.553	127 127;180;15	0.001532
1	1	44.7	16.7	16.7	17.107	150 150;180;40	0.000539
2	3	24.6	24.6	24.6	20.082	175 175	0
1	1	10.2	10.2	4.8	21.539	186 186	0
2	3	20.6	20.6	20.6	19.961	180 180;186;23	0
1	2	2.3	2.3	2.3	88.583	797 797	0
4	4	4.2	4.2	4.2	202.29	1930 1930;1963;	0
1	1	4.2	4.2	4.2	37.636	330 330	0
0	1	6.8	6.8	6.8	16.008	146 146;1745;2	1
2	2	6.4	6.4	6.4	38.518	358 358;422;51	0
5	5	10.4	10.4	10.4	106.81	968 968;992;28	0
3	3	13.8	13.8	13.8	36.573	325 325;119;14	0
3	4	14.2	14.2	14.2	39.724	374 374;115;26	0
15	16	35.2	35.2	32	56.108	512 512;405;14	0
0	1	9.7	6.6	6.6	57.206	517 517	0
0	0	45.8	45.8	0	36.788	323 323;248	0
2	2	44.1	7.4	7.4	33.834	297 297;323;20	0
1	1	31.3	11.8	11.8	36.867	323 323;323;30	0
5	5	18.7	18.7	18.7	35.853	316 316;102;26	0
8	7	24	24	24	72.911	658 658;543;18	0
0	0	3.7	3.7	3.7	37.017	323 323;416	0.002021
1	1	1.5	1.5	1.5	94.069	819 819;754;81	0
1	0	7.3	7.3	7.3	41.465	357 357	0
20	18	50.8	50.8	34.6	103.06	892 892;914;88	0
20	20	46	30.2	30.2	104.85	911 911;692;52	0
3	5	19.8	19.8	19.8	51.853	479 479;521;53	0
1	1	5.4	5.4	5.4	37.433	332 332;376	0
0	1	14.3	14.3	14.3	13.133	119 119;140;18	0.002004
19	18	65.2	65.2	65.2	47.168	434 434;341;19	0
0	1	2.1	2.1	2.1	131.14	1144 1144	0
0	1	3	3	3	35.66	329 329;793;79	0.005731
3	3	28.5	28.5	28.5	29.163	256 256;295;26	0
1	1	3.5	3.5	3.5	61.89	546 546	0
4	4	9.9	9.9	9.9	59.681	527 527;394;41	0
4	4	18.6	18.6	18.6	34.352	312 312;336;15	0
3	3	17.2	17.2	17.2	35.348	320 320;242;25	0
5	4	12.8	12.8	12.8	68.168	611 611;650;17	0
2	2	5.7	5.7	5.7	57.933	522 522	0
7	5	14.7	14.7	13.6	80.832	714 714;733;74	0

6	5	11.7	10.7	10.7	85.486	751 751;761;76	0
0	1	3.2	3.2	3.2	41.385	373 373;410;47	0
1	1	1.1	1.1	1.1	118.01	1123 1123;1565;	0.001526
23	20	64.5	64.5	64.5	38.714	346 346;204;11	0
1	1	4.9	4.9	4.9	37.277	324 324	0
6	7	17.6	17.6	17.6	51.242	472 472;505;14	0
25	24	58.4	58.4	58.4	38.604	339 339;357;25	0
11	12	38.4	38.4	38.4	36.375	323 323;284;15	0
11	10	40.4	40.4	40.4	35.882	319 319;299;23	0
10	9	35.6	35.6	35.6	35.936	320 320;260;22	0
7	9	26.6	26.6	26.6	50.315	466 466;488	0
6	7	41.6	41.6	41.6	36.881	327 327;365;32	0
6	7	8.5	8.5	8.5	319.44	2896 2896;3256	0
2	1	3.1	3.1	3.1	87.175	808 808;808	0
2	3	8.5	8.5	3.8	101.35	919 919;939;94	0
2	2	13.1	13.1	13.1	22.065	191 191;158;13	0
1	2	4.5	4.5	4.5	105.36	955 955;977;63	0
2	2	13.3	6.8	6.8	74.136	663 663;677;88	0
2	1	9	9	9	49.526	434 434;460;43	0
0	1	1.5	1.5	1.5	111.24	984 984;1021;1	0.002005
1	1	5.5	5.5	5.5	46.939	418 418	0.000529
1	1	13.5	13.5	13.5	21.732	193 193;162	0.00293
3	4	1.7	1.1	1.1	515.6	4563 4563	0
1	1	13.7	13.7	13.7	12.815	117 117;99	0
2	1	4.9	4.9	4.9	48.915	449 449;337;12	0
1	0	22.8	22.8	22.8	13.101	114 114;178;18	0
4	4	10.3	10.3	10.3	56.769	504 504;510;44	0
2	3	22.6	22.6	22.6	18.129	164 164;173;17	0
5	5	18.6	18.6	18.6	66.294	609 609;613;27	0
6	7	9.9	9.9	9.9	145.44	1283 1283;1301;	0
1	1	2.9	2.9	2.9	41.595	374 374;256;30	0.009341
7	7	17.7	17.7	17.7	75.378	660 660;588;11	0
3	5	13.3	13.3	13.3	62.168	540 540;561;47	0
4	6	14.6	14.6	14.6	62.942	548 548;162;16	0
3	3	14.3	14.3	14.3	46.247	413 413;392	0
12	11	33.5	33.5	33.5	47.517	430 430;387	0
19	18	42.5	42.5	42.5	57.136	501 501;401;17	0
1	1	2.8	2.8	2.8	73.562	645 645	0
3	4	8.8	8.8	8.8	85.862	758 758;729;11	0
1	1	9.3	9.3	9.3	12.53	108 108;130;15	0.001531
1	0	3.3	3.3	3.3	102.89	968 968;1044;1	0.001564
2	2	13.1	13.1	13.1	47.4	413 413;412;56	0
2	2	9	9	9	58.772	523 523;541;16	0
4	4	36.4	36.4	36.4	22.275	195 195;256	0
1	1	4.4	4.4	4.4	24.817	226 226	0.001565
17	17	45	45	45	59.75	553 553;503;53	0
19	17	52.6	52.6	52.6	56.559	529 529;362;28	0
4	5	60.2	60.2	60.2	18.491	161 161;137;81	0
2	2	13.7	13.7	13.7	17.49	168 168	0
2	2	30.4	30.4	30.4	7.9331	69 69	0

2	0	47.3	47.3	47.3	6.2953	55 55;94;54;9;	0
2	2	51.3	51.3	51.3	8.4518	76 76;103	0
7	9	33.3	33.3	33.3	32.881	297 297;298	0
6	6	46.5	46.5	46.5	23.277	213 213;242;86	0
4	4	45.4	45.4	45.4	12.587	108 108;116;11	0
3	4	13	13	13	66.217	586 586;634;57	0
0	1	5.3	5.3	5.3	20.616	188 188;702;71	0.008527
1	1	4.4	4.4	4.4	75.475	659 659;236;54	0
4	3	9.5	9.5	9.5	67.314	599 599;421;14	0
2	2	4.7	4.7	4.7	67.55	596 596;807;84	0
1	1	2.2	2.2	2.2	71.289	623 623;634	0
1	1	1.6	1.6	1.6	78.983	703 703;709	0
18	22	25.1	25.1	25.1	119.77	1091 1091;1101;	0
2	2	7.8	4.2	4.2	85.018	780 780;827	0
2	2	6.5	5.3	5.3	81.775	749 749;780;85	0
10	9	24.9	24.9	21.3	85.595	784 784;776;20	0
3	3	9.8	9.8	9.8	69.223	633 633;268;13	0
1	0	22.1	22.1	22.1	20.568	190 190;277;16	0
2	2	5.1	5.1	5.1	73.457	649 649	0
22	22	27.2	27.2	27.2	140.96	1270 1270;235	0
9	6	20.2	20.2	20.2	73.915	659 659;659;74	0
7	7	17.5	17.5	17.5	75.406	670 670;214	0
2	2	7.2	7.2	7.2	50.519	447 447;479;48	0
3	2	14.3	14.3	14.3	91.48	816 816;804;85	0
1	1	23.7	2.1	2.1	49.129	427 427;189;26	0
11	8	25.8	24.1	24.1	70.839	640 640;647;73	0
1	1	3	3	3	77.813	708 708;819;93	0.001577
3	5	11.4	11.4	11.4	98.594	881 881;882;82	0
1	1	4.1	4.1	4.1	87.99	786 786	0
1	0	20.3	20.3	20.3	7.6758	69 69;123;172	0
1	1	5.2	5.2	5.2	23.772	211 211	0
3	3	7.5	7.5	7.5	61.594	575 575	0
2	1	3.1	3.1	3.1	98.374	880 880;701;77	0
1	1	27	27	27	10.058	89 89	0
0	0	0.3	0.3	0.3	468.83	4391 4391	0.001995
4	4	11.3	11.3	11.3	40.538	353 353;419;42	0
2	2	13.9	13.9	13.9	31.247	274 274;408;41	0
4	5	51.2	51.2	51.2	22.764	205 205;269;38	0
3	3	23.2	23.2	23.2	27.991	246 246;313;18	0
1	1	22.2	22.2	22.2	16.872	153 153;211	0
4	3	13.3	13.3	13.3	52.917	467 467;703;72	0
3	2	11.1	11.1	11.1	48.871	461 461;509;32	0
3	3	35.3	35.3	35.3	13.714	119 119;71;101	0
1	1	2.4	2.4	2.4	57.949	540 540	0
1	1	4	4	4	42.293	376 376	0
2	2	13.9	13.9	13.9	32.805	288 288	0
3	2	26.7	26.7	26.7	21.994	195 195;241;12	0
3	2	6.7	6.7	6.7	62.328	564 564;593;96	0
21	21	20	20	20	170.59	1512 1512;968;1	0
1	0	14.1	14.1	14.1	26.849	248 248;350;22	0

13	13	31.6	31.6	31.6	64.523	591 591;592;23	0
0	1	0.3	0.3	0.3	330.46	3051 3051	0
2	1	16.4	16.4	16.4	16.932	152 152;86;88;1	0
1	1	16.3	16.3	16.3	10.863	98 98;125	0
4	3	12.9	12.9	12.9	56.882	511 511	0
1	1	4.6	4.6	4.6	36.297	325 325;349;38	0
1	2	13.4	13.4	13.4	33.242	292 292;292;31	0
2	1	14.3	14.3	14.3	27.835	251 251	0
1	2	1.8	1.8	1.8	175.38	1524 1524;1556	0
4	4	17.8	17.8	17.8	35.7	325 325	0
1	0	4.9	4.9	4.9	27.126	246 246;234	0.008065
4	4	9.3	9.3	9.3	52.541	493 493;497;46	0
14	12	20	20	20	110.61	1020 1020;935;1	0
4	3	10.5	10.5	10.5	54.812	475 475	0
1	1	6.8	6.8	6.8	22.712	206 206;308;32	0.008929
17	17	13.1	13.1	13.1	236.02	2162 2162;2225;	0
1	1	3.1	3.1	3.1	100.03	903 903;821;88	0
3	4	8	8	8	86.551	784 784;829	0
2	1	24.6	24.6	24.6	22.456	195 195;91;123	0
1	0	2.2	2.2	2.2	40.189	357 357;385	0.008945
15	12	28.6	28.6	28.6	74.175	675 675;676;57	0
3	4	15.7	15.7	15.7	51.354	458 458;477	0
6	6	10.8	10.8	10.8	104.71	953 953;903;91	0
6	6	45.4	45.4	45.4	21.228	185 185;228	0
17	17	31.2	31.2	31.2	67.567	592 592;627;48	0
4	4	38	38	38	15.958	163 163;196;19	0
7	7	12.9	12.9	12.9	81.889	714 714;122;13	0
6	6	11.4	11.4	11.4	79.994	700 700;622	0
3	5	17.3	17.3	17.3	46.133	423 423;431;43	0
7	6	35.6	35.6	35.6	32.616	298 298;330;30	0
14	15	47	47	47	48.141	417 417;247;16	0
1	2	18.8	18.8	18.8	26.326	224 224;265;31	0
2	1	10	10	10	42.981	381 381;153;33	0
1	1	10	10	10	22.873	200 200;382;40	0
4	4	7.3	7.3	7.3	70.353	628 628;694;70	0
4	3	19.2	19.2	19.2	29.246	260 260;97;101	0
10	11	62.8	62.8	62.8	30.375	277 277;178;22	0
4	4	9.6	9.6	9.6	152.93	1380 1380;1133;	0
7	6	14	14	14	86.238	756 756;773;11	0
1	4	9.6	9.6	9.6	73.776	658 658;635;64	0
2	3	13.6	13.6	13.6	27.741	236 236;264;32	0
0	2	9.9	9.9	9.9	45.31	385 385;391;39	0
2	1	11	11	11	26.673	228 228;234;30	0
2	1	6.2	6.2	6.2	54.822	501 501;712;50	0.002973
1	0	8.4	8.4	8.4	43.588	393 393;423	0.002928
4	6	20.7	20.7	20.7	59.755	527 527	0
5	5	51.6	51.6	51.6	24.449	221 221;271;22	0
16	18	31.8	31.8	31.8	100.07	906 906;930;84	0
2	5	11.4	8.4	8.4	84.765	774 774;781	0
14	12	21.5	21.5	21.5	104.85	938 938;832;83	0



3	5	20.7	20.7	20.7	43.688	405 405;406;40	0
2	3	11.2	11.2	11.2	30.993	277 277;122;19	0
5	5	4.7	4.7	4.7	274.37	2491 2491	0
7	8	51.1	51.1	51.1	20.471	178 178;167;13	0
2	1	2.3	2.3	2.3	120.97	1054 1054	0
0	1	3.1	3.1	3.1	152.66	1368 1368;1445;	0
2	2	15.7	15.7	15.7	38.138	344 344;532;30	0
2	2	10.3	10.3	10.3	41.767	388 388;493;53	0
6	6	31.6	31.6	31.6	22.683	206 206;287;34	0
3	3	29.6	29.6	29.6	11.985	108 108;130;12	0
2	3	17.4	17.4	17.4	26.818	242 242;267;15	0
1	2	6.3	6.3	6.3	81.742	742 742;786;83	0
2	2	42.6	42.6	42.6	5.1441	47 47;135	0
1	1	8.9	8.9	8.9	25.946	237 237;168;21	0
2	4	6.9	6.9	6.9	103.14	923 923;923;59	0
4	3	26.7	20.9	20.9	21.258	191 191;136;19	0
3	4	7.4	7.4	7.4	92.25	802 802	0
2	2	7.1	7.1	7.1	43.614	379 379;79	0
1	1	36.5	36.5	8.2	18.742	170 170;177;16	0
1	0	2.6	2.6	2.6	53.082	460 460;2319;2	1
1	1	28	28	28	13.415	118 118;272;27	0
2	1	41.6	41.6	41.6	8.6227	77 77;105;108	0
1	1	6.3	6.3	6.3	18.739	159 159;227;22	0.002937
5	5	25.9	25.9	25.9	24.95	224 224;233	0
9	9	52.3	52.3	52.3	26.922	241 241	0
2	2	6	6	6	73.011	652 652;654;65	0
1	1	1.7	1.7	1.7	79.845	704 704;706;71	0
1	0	3.9	3.9	3.9	31.293	280 280;416	0
0	1	15.3	15.3	15.3	15.769	137 137;201;29	0
1	1	17.1	17.1	17.1	8.5199	76 76;223;202	0
5	6	36.1	36.1	36.1	20.811	183 183;107;62	0
2	2	1.7	1.7	1.7	217.1	1905 1905;1937;	0
5	6	20.5	20.5	18.5	50.431	453 453;466;40	0
34	32	34.5	34.5	27.6	192.06	1679 1679;1639;	0
2	2	17.4	17.4	17.4	23.662	218 218;260;16	0
2	1	7.1	7.1	7.1	23.181	211 211;229	0.001575
1	1	25.6	25.6	25.6	13.649	129 129;145;19	0
3	3	19	19	19	22.744	211 211	0
1	1	6.1	6.1	6.1	27.11	244 244	0
2	2	12.9	12.9	12.9	22.077	209 209;217;22	0
3	3	14.5	14.5	14.5	26.227	227 227;71;149	0
3	2	11.9	11.9	11.9	52.269	478 478;478;55	0
1	1	5.4	5.4	5.4	22.62	204 204;219;28	0.001545
1	1	4.9	4.9	4.9	24.717	225 225;438;59	0
2	2	10	10	10	76.096	669 669;655;17	0
2	1	10.8	10.8	10.8	43.28	369 369;502;53	0
1	3	3.1	3.1	3.1	138.23	1236 1236;1251;	0
4	5	43.7	43.7	43.7	15.945	142 142;73	0
0	0	11.6	11.6	11.6	15.951	138 138;185;73	0.002948
9	8	10.4	10.4	10.4	138.34	1224 1224;1233	0

2	2	7	7	7	107.14	953 953;485	0
8	9	15.8	15.8	15.8	99.045	877 877;906;15	0
5	5	14.9	14.9	14.9	57.21	511 511;552;18	0
3	3	13	13	13	36.923	331 331;308;25	0
2	4	5.7	5.7	5.7	97.717	874 874;188	0
11	11	64.5	64.5	60.2	18.502	166 166;149;15	0
0	0	2.2	2.2	2.2	115.01	998 998;1221;1	0.001539
4	5	13.5	13.5	13.5	55.317	480 480;483	0
1	1	7.3	7.3	7.3	33.657	302 302;411	0
1	0	8.5	8.5	8.5	15.296	130 130;141;14	0.008515
1	1	26.1	26.1	26.1	9.1349	88 88;360	0.002944
2	3	31.1	31.1	31.1	15.512	151 151;151	0
5	4	7.8	7.8	7.8	85.746	767 767;798;81	0
9	5	10	10	10	142.34	1415 1415;1497;	0
7	6	33.7	33.7	33.7	31.362	282 282;177;17	0
0	1	1	1	1	157.18	1401 1401	0
3	4	7.1	7.1	7.1	81.572	730 730;741;60	0
2	2	3.6	3.6	3.6	114.33	1015 1015;269	0
0	0	7.2	7.2	7.2	50.539	444 444;828	0.000532
7	8	11.6	11.6	11.6	121.89	1118 1118;1146;	0
2	1	5.7	5.7	5.7	53.371	471 471;486;49	0
1	2	6.7	6.7	6.7	47.726	420 420;352;40	0
2	1	20.8	20.8	20.8	19.344	173 173;160;20	0.004799
8	8	24.4	24.4	22.7	60.13	537 537;234;13	0
0	0	4.2	2.5	2.5	62.233	552 552;553;56	0.004831
8	6	33.3	33.3	30.9	39.183	369 369;371;37	0
1	0	17.8	17.8	17.8	14.013	129 129;137;14	0
2	1	7.6	7.6	7.6	54.234	489 489	0
6	5	15.2	15.2	15.2	53.248	474 474;480;52	0
0	1	2.3	2.3	2.3	59.763	525 525	0.007594
1	1	23.9	23.9	23.9	7.5164	67 67;81	0
3	3	14	14	14	38.123	344 344;352;36	0
3	2	14.9	14.9	14.9	47.036	417 417;448;10	0
1	2	9.9	9.9	9.9	33.777	303 303	0
1	1	10.2	10.2	10.2	13.328	118 118;807	0.002975
2	2	7.6	7.6	7.6	56.101	513 513;445;51	0
5	5	12.4	12.4	12.4	66.69	591 591;360	0
1	2	4.9	4.9	4.9	92.931	836 836;649;34	0
1	1	2.5	2.5	2.5	55.142	514 514;468;48	0
1	1	1.3	1.3	1.3	102.75	900 900;717;89	0.001571
6	6	7.6	7.6	7.6	136.37	1230 1230;1062;	0
3	4	14.1	11.4	11.4	34.081	297 297;297;18	0
5	5	22.4	22.4	19.9	36.938	326 326	0
1	1	18.4	18.4	18.4	11.006	98 98	0
3	3	49	49	49	11.139	98 98;83	0
1	0	11.6	11.6	11.6	15.799	146 146	0.001527
5	6	46.6	46.6	46.6	20.567	193 193;153;16	0
2	2	9	9	9	37.489	332 332;116;12	0
1	0	10.3	10.3	10.3	10.631	97 97	0.004847
2	2	4.8	4.8	4.8	113.74	1036 1036;175;2	0

1	1	16.7	16.7	16.7	20.6	192 192;208;28	0
1	1	4.9	4.9	4.9	35.288	325 325;353;37	0.008941
0	0	21.4	21.4	21.4	11.268	98 98;124;134	0.001559
2	2	37.9	37.9	37.9	15.716	140 140;150;14	0
10	13	43.5	43.5	42.1	52.645	480 480	0
12	11	38.2	38.2	38.2	48.442	453 453;412;33	0
3	2	36.3	36.3	36.3	10.739	91 91;91	0
2	1	25.2	25.2	25.2	13.53	111 111;76;161	0
1	1	27	27	27	7.3084	63 63	0
2	2	25.5	25.5	25.5	29.668	274 274;283	0
2	2	24.8	24.8	24.8	11.333	101 101;105;10	0.001054
2	3	26.4	26.4	26.4	11.731	106 106;71	0
0	0	4.4	4.4	4.4	43.835	388 388;410	0.00054
1	1	16.3	16.3	16.3	10.853	98 98;63	0
2	3	14.5	14.5	14.5	25.565	227 227	0
4	4	26	26	26	19.576	169 169;83;126	0
2	2	15.7	15.7	15.7	17.235	153 153;150;69	0
3	2	25.6	25.6	25.6	13.696	129 129	0
3	3	55.8	55.8	55.8	10.192	86 86	0
3	2	28	28	28	8.7813	75 75	0
2	2	25.3	25.3	25.3	10.264	91 91;103;115	0
1	1	36.8	36.8	36.8	12.615	114 114;79;95	0
2	2	32.1	32.1	32.1	6.3824	56 56;63	0
2	2	27.2	27.2	27.2	9.3697	81 81	0
1	2	12.3	12.3	12.3	35.422	325 325	0
3	3	26.5	26.5	26.5	30.601	268 268	0
38	36	11.7	11.7	11.7	532.4	4646 4646;180	0
2	2	7.5	7.5	7.5	68.297	611 611;612;63	0
3	3	26.9	26.9	26.9	17.778	167 167;415;49	0
3	4	4.1	4.1	4.1	145.18	1253 1253;862;8	0
16	17	43.4	43.4	43.4	66.022	602 602	0
1	2	7.4	7.4	7.4	52.771	488 488;519;20	0
1	2	12.6	12.6	12.6	27.041	246 246;283;33	0.001994
5	4	14.9	14.9	14.9	52.878	475 475;391;20	0
1	2	31.5	31.5	31.5	16.474	146 146;532;56	0
9	8	24.3	24.3	24.3	55.938	526 526;532;53	0
3	3	14.4	14.4	14.4	35.02	327 327;406;40	0
1	2	51.4	51.4	51.4	7.6679	70 70;582;53;	0
2	2	15.3	15.3	15.3	18.681	170 170	0
1	1	4	4	4	67.55	597 597;445;22	0
4	4	35.6	35.6	35.6	12.712	118 118;132;16	0
2	2	10.7	10.7	10.7	33.939	298 298;313;31	0
1	2	14.2	14.2	14.2	32.267	289 289;339;16	0
4	4	10.5	10.5	10.5	49.436	427 427;475;51	0
3	3	17.4	17.4	9.1	35.816	328 328;267;18	0
1	1	6.1	6.1	6.1	56.042	512 512;563;21	0
9	11	20.4	20.4	20.4	87.088	793 793;795	0
0	1	8.6	8.6	8.6	22.092	198 198	0
2	3	6.8	6.8	6.8	66.174	601 601;756;16	0
0	1	5.2	5.2	5.2	25.113	230 230;275;31	0

4	5	43.3	43.3	43.3	15.395	141 141;167;16	0
1	1	7.3	7.3	7.3	17.221	151 151;151;23	0.001572
1	1	19	19	19	18.038	158 158;239	0
1	0	1.2	1.2	1.2	93.768	847 847;901	0.003899
2	2	7.2	7.2	7.2	93.453	839 839;896;21	0
10	12	19.5	19.5	19.5	122.29	1118 1118	0
4	7	18.5	18.5	18.5	107.53	999 999	0
34	30	20.3	20.3	20.3	331.77	2871 2871;2428;	0
6	7	44.2	40	40	18.506	165 165;135;14	0
2	2	6.3	6.3	6.3	40.542	367 367	0
4	3	12.2	12.2	12.2	54.177	509 509;486;41	0
3	4	10.5	10.5	10.5	68.996	647 647;479;54	0
8	4	23.8	23.8	23.8	48.755	453 453;367;27	0
1	1	3.3	3.3	3.3	84.304	756 756;757;70	0
2	1	3.1	3.1	3.1	84.141	748 748	0
4	3	11.9	11.9	11.9	69.323	628 628;712;65	0
1	1	13.9	13.9	13.9	12.672	115 115;411;47	0
8	9	11.4	11.4	11.4	126.97	1140 1140;1092;	0
1	1	8.3	8.3	8.3	29.766	266 266	0.008891
5	5	13.9	13.9	13.9	57.208	490 490;357;38	0
4	5	10.9	10.9	10.9	77.592	691 691;734;15	0
3	3	3.5	3.5	3.5	103.19	921 921;868;93	0
2	2	4.2	4.2	4.2	119.79	1058 1058;1230;	0
0	0	9.9	9.9	9.9	22.653	192 192;223	0.003895
11	11	18.4	18.4	18.4	93.998	836 836;904	0
6	7	12.3	12.3	12.3	90.98	808 808;853;81	0
11	9	18.9	18.9	18.9	96.557	863 863;278;21	0
7	6	11.3	11.3	11.3	92.888	821 821	0
13	12	29.3	29.3	29.3	81.307	719 719;543;38	0
11	9	21.6	21.6	21.6	90.725	765 765;376;50	0
13	11	11.8	11.8	11.8	174.38	1531 1531;1557;	0
5	5	29.3	29.3	29.3	27.125	242 242;263;31	0
50	51	16.3	16.3	16.3	469.08	4128 4128;4097	0
1	0	2.3	2.3	2.3	194.81	1720 1720;1659	0
1	1	7.5	7.5	7.5	54.985	510 510;512	0
0	1	3.2	3.2	3.2	63.64	566 566;1970	0.008908
1	1	6.9	6.9	6.9	38.883	347 347;1230	0
2	1	3.7	3.7	3.7	133.06	1167 1167;1174;	0
1	1	8.2	8.2	8.2	38.646	342 342;346;12	0.001524
1	0	9.2	9.2	9.2	21.459	184 184;204;21	0.00157
2	2	14.8	14.8	14.8	37.044	331 331;397	0
1	1	17	17	17	45.745	412 412;134;47	0
2	1	8.8	8.8	8.8	49.611	453 453;480;30	0
3	2	13.5	13.5	13.5	38.044	340 340;183;24	0
3	4	18.4	18.4	18.4	40.513	358 358;167	0
0	0	6.4	6.4	6.4	19.777	172 172;276;40	0.001558
0	1	9.1	9.1	9.1	57.196	507 507;559;52	0
0	1	17.7	17.7	17.7	10.302	96 96;2243	0
0	1	11.5	11.5	11.5	51.911	453 453;504	0
1	1	17.2	17.2	17.2	22.149	198 198	0

3	3	9.1	9.1	9.1	50.096	438 438;494;55	0
0	1	4.2	4.2	4.2	29.909	260 260	0.004789
2	3	13.2	13.2	13.2	32.426	287 287;295;26	0
2	2	23.9	23.9	23.9	10.094	92 92;122	0
6	6	20.3	20.3	20.3	48.799	439 439;456;43	0
22	19	42.8	42.8	42.8	68.569	607 607;435;12	0
9	11	27.9	27.9	27.9	69.283	631 631;615;34	0
3	3	47.1	47.1	47.1	9.5541	85 85;113;65;	0
2	4	7.1	7.1	7.1	80.529	705 705;613;10	0
0	0	2.7	2.7	2.7	93.673	826 826	0
0	1	4.1	4.1	4.1	33.525	294 294;324	0.000539
2	2	6.1	6.1	6.1	54.945	493 493;494;49	0
1	2	2.8	2.8	2.8	132.65	1195 1195;931;1	0
0	0	4.7	4.7	4.7	19.15	172 172;249;27	1
2	1	11.1	11.1	11.1	40.16	359 359;406;32	0
1	1	3.3	3.3	3.3	40.763	367 367;393	0
0	1	8.8	8.8	8.8	44.424	400 400	0
2	1	12.3	12.3	12.3	36.172	318 318;347;35	0
2	1	2.9	2.9	2.9	139.09	1256 1256;1139;	0
3	3	5.6	5.6	5.6	79.621	712 712;699;71	0
2	2	4.4	4.4	4.4	113.68	979 979;924;96	0
0	0	0.3	0.3	0.3	538.59	4707 4707;4454;	1
1	1	49.4	24.7	24.7	10.366	89 89;42;47;6	0.002003
1	1	49.4	49.4	24.7	10.35	89 89	0
3	2	38.5	38.5	38.5	10.921	96 96;148;96;	0
0	1	1.5	1.5	1.5	132.29	1143 1143;1479;	0
1	0	4.5	4.5	4.5	97.44	895 895	0
14	15	11.4	11.4	11.1	358.2	3224 3224;1760;	0
7	7	14.1	14.1	14.1	70.973	630 630	0
1	1	6.5	6.5	6.5	21.392	185 185;213;23	0.004808
4	3	1.5	1.5	1.5	480.19	4358 4358;4365;	0
2	2	12.8	12.8	12.8	43.061	398 398;400	0
0	1	8.1	8.1	8.1	19.188	172 172;653	0
2	2	10.2	10.2	10.2	34.193	294 294;474;50	0
2	1	6.3	6.3	6.3	91.099	806 806;857;79	0
7	7	33.8	33.8	33.8	26.697	240 240;179;14	0
2	2	8.7	8.7	8.7	52.747	470 470;480	0.001521
0	1	8.5	8.5	4.9	34.721	306 306;548;53	0
4	5	13.3	13.3	11.3	61.174	541 541;175	0
6	7	25.8	25.8	25.8	36.091	326 326;353;15	0
3	4	28.4	28.4	28.4	30.22	289 289;303;33	0
8	9	44.7	44.7	44.7	27.843	255 255;346;17	0
1	1	20.7	5.2	5.2	50.47	463 463	0.002931
5	5	38.7	38.7	38.7	24.763	225 225;68;123	0
1	1	46.4	46.4	9.2	28.821	261 261;281;63	0
1	1	45.9	8.2	8.2	28.558	257 257;187;10	0
14	14	34.3	34.3	34.3	50.118	437 437;487	0
31	31	43	43	41.8	95.337	858 858	0
3	3	10.7	10.7	10.7	66.034	591 591;751;77	0
3	2	17.5	17.5	17.5	35.39	325 325;346;14	0

17	15	46	46	46	49.541	452 452;101	0
1	1	5	5	5	32.662	279 279	0
1	1	5	5	5	30.742	262 262;88;299	0
1	1	2.2	2.2	2.2	111.47	983 983;1332	0
4	4	22.8	22.8	22.8	28.994	254 254;219	0
2	2	9.8	9.8	9.8	55.016	500 500	0
0	1	10.2	10.2	10.2	14.245	128 128;139;32	0.002013
5	5	9.5	9.5	9.5	107.23	941 941;948;12	0
3	3	5.1	5.1	5.1	93.159	841 841;904;35	0
6	5	31.4	31.4	27.6	28.993	261 261;160;53	0
3	4	16.7	16.7	16.7	46.971	406 406	0
2	2	15.3	15.3	15.3	36.851	326 326;397;38	0
22	21	38.2	36.5	36.5	92.468	803 803;315;31	0
2	2	12.9	12.9	12.9	15.48	139 139;141;14	0.008971
3	2	37.5	37.5	37.5	12.259	104 104;71	0
4	4	18.6	18.6	18.6	30.895	285 285;302;24	0
2	2	18.7	18.7	18.7	40.183	364 364;359;39	0
8	6	34.5	34.5	34.5	31.387	290 290	0
0	0	5.2	5.2	5.2	38.006	346 346	0
27	22	35.2	35.2	35.2	134.28	1210 1210;1165;	0
2	3	40.2	40.2	40.2	13.078	122 122;148;17	0
5	5	26.3	26.3	26.3	37.893	342 342;314;19	0
1	1	5.2	5.2	5.2	56.035	502 502;522;60	0
4	5	18	18	18	52.948	455 455	0
1	1	2.2	2.2	2.2	50.219	456 456;535	0
1	2	8.6	8.6	8.6	24.844	220 220;186;21	0
0	1	3.8	3.8	3.8	111.69	992 992;992;99	0
3	3	11.8	11.8	11.8	34.833	297 297;135	0
1	1	17.9	17.9	17.9	9.1037	78 78;219;261	0.000533
1	1	8.1	8.1	8.1	23.773	210 210;100;12	0.004836
2	2	15.9	6.9	6.9	38.925	346 346;275;15	0
2	1	21.6	21.6	12.4	37.725	338 338;339;19	0
10	10	31.2	31.2	31.2	54.392	468 468;257;12	0
1	1	25.5	25.5	25.5	14.417	137 137;182;19	0
0	1	1.5	1.5	1.5	98.795	851 851	0.001999
0	0	5.7	5.7	5.7	26.973	261 261	0.001522
15	16	53.7	53.7	47.8	46.153	406 406;341;34	0
4	4	16.8	10.9	10.9	46.871	411 411;125	0
6	6	14.5	14.5	14.5	68.6	636 636;637;47	0
5	5	16.5	16.5	16.5	47.475	423 423;404;43	0
2	0	14	14	14	16.686	150 150;151;13	0
1	2	33.1	33.1	33.1	13.607	121 121;113;11	0
3	2	21.5	21.5	21.5	16.46	144 144;116;12	0
5	3	19.7	19.7	19.7	36.112	315 315;252;27	0
7	7	26.7	26.7	26.7	38.388	333 333	0
7	6	22.2	22.2	22.2	51.109	472 472;472;46	0
2	2	11.4	11.4	11.4	26.008	236 236;580;52	0.001553
9	9	9.7	9.7	9.7	166.57	1382 1382;1348	0
8	8	11.2	11.2	11.2	92.48	814 814;873;15	0
6	6	9.3	9.3	9.3	104.1	903 903;913;91	0

7	6	26.5	26.5	26.5	58.14	499 499;533;54	0
7	6	19.6	19.6	19.6	52.22	445 445;352;15	0
3	3	8.4	8.4	8.4	37.563	357 357;100	0
3	2	19.8	19.8	19.8	29.283	262 262;320;22	0
4	2	13.2	13.2	13.2	39.589	349 349;366;35	0
8	8	39.4	39.4	39.4	36.501	325 325;125	0
2	2	18.9	18.9	18.9	11.959	106 106;117;20	0
1	1	10.2	10.2	10.2	15.875	137 137;192;21	0.001567
7	6	15	15	15	70.901	607 607;564;51	0
1	0	13.5	13.5	13.5	8.4675	74 74;191;220	0.001567
15	13	15.3	15.3	15.3	158.52	1435 1435;1512;	0
1	2	5.4	5.4	5.4	49.652	444 444;869;90	0.002008
3	3	9.6	9.6	9.6	69.697	616 616;572;61	0
6	6	34.6	34.6	34.6	25.2	228 228;248	0
2	2	6.5	6.5	6.5	49.222	431 431;101;10	0
7	7	37.7	37.7	37.7	16.019	146 146;186;15	0
4	4	8.1	8.1	8.1	138.68	1220 1220;1220	0
5	5	33.1	33.1	33.1	26.599	245 245;108;22	0
1	1	11.5	11.5	11.5	15.105	139 139;143;16	0
3	4	23.5	23.5	23.5	28.235	272 272	0
1	1	5.7	5.7	5.7	29.408	263 263;293	0
1	2	12.4	12.4	12.4	31.821	291 291	0
2	2	7.9	7.9	7.9	63.616	559 559;796;92	0.001535
6	5	10.1	10.1	10.1	123.38	1071 1071;132;1	0
10	10	14	14	14	107.78	945 945;971;91	0
1	2	2.2	2.2	2.2	136.31	1204 1204;24;76	0
7	8	14.9	14.9	14.9	122.85	1104 1104;1114	0
7	9	23.5	15.7	15.7	69.371	586 586;586;58	0
8	10	12.8	12.8	12.8	119.91	1047 1047;66;81	0
9	9	19	19	19	81.074	709 709;173;89	0
5	5	39.5	39.5	36	32.922	286 286	0
4	5	32.9	29.4	29.4	32.949	286 286;146;17	0
9	9	35.3	35.3	35.3	30.628	272 272;260;30	0
10	9	24.3	23.1	23.1	68.604	653 653;655;64	0
12	13	28.3	28.3	27.1	73.027	711 711;711;27	0
6	7	25.5	24.1	24.1	61.64	572 572;261	0
3	3	11.3	11.3	11.3	40.532	353 353;419;80	0
4	4	22.2	22.2	22.2	52.623	445 445	0
19	16	44.4	44.4	44.4	54.529	493 493;132;13	0
41	40	27.2	27.2	27.2	273.2	2509 2509;2511;	0
4	4	47.4	47.4	47.4	15.164	135 135;101;10	0
2	2	11.3	11.3	11.3	37.481	335 335;515	0
4	6	21.9	21.9	21.9	44.648	393 393;485;50	0
3	3	11.9	11.9	11.9	48.295	420 420;677;49	0
5	5	35.5	35.5	35.5	21.225	183 183;113;15	0
0	0	0.5	0.5	0.5	198.69	1831 1831;1894	1
71	70	48.2	48.2	45	280.01	2639 2639;2647;	0
39	35	27.4	25.9	24.6	275.66	2578 2578;2591;	0
2	2	12.3	12.3	12.3	30.77	276 276;373;37	0
6	5	26.8	26.8	26.8	42.592	380 380;316;16	0

4	5	32.5	32.5	32.5	22.119	206 206;163;15	0
5	5	15.3	15.3	15.3	42.08	379 379;427;18	0
4	5	18	18	18	47.142	428 428;483;42	0
2	2	6.2	6.2	6.2	44.205	389 389;395;27	0.000533
4	4	13	13	13	68.326	608 608;539;62	0
1	2	22.2	22.2	22.2	11.901	108 108;135;21	0
0	0	2.7	2.7	2.7	75.579	674 674;706	0
17	17	63.2	63.2	51.4	39.42	364 364;418;36	0
2	2	19	7.1	7.1	39.455	364 364;135;14	0
7	7	31.7	31.7	31.7	50.212	467 467;510	0
1	1	16.4	16.4	16.4	12.43	116 116;87;113	0
4	4	18.6	18.6	18.6	32.632	290 290;317;35	0
6	8	71.9	71.9	71.9	14.716	135 135;38	0
2	2	9.6	9.6	9.6	26.152	250 250;233	0
3	4	8.5	8.5	8.5	65.33	585 585;144;20	0
2	1	18.8	18.8	18.8	13.667	117 117;57;70;	0
3	2	33	33	33	10.504	94 94;188;103	0
6	6	16.6	16.6	16.6	75.935	673 673;729;78	0
1	1	7.5	7.5	7.5	43.955	388 388;194	0
6	5	21.3	21.3	21.3	85.686	781 781;748;76	0
1	1	1.2	1.2	1.2	236.28	2084 2084;2109	0.00295
5	6	12.5	12.5	12.5	107.97	957 957;977;97	0
2	1	2.9	2.9	2.9	107.89	962 962;973	0.001053
1	1	15.3	15.3	15.3	17.512	150 150;142	0
1	1	6.9	6.9	6.9	54.389	478 478	0
1	1	9.7	9.7	9.7	12.976	113 113;163;18	0.000538
2	5	24.9	24.9	24.9	26.987	237 237;274;28	0
13	14	35.9	35.9	35.9	59.256	515 515;545;56	0
10	7	20.2	20.2	20.2	64.824	573 573;558;56	0
13	12	37.9	37.9	37.9	60.192	535 535;525;52	0
15	15	37.3	37.3	37.3	61.397	558 558;425;39	0
1	2	3.3	3.3	3.3	68.629	599 599;637;17	0
1	1	5.2	5.2	5.2	28.135	252 252;274	0.009767
3	1	8.7	8.7	8.7	49.419	446 446;228	0
9	10	22.6	22.6	22.6	65.459	598 598;669;16	0
3	4	9	9	9	76.758	681 681;699	0
2	2	10.7	10.7	3.7	86.578	764 764;775;17	0
2	2	7.8	7.8	7.8	37.432	335 335	0.001554
1	1	8.9	8.9	8.9	16.628	157 157	0
4	4	14.1	14.1	14.1	50.496	469 469;479;52	0
1	1	20	20	20	21.707	190 190;183;22	0
5	5	24.1	24.1	24.1	27.566	241 241;200;20	0
8	8	57.6	57.6	57.6	23.356	210 210;174;79	0
13	14	56	56	56	31.548	293 293;335;26	0
1	0	2.8	2.8	2.8	48.705	434 434	0.004845
6	6	14.4	14.4	14.4	80.852	727 727;601;37	0
2	1	30	30	30	10.999	100 100;118;17	0
2	4	9.2	9.2	9.2	83.165	739 739;77;79	0
1	0	5.7	5.7	5.7	46.744	420 420;433	0
1	1	7.3	7.3	7.3	21.51	193 193;265;27	0



3	3	6.6	6.6	6.6	54.719	502 502;298;31	0
1	1	6.7	6.7	6.7	38.695	358 358;328	0
4	5	18.3	18.3	18.3	61.68	558 558;486;29	0
6	7	14.1	14.1	14.1	65.928	594 594;693	0
5	2	7.5	7.5	7.5	134.55	1179 1179;1192;	0
1	1	4.9	4.9	4.9	78.759	668 668;696	0
1	1	10.4	10.4	10.4	33.81	298 298;285	0
3	2	14.8	14.8	14.8	39.768	384 384;452;46	0
1	1	2.5	2.5	2.5	60.593	528 528 0.008916	
1	0	16	16	16	9.4134	81 81;174;236	0
1	2	8.7	8.7	8.7	70.472	620 620;1002;3	0
1	1	11.2	11.2	11.2	15.578	134 134;137	0
0	0	7.3	7.3	7.3	20.969	193 193;463;48	0.002967
1	0	5.6	5.6	5.6	58.041	518 518;687;69	0
0	0	7.2	7.2	7.2	47.27	417 417;424;45	0
0	1	6.4	6.4	6.4	37.205	345 345 0.001996	
5	2	28.6	28.6	28.6	24.279	217 217	0
1	1	9.6	9.6	9.6	18.192	157 157;187;22	0
2	2	12.2	12.2	12.2	21.424	188 188;189;18	0
5	4	30.5	30.5	30.5	26.224	233 233;216;23	0
1	0	20.3	20.3	20.3	8.6739	79 79;184	0
1	0	10.4	10.4	10.4	12.964	115 115;155;19	0
2	2	4.3	4.3	4.3	97.031	839 839;868;87	0.001529
3	3	27.1	15.5	15.5	40.361	354 354;302;14	0
4	2	28.2	16.6	16.6	40.45	355 355;366;30	0
3	1	69.4	69.4	69.4	8.0061	72 72	0
2	4	26.5	13.5	13.5	37.377	340 340;332;10	0
5	5	30.3	30.3	17.4	37.331	340 340;232;25	0
3	3	26.6	26.6	15	40.532	354 354;350;35	0
1	1	7.2	7.2	4.2	42.142	359 359;170	0
3	2	11.3	8.4	8.4	44.179	379 379;380;39	0
0	1	7	3.9	3.9	42.123	359 359;355	0.00153
0	0	4.3	4.3	4.3	33.287	282 282;377	0.004824
14	13	68.1	68.1	68.1	35.076	317 317;273;19	0
2	2	6.3	6.3	6.3	60.54	537 537;549	0
0	0	1.2	1.2	1.2	97.23	901 901;781;80	0.001519
2	2	14.6	14.6	14.6	20.834	199 199;217	0
3	2	31.4	31.4	31.4	17.201	153 153;90;132	0
3	5	13.4	13.4	13.4	57.673	514 514;420;20	0
4	6	6.4	6.4	6.4	233.27	2063 2063;2144;	0
0	1	2.2	2.2	2.2	54.794	509 509 0.007605	
15	11	52.5	52.5	29.4	70.108	642 642;641;64	0
13	15	32	30.4	30.4	94.33	840 840;699;47	0
1	1	15.4	1.7	1.7	71.027	643 643;367	0
17	16	50.5	46.3	36.4	70.897	646 646;627;49	0
1	1	32.9	32.9	32.9	8.5435	76 76	0
17	19	35.6	35.6	33.9	92.115	814 814;858;81	0
9	9	24.9	24.9	24.9	74.267	651 651;704;49	0
13	12	75.6	75.6	75.6	22.782	205 205;186;37	0
19	19	45.2	27.2	27.2	84.659	732 732;854;17	0

17	17	56.5	56.5	31.8	83.263	724 724;597	0
1	1	16.1	1.9	1.9	70.02	639 639	0
4	4	54.8	54.8	54.8	11.012	104 104;154;18	0
2	1	27	27	27	12.23	115 115;116;16	0
1	3	15.5	15.5	15.5	36.032	316 316;370;28	0
1	1	12.9	12.9	12.9	12.649	116 116;205	0.008887
3	4	48.6	48.6	48.6	15.184	142 142;110;14	0
0	0	27.9	21.8	21.8	15.998	147 147;90	0
3	2	7.7	7.7	7.7	67.703	634 634;662;65	0
1	1	4.2	4.2	4.2	30.004	263 263;690;77	0.002015
4	5	34.2	34.2	34.2	26.788	240 240;233;25	0
4	4	22.1	22.1	22.1	28.515	253 253;515;55	0
3	4	16.4	16.4	16.4	30.302	280 280;283;32	0
5	5	23.6	23.6	23.6	30.84	305 305	0
9	7	40.7	37.8	37.8	33.155	307 307;267;32	0
7	6	28.1	28.1	28.1	37.029	356 356;378;11	0
5	7	38.6	38.6	38.6	23.811	210 210;287;30	0
3	2	10.7	10.7	10.7	40.04	363 363;244;30	0
9	7	37.3	37.3	30.8	45.671	415 415;98	0
4	4	33.6	27.3	14.9	47.087	429 429;472;44	0
2	4	27.8	13.8	13.8	49.263	449 449	0
7	4	29	29	29	35.238	331 331;346;29	0
15	16	43.2	43.2	43.2	48.562	440 440;463;46	0
6	6	40.6	40.6	27.2	64.132	589 589;530;45	0
22	22	41.5	41.5	41.5	73.62	691 691;730;73	0
10	6	35.7	35.7	26.6	58.735	527 527;562;58	0
9	9	25.6	18	18	70.942	633 633;636;59	0
22	21	34.1	34.1	34.1	90.583	825 825;804;80	0
2	3	5.6	5.6	5.6	71.611	641 641;766;76	0
11	10	23.3	23.3	23.3	85.104	747 747;746	0
15	11	56.4	56.4	53.8	37.429	353 353;341;26	0
13	11	47.7	47.7	47.7	28.916	262 262;288;29	0
3	5	13.7	12.5	12.5	98.972	889 889;917	0
9	10	19.4	19.4	18.2	101.08	905 905;916;91	0
1	2	2.9	2.9	2.9	67.638	629 629	0
4	3	37.3	37.3	29.7	18.311	158 158;215;21	0
1	0	19.4	10.4	10.4	15.404	134 134;209	0
1	1	8.5	8.5	8.5	17.522	153 153;188;19	0
3	2	30.8	30.8	30.8	11.676	107 107;179;96	0
0	1	23.2	23.2	23.2	10.767	99 99;118;147	0
4	4	35.7	35.7	35.7	13.802	126 126;78;78;	0
0	0	10.5	10.5	10.5	20.598	181 181;440;44	0.002
1	1	3.9	3.9	3.9	39.786	334 334;419	0.001517
2	1	11.4	11.4	6.1	51.998	458 458;488	0
2	3	17	17	17	20.863	194 194;177	0
2	2	36.2	36.2	16	21.364	213 213	0
2	2	31.1	11.4	11.4	21.865	219 219;221;20	0
5	6	26.1	22.1	22.1	22.58	226 226	0
2	2	10.3	10.3	10.3	22.487	213 213	0
1	1	27.2	27.2	6.5	18.481	169 169;170;12	0

2	2	31.2	18.8	18.8	13.509	128 128;128;12	0
0	1	14.5	10.7	10.7	26.153	242 242;372	0.006667
1	1	21.7	5.6	5.6	15.144	143 143;131;14	0.002001
0	0	53.2	5.6	0	13.952	126 126;127	1
0	0	52.4	7.1	0	13.92	126 126;126;12	1
0	0	52.4	5.6	5.6	13.908	126 126	1
0	0	40.4	40.4	0	18.804	166 166;126;12	0
0	0	26.5	26.5	8.1	15.43	136 136	0
7	8	52.4	52.4	52.4	11.367	103 103	0
4	4	22	22	13.2	46.158	410 410;425;42	0
2	1	19.5	11.1	11.1	47.82	425 425;469;41	0
0	0	43	6.8	0	41.003	365 365;326;36	0
0	0	43	43	0	41.054	365 365;371;36	0
1	1	6.8	3	3	38.254	338 338;343;34	0.004852
0	0	25.7	8	0	40.539	362 362;362;24	0
0	0	30.3	16.7	0	40.885	366 366;325;33	0
0	0	26.3	7	0	41.238	372 372	0
7	7	20.9	20.9	20.9	41.331	369 369;211;36	0
6	5	26.7	26.7	26.7	44.468	378 378;230;35	0
1	1	8	8	8	29.578	264 264;281;55	0
4	3	14.8	14.8	14.8	35.236	318 318;390;31	0
1	1	8	8	8	34.36	325 325	0
7	8	18.5	18.5	18.5	57.293	520 520;95	0
4	3	20.6	20.6	20.6	37.32	345 345;418	0
5	5	28	28	28	24.579	218 218	0
6	6	13.6	13.6	13.6	104.78	937 937;999;65	0
1	1	29	29	29	7.6079	69 69;82	0
8	8	24.6	24.6	24.6	57.861	529 529;134;14	0
4	3	22.1	22.1	19.4	57.886	521 521;170	0
1	1	4.6	1.9	1.9	57.81	521 521	0.001548
1	1	4.6	4.6	4.6	60.221	538 538;169;17	0
13	12	23.1	23.1	23.1	97.169	876 876;690;73	0
8	9	14.6	14.6	14.6	123.75	1099 1099;1037;	0
3	4	6.5	6.5	6.5	119.52	1038 1038	0
1	0	1.9	1.9	1.9	115.96	1041 1041	0
2	1	2.2	2.2	2.2	103.58	940 940;1014;1	0
1	1	6.9	3.4	3.4	39.309	350 350;244	0
0	1	6.6	6.6	3.4	43.083	377 377	0
1	1	3.1	3.1	3.1	104.99	914 914;918	0
1	0	4.5	4.5	4.5	99.996	911 911	0
9	8	47.4	47.4	47.4	32.66	289 289;178	0
2	2	18.6	18.6	18.6	19.603	177 177;194;15	0
11	10	31.9	31.9	30.2	50.957	470 470;514;27	0
2	3	3.8	3.8	3.8	304.1	2671 2671;721;2	0
4	4	10	10	10	63.704	579 579;198;60	0
2	3	18.8	18.8	18.8	30.338	266 266;160	0
1	0	2.6	2.6	2.6	38.463	342 342;502;50	0.002488
13	10	18.8	18.8	18.8	129.29	1181 1181;942;8	0
4	3	5	5	5	116.61	1051 1051;1066;	0
16	15	30.4	30.4	30.4	119.09	1068 1068;1073;	0

2	3	8.2	8.2	8.2	111.13	1002 1002;1012;	0
2	2	3.5	3.5	3.5	75.849	693 693;746;78	0.00054
12	11	20.8	20.8	20.8	88.414	798 798;789;80	0
32	31	28.1	28.1	28.1	194.46	1745 1745;1752;	0
2	2	5.3	5.3	5.3	57.825	532 532;310	0
1	2	8.8	8.8	8.8	54.404	489 489;161;21	0
2	3	10.5	10.5	10.5	31.356	276 276;467;37	0
1	1	21.6	21.6	21.6	8.0866	74 74;112;112	0
4	5	10.3	10.3	10.3	62.094	551 551;510;10	0
6	8	32.7	32.7	32.7	38.91	352 352;390;11	0
18	18	32.3	32.3	32.3	95.337	894 894;898;69	0
0	1	0.9	0.9	0.9	134.62	1240 1240;1249	0.001521
1	1	5.9	5.9	5.9	20.239	188 188;298	0.00152
5	5	27.2	27.2	27.2	35.786	331 331;366;13	0
2	3	16.5	16.5	16.5	42.794	393 393;199;28	0
12	11	37.4	37.4	37.4	46.659	414 414;157;62	0
9	9	12.3	12.3	12.3	144.5	1262 1262;1152;	0
6	6	8.7	8.7	8.7	113.79	1012 1012	0
1	1	25.8	25.8	25.8	13.651	120 120;122;22	0
18	17	37.2	37.2	34.1	81.744	745 745;235;27	0
7	6	35.8	35.8	35.8	32.583	299 299;279;25	0
1	1	9.4	9.4	9.4	13.999	128 128;341;46	0
3	2	12.1	8.9	8.9	59.51	593 593;584;45	0
9	9	60.3	56.8	26.4	49.586	458 458;458;41	0
5	3	31.6	16.9	12.7	49.167	456 456;456;29	0
18	18	57.2	55.1	45.8	48.057	430 430;391;29	0
21	15	80.2	80.2	60	44.091	400 400;400;18	0
3	2	14	12.8	12.8	62.064	623 623;623;39	0
1	0	12.7	7.8	4.5	66.017	644 644;644	0
1	1	10.9	2.2	2.2	65.865	645 645;639;70	0.001528
5	5	48.3	44.2	10.5	62.378	590 590;590;17	0
2	2	42.7	25.7	4.8	60.044	564 564;564;56	0
0	0	36.3	1.8	0	60.066	564 564	0.004805
2	3	64.8	64.8	6.4	51.385	469 469;469	0
23	23	62.1	57.6	51.8	53.704	483 483;483;51	0
3	3	9.1	9.1	9.1	45.86	418 418;443;40	0
2	4	5.2	5.2	5.2	149.61	1300 1300;1306;	0
6	6	8.3	8.3	8.3	109.68	963 963;860;94	0
0	0	1.1	1.1	1.1	186.49	1648 1648	0.001518
4	4	7.7	7.7	7.7	109.13	952 952;856;96	0
0	0	3.7	3.7	3.7	36.788	324 324;381	0.00201
2	1	32.7	32.7	26.7	22.828	202 202;195;25	0
1	0	2.4	2.4	2.4	52.351	465 465	0.003893
2	2	16	16	16	19.043	169 169;184	0
6	4	20.3	20.3	20.3	58.677	531 531;517;18	0
2	2	23.6	9.7	9.7	75.491	694 694;248	0
5	6	38.8	38.8	17.4	50.67	454 454;414;34	0
4	2	7.5	7.5	7.5	70.702	615 615;213;51	0
25	22	53.6	52.2	50.9	66.408	586 586;387;32	0
20	16	46.1	43.5	43.5	69.948	620 620	0

0	1	1.9	1.9	1.9	128.17	1147 1147;1668;	0
0	0	1.4	1.4	1.4	399.73	3695 3695;561	0
5	3	7.9	7.9	7.9	129.57	1172 1172;188	0
3	2	5.2	5.2	5.2	177.6	1609 1609	0
5	4	9.8	9.8	9.8	121.6	1111 1111;1193	0
1	1	14.6	14.6	14.6	9.2824	82 82;196;399	0.001569
6	5	14.1	14.1	14.1	57.278	509 509;503;40	0
0	2	5.4	5.4	5.4	82.198	721 721;732;26	0
3	5	9.9	9.9	9.9	55.01	507 507	0
1	3	3.7	3.7	3.7	113.46	1077 1077;1126;	0
1	2	14.5	14.5	14.5	26.076	234 234	0
1	1	11.9	11.9	11.9	23.52	201 201;503;53	0
3	4	11.1	11.1	11.1	83.353	739 739	0
26	27	29.1	29.1	29.1	157.9	1394 1394;504;5	0
4	3	8.4	8.4	8.4	82.688	752 752;784;80	0
1	1	1.1	1.1	1.1	92.005	835 835;883;90	0.008895
0	3	8.7	8.7	8.7	63.472	583 583	0
7	8	32.2	32.2	32.2	34.93	307 307;62	0
4	5	6.1	6.1	6.1	128.04	1122 1122;1176;	0
0	0	4.4	4.4	4.4	115.06	1006 1006;1011;	0
4	4	13.2	13.2	13.2	42.741	379 379;228	0
2	3	9.6	9.6	9.6	31.742	292 292;305;31	0
6	5	12.6	12.6	12.6	69.284	611 611;532;58	0
6	7	41	41	41	29.717	261 261;323;16	0
12	9	25.6	25.6	25.6	66.99	598 598;599;60	0
0	1	6.7	6.7	6.7	66.175	601 601;493;58	0
12	12	42.2	42.2	38.6	36.688	332 332;361;27	0
7	8	32.9	29.3	29.3	36.638	334 334;232;13	0
2	3	11	11	11	93.296	829 829;845;76	0
3	2	9.5	9.5	9.5	72.063	643 643;237	0
8	9	24.4	24.4	20.4	80.419	720 720;141	0
2	2	10.1	5.8	5.8	74.435	670 670;711;15	0
3	3	20.3	20.3	20.3	18.042	158 158;70;80;	0
2	3	6.8	6.8	6.8	104.56	945 945;682;69	0
0	0	2.9	2.9	2.9	76.193	713 713	0
3	2	8.8	8.8	8.8	58.22	489 489;432;18	0
4	3	10.8	10.8	10.8	46.836	408 408;120;18	0
1	1	20	20	20	8.2474	70 70;74;96;1	0.004822
8	8	14.9	14.9	14.9	68.047	597 597;625;10	0
3	3	8.8	8.8	8.8	44.561	376 376;414;15	0
0	1	9.4	9.4	9.4	25.74	234 234;489;53	0
0	0	5.3	5.3	5.3	60.207	544 544;274;18	0
1	0	2.5	2.5	2.5	46.765	407 407;487	0.004803
4	3	13.3	13.3	13.3	44.732	399 399;472;34	0
0	0	9.4	9.4	9.4	12.06	106 106;141;14	0.00485
4	4	8.6	8.6	8.6	44.882	417 417;364	0
2	2	4.1	4.1	4.1	44.955	410 410;410;41	0
2	1	17.9	17.9	17.9	22.279	207 207;774	0
2	2	17.4	17.4	17.4	12.476	115 115	0
4	4	14.1	14.1	14.1	36.856	333 333;348;10	0

2	2	9	9	9	41.531	367 367;335;13	0
0	1	9.8	9.8	9.8	65.171	599 599	0
0	1	2.5	2.5	2.5	38.247	356 356;366;48	0.004787
1	1	5.2	5.2	5.2	28.973	249 249;296;34	0.001555
2	2	8	8	8	27.278	249 249;246;25	0
8	11	16	16	16	99.326	893 893;94;107	0
5	6	39	39	39	23.038	210 210;245;33	0
16	17	65.7	65.7	65.7	35.503	338 338;296;23	0
3	1	19.2	19.2	19.2	32.233	292 292;146;17	0
1	1	11.2	11.2	11.2	19.228	169 169;181;18	0.000536
0	1	3.3	3.3	3.3	39.834	360 360;387	0.004843
1	1	38.5	38.5	38.5	5.7856	52 52;61;75;1	0
1	3	10.7	10.7	10.7	80.702	731 731;837;49	0
1	0	6.9	6.9	6.9	24.269	245 245	0
1	2	14.4	14.4	14.4	19.529	195 195	0
15	15	25	25	25	94.622	847 847;895;84	0
2	4	8.4	8.4	8.4	65.893	582 582;194	0
4	3	11	11	11	197.6	1825 1825;2089;	0
0	0	6.3	6.3	6.3	12.853	111 111;134;13	1
1	1	6.5	6.5	6.5	42.426	385 385;454;42	0
0	0	4.9	4.9	4.9	80.214	738 738	0
1	1	18.3	18.3	18.3	14.686	131 131;196	0
3	3	26.2	21.5	21.5	21.671	195 195;143	0
3	3	16.6	16.6	12.6	23.818	223 223;247;91	0
0	0	18.4	18.4	18.4	16.389	147 147;169;21	0.00572
4	3	26.5	26.5	26.5	21.143	185 185;182;71	0
2	2	5	5	5	50.628	457 457;456;48	0
2	1	32.8	32.8	32.8	6.0683	61 61;61;61;6	0
2	2	7.8	7.8	7.8	75.022	668 668;495	0
3	2	15.5	15.5	15.5	35.777	317 317;466;43	0
2	1	13.1	13.1	13.1	25.717	229 229;253;26	0
1	1	6.6	6.6	6.6	22.063	198 198;259;30	0.001998
3	2	11.1	11.1	11.1	43.215	386 386;38;170	0
2	2	11.3	11.3	11.3	35.991	328 328;455;47	0
5	6	9.7	9.7	9.7	101.11	900 900;546;58	0
1	1	5.8	5.8	5.8	24.618	241 241;302;41	0
2	1	9.7	9.7	9.7	57.518	525 525;563;28	0
1	1	3	3	3	48.216	434 434;575;59	0
1	1	5.4	5.4	5.4	29.651	278 278;342	0.002979
0	0	18.6	18.6	18.6	18.259	167 167;203;23	0.001568
2	2	11.3	11.3	11.3	37.171	344 344;346;39	0.002954
0	1	24.2	24.2	24.2	7.036	62 62;24;78;4	0.002963
4	2	28.9	28.9	28.9	26.753	232 232;227;24	0
0	1	17.1	17.1	17.1	15.303	140 140;256;23	0.003891
10	10	27.3	27.3	27.3	82.624	747 747;758;71	0
1	1	18.2	18.2	18.2	8.3587	77 77;147	0
1	1	18.1	18.1	18.1	18.416	166 166;152;12	0
1	0	0.6	0.6	0.6	199.08	1823 1823;1827	1
6	7	48.9	48.9	48.9	29.999	268 268	0
3	3	9.3	9.3	9.3	48.646	463 463;493;76	0

2	0	23.7	23.7	23.7	14.374	131 131;156;14	0
1	1	3	3	3	72.748	640 640;642	0.005723
3	3	13.4	13.4	13.4	36.813	335 335;377;27	0
1	1	2	2	2	143.64	1275 1275;1295;	0
5	5	21.3	21.3	21.3	32.182	296 296;263;31	0
3	1	12.5	12.5	12.5	40.467	399 399;540	0
2	3	10.2	10.2	10.2	43.121	394 394;372;38	0
4	5	29	29	29	33.331	303 303;262	0
1	0	15.7	3.5	3.5	31.282	287 287;296;40	0.00053
2	2	16.4	16.4	16.4	16.937	152 152	0
1	1	7.3	7.3	7.3	33.281	313 313;323;97	0
1	1	26.3	26.3	26.3	10.5	95 95	0
4	4	16.2	16.2	16.2	51.355	452 452;273;13	0
1	1	7	7	7	25.028	227 227;353;45	0
2	2	22.7	22.7	22.7	10.998	97 97	0
1	1	25	25	25	5.1438	44 44;60;61;6	0
5	5	65.5	65.5	65.5	15.521	142 142	0
2	3	17.2	17.2	17.2	34.559	309 309	0
7	7	39.6	39.6	39.6	37.893	361 361;329;21	0
6	6	17.9	17.9	17.9	67.454	608 608	0
1	1	10.7	10.7	10.7	12.728	112 112;408;43	0
0	1	1.3	1.3	1.3	80.64	713 713	0.008962
3	3	16	16	16	36.828	312 312;403	0
2	2	11.6	11.6	11.6	58.252	525 525;394;27	0
1	3	10.8	9.4	9.4	54.366	489 489;490;11	0
2	2	8.5	8.5	8.5	36.432	316 316;360	0
5	5	20.9	20.9	20.9	31.703	278 278;326;32	0
2	1	4.6	4.6	4.6	75.356	679 679	0
3	3	14.3	14.3	14.3	34.222	293 293;102;16	0
14	14	38.1	38.1	30.2	67.819	577 577;103	0
2	2	4.2	4.2	4.2	53.944	500 500	0
1	2	4.6	4.6	4.6	99.31	913 913;979;97	0
1	2	11.3	11.3	11.3	23.844	213 213;431;32	0
4	4	33.6	33.6	33.6	24.061	217 217;437;36	0
2	2	16.3	16.3	16.3	27.56	239 239	0
0	0	3.2	3.2	3.2	53.004	473 473;1394;1	0.002976
1	0	17.3	17.3	17.3	9.2555	81 81;106;120	0
7	5	24.9	24.9	24.9	45.651	413 413;425;43	0
2	1	8.6	8.6	8.6	37.898	348 348;400;38	0.001562
12	13	16.7	16.7	16.7	148.85	1328 1328;1332;	0
1	1	7.8	7.8	7.8	33.932	306 306;149;20	0
2	3	33.8	33.8	33.8	15.947	145 145;268;26	0
0	1	6	6	6	24.484	215 215	0
2	2	22.6	22.6	22.6	15.864	146 146;188;24	0
46	44	29.7	29.7	29.7	233.47	2048 2048;2061;	0
0	1	8	8	8	16.684	150 150;194;19	0.002934
6	5	62.8	62.8	46.2	16.29	145 145;161;15	0
0	1	3	3	3	95.928	844 844;1794;1	0
8	8	60.5	60.5	60.5	20.457	177 177;171;17	0
1	1	6.7	0.4	0.4	229	1976 1976;1985;	0.002969

0	0	6	0.5	0.5	223.57	1938 1938;1945;	0.004838
1	1	4.7	1.3	1.3	227.87	1995 1995;2003;	0
72	74	52.1	52.1	44	226.53	1960 1960;1382;	0
2	2	51.9	51.9	51.9	5.7044	52 52;118	0
7	7	38.6	38.6	38.6	31.554	332 332	0
2	2	7.8	7.8	7.8	38.868	358 358;215;20	0.002007
1	1	4.6	4.6	4.6	75.388	657 657;199;38	0
11	8	15.2	15.2	15.2	115.73	1025 1025;953;8	0
3	2	5.4	5.4	5.4	96.352	846 846;879;88	0
1	1	4.4	4.4	4.4	113.89	1086 1086;199;2	0
4	4	23.3	23.3	23.3	22.793	202 202;269;23	0
3	3	8.8	8.8	8.8	53.662	480 480;530;53	0
1	1	6	6	6	20.35	184 184	0
0	0	12.9	12.9	12.9	7.8423	70 70;93;101;:	0.008904
1	0	14.7	14.7	14.7	15.733	136 136;377	0.00156
1	2	13.7	13.7	13.7	19.258	161 161;172;14	0
0	1	13.1	13.1	13.1	27.907	252 252;249	0
0	2	4.4	4.4	4.4	51.851	457 457;463	0
0	0	4.9	4.9	4.9	30.241	264 264	0
1	1	4.9	4.9	4.9	24.793	226 226;305	0.004854
4	5	27.7	27.7	27.7	31.628	278 278;301;33	0
1	0	2.2	2.2	2.2	55.165	497 497;572	0.009337
1	1	7.1	7.1	7.1	48.027	439 439;463;48	0
2	3	8.3	8.3	8.3	76.689	677 677;418;72	0
2	2	16.7	16.7	16.7	19.311	168 168;169;48	0
2	2	20.6	20.6	20.6	15.016	136 136;198;21	0
0	1	1.2	1.2	1.2	128.79	1128 1128;1134	0.008912
0	0	8.1	8.1	8.1	24.899	221 221	0.004833
2	1	22.6	22.6	22.6	15.727	146 146;222;24	0
3	2	15.8	15.8	15.8	20.9	183 183;69;114	0
1	0	15.1	15.1	15.1	18.856	172 172	0
113	120	46.4	46.4	46.4	629.09	5890 5890;121;1	0
1	1	2.7	2.7	2.7	46.91	414 414;600;70	0.000538
2	2	14.9	14.9	14.9	31.291	282 282;398;18	0
1	1	29.1	29.1	2.2	106.87	944 944;847	0
1	1	28.3	2	2	109.44	966 966;852;11	0
1	1	7.1	7.1	7.1	55.722	532 532;234	0
6	6	21.8	21.8	21.8	56.598	541 541;365;31	0
4	3	11.8	11.8	11.8	49.062	440 440;448;40	0
4	4	32	32	32	22.788	200 200;198;19	0
1	0	2.4	2.4	2.4	92.948	837 837;937;96	0
3	3	25.8	25.8	25.8	14.627	132 132;128	0
3	3	4.6	4.6	4.6	82.682	733 733;746	0
0	1	8.7	8.7	8.7	62.846	562 562;563;32	0
6	7	21.8	21.8	21.8	55.52	491 491;368;60	0
1	1	2.3	2.3	2.3	56.099	525 525;538	0.000539
0	0	1.2	1.2	1.2	108.06	971 971;960;12	0
6	5	5.5	5.5	5.5	139.38	1267 1267;1267;	0
1	2	38.9	38.9	38.9	9.3926	90 90;130;77;'	0
11	12	33.8	32.1	32.1	54.231	471 471;382;23	0



4	4	29.3	29.3	29.3	15.079	140 140;143;46	0
1	1	9.7	9.7	9.7	61.386	548 548;543;48	0
6	6	24.3	24.3	24.3	40.572	370 370;372;27	0
1	0	10.3	10.3	10.3	15.896	145 145;223	0
3	3	21.1	21.1	21.1	18.76	175 175;422;44	0
3	4	7	7	7	91.838	790 790	0
1	1	20.4	20.4	20.4	6.199	54 54;103;156	0
1	1	11.6	11.6	11.6	21.87	198 198;968;96	0
3	3	6.5	6.5	6.5	76.12	695 695	0
4	3	16.9	16.9	16.9	38.242	331 331;133;18	0
28	35	29.7	29.7	29.7	236.51	2101 2101;2099;	0
2	3	11	11	11	106.37	925 925;686;89	0
4	3	8.4	8.4	8.4	128.98	1156 1156	0
2	3	5.9	5.9	5.9	149.39	1433 1433;1475;	0
10	10	15.6	15.6	15.6	148.09	1327 1327;1391;	0
4	3	6.2	6.2	6.2	148.86	1314 1314;1436;	0
5	7	6	6	6	227.92	2012 2012;273	0
4	3	5.7	5.7	5.7	152.57	1519 1519;2079;	0
1	1	3.4	3.4	3.4	46.862	440 440;468	0
0	2	4.4	4.4	4.4	62.101	544 544;462;61	0
4	4	12.4	12.4	12.4	78.77	696 696;741;11	0
7	7	13.4	13.4	13.4	99.554	880 880;819;69	0
3	2	4.2	4.2	4.2	186.27	1714 1714;1800;	0
2	2	9.2	9.2	9.2	53.254	522 522;446	0
0	0	3.3	3.3	3.3	205.11	1887 1887;967	0
1	1	1.6	1.6	1.6	68.119	608 608;617 0.003885	
2	3	15.3	15.3	15.3	69.725	614 614;630;65	0
5	3	56.7	56.7	56.7	14.478	127 127;107	0
3	3	11.9	11.9	11.9	27.296	243 243;203	0
0	1	2.3	2.3	2.3	72.732	659 659;667;75 0.001539	
5	5	42.6	42.6	31.5	35.924	324 324;374;21	0
1	1	8.2	8.2	8.2	53.879	461 461;267	0
2	3	7.8	7.8	7.8	74.543	708 708;699;70	0
1	1	5.6	5.6	5.6	84.918	749 749	0
0	0	1.9	1.9	1.9	92.547	800 800 0.002959	
4	9	15	15	15	73.964	634 634;587;51	0
0	0	0.7	0.7	0.7	254.39	2271 2271 0.004794	
2	2	3.9	3.9	3.9	81.123	719 719;189;27	0
1	1	1.8	1.8	1.8	88.865	788 788;806;85	0
0	0	14.7	14.7	14.7	10.701	95 95;150;231 0.001552	
10	8	19.4	19.4	19.4	66.049	594 594;219;25	0
10	10	23.8	23.8	23.8	59.578	529 529;187;68	0
1	1	2.4	2.4	2.4	127.32	1143 1143;1146;	0
14	16	30.8	30.8	28.9	87.343	783 783;715;73	0
1	2	5.2	5.2	5.2	87.435	745 745;727;76	0
23	20	30.7	30.7	30.7	76.613	710 710;296;14	0
1	0	11.4	11.4	11.4	13.052	114 114;285;38	0
11	11	39.5	39.5	39.5	32.575	294 294;259;26	0
0	0	5.3	5.3	5.3	23.266	208 208;326 0.001554	
3	1	10.5	10.5	10.5	42.15	380 380;284	0

5	3	24.3	24.3	24.3	33.12	309 309;326;11	0
2	1	14.1	14.1	14.1	33.179	291 291;459;50	0
3	4	24.4	24.4	24.4	39.648	360 360;421;26	0
9	12	9.1	9.1	9.1	267.29	2363 2363;726	0
1	1	20	20	20	12.832	120 120;435	0
1	0	40.8	9.2	9.2	17.149	152 152;177;82	0
4	2	45.9	45.9	16.4	32.642	292 292;267;15	0
3	3	23.2	23.2	23.2	23.417	198 198;207;20	0
4	3	23.7	23.7	23.7	31.839	278 278;375;38	0
2	1	4.4	4.4	4.4	56.613	496 496;554;58	0
1	1	8.3	8.3	8.3	14.745	132 132;157	0.002018
1	1	9.5	9.5	9.5	12.302	116 116;416;27	0
2	2	17.5	17.5	17.5	16.953	154 154;61;88;!	0
1	1	14.5	14.5	14.5	9.369	83 83;149;171	0
6	7	37.3	37.3	37.3	30.608	276 276;265;92	0
1	1	5.3	5.3	5.3	39.503	342 342;979	0
0	1	13.9	13.9	13.9	12.157	108 108;109;15	0
0	0	11.6	11.6	11.6	14.788	129 129;137;15	0.001057
9	9	26.7	26.7	26.7	48.534	439 439;301	0
0	1	11.7	11.7	11.7	23.787	214 214	0.002982
5	4	13	13	13	50.151	454 454;70;287	0
0	0	2.3	2.3	2.3	43.963	392 392	0.00979
2	3	7.4	7.4	7.4	48.55	432 432;249;19	0
1	1	17.2	17.2	17.2	10.016	87 87;208;305	0.001055
1	1	5.8	5.8	5.8	33.743	292 292;365	0.007612
3	3	10.7	10.7	10.7	45.57	393 393;523;24	0
9	8	48	48	48	36.071	329 329	0
1	1	7.5	7.5	7.5	36.049	333 333;40;128	0
1	1	4.6	4.6	4.6	78.549	689 689;280	0
1	1	78.1	8.6	8.6	11.418	105 105	0.008979
3	4	70.9	70.9	26.7	18.012	165 165;120;12	0
9	9	44.9	44.9	44.9	23.742	216 216	0
1	1	6.1	6.1	6.1	22.763	212 212	0
0	1	25.1	21.7	21.7	22.04	207 207;145;15	0
3	3	40.7	40.7	40.7	11.951	108 108;103;12	0
2	2	18.3	18.3	18.3	15.649	142 142;102	0
3	3	14.7	14.7	14.7	25.177	224 224	0
11	9	32.2	32.2	32.2	51.804	459 459;84;86;!	0
1	1	6.2	6.2	6.2	27.527	257 257;412;41	0
1	1	18.7	18.7	18.7	18.237	166 166	0.001577
0	1	2.8	2.8	2.8	57.224	492 492	0.001528
2	2	23.3	23.3	23.3	19.325	180 180;179	0
0	1	4.4	4.4	4.4	46.348	408 408;530;74	0.004829
7	5	30.6	30.6	30.6	45.803	422 422;433;43	0
2	1	6.5	6.5	6.5	102.45	919 919;919;18	0
10	9	72.9	72.9	59.8	22.11	199 199;171;97	0
7	6	53.5	48	48	21.892	198 198;136;14	0
7	7	50.9	45.4	45.4	30.54	271 271;161;18	0
6	6	48.1	48.1	48.1	17.031	162 162;214;17	0
9	8	40.2	40.2	40.2	25.035	224 224	0

1	0	28.2	28.2	28.2	7.8376	71 71;156;223	0
0	0	2.5	2.5	2.5	44.129	403 403	0.001543
0	1	6.3	6.3	6.3	36.701	334 334;377	0.008899
12	13	33.8	33.8	33.8	79.685	736 736;712;71	0
0	1	4.6	4.6	4.6	28.444	260 260;254	0.002014
3	2	20	20	20	66.077	571 571;588;44	0
0	0	38.2	38.2	38.2	3.692	34 34;70;434;!	0.008061
2	2	26.4	26.4	26.4	12.405	110 110	0
2	3	6.2	6.2	6.2	62.395	548 548;508;23	0
9	9	17.1	17.1	17.1	66.115	589 589;490	0
1	2	1.4	1.4	1.4	206.69	1821 1821	0
8	7	22.4	22.4	22.4	39.958	361 361;362;32	0
0	1	4.3	4.3	4.3	51.417	445 445	0
6	6	54.5	54.5	54.5	21.057	187 187	0
0	1	14.3	14.3	14.3	13.552	112 112;287;48	0
3	3	19.6	19.6	19.6	31.581	271 271;271;27	0
4	4	12.5	12.5	12.5	59.918	551 551;610;63	0
1	1	4	4	4	34.579	301 301;327;47	0.001055
3	2	10	10	10	70.698	640 640;441;50	0
7	6	18.3	18.3	18.3	61.448	562 562;580;36	0
1	1	8.2	8.2	8.2	32.724	291 291;612	0.00481
14	13	49.9	49.9	49.9	41.428	389 389;417;41	0
8	11	49.2	49.2	49.2	28.804	254 254;253;25	0
0	1	6.9	6.9	6.9	54.705	490 490;71	0
1	1	7.4	7.4	7.4	34.217	311 311;237;31	0
1	1	8	8	8	19.878	176 176;194;24	0.001544
8	7	26.5	26.5	26.5	40.422	370 370;324	0
1	1	7	7	7	20.745	187 187;225	0
3	2	6.1	6.1	6.1	81.627	717 717	0
0	1	3.1	3.1	3.1	32.113	290 290	0.002953
2	2	5.2	5.2	5.2	80.496	726 726;747	0
2	1	3.7	3.7	3.7	92.755	837 837;881;36	0
7	6	16	16	16	88.654	812 812;797;24	0
2	1	3.8	3.8	3.8	129.15	1171 1171;1176;	0
9	11	37.4	37.4	37.4	43.135	393 393;408;38	0
6	5	18.8	18.8	18.8	46.596	415 415;253;28	0
11	13	36.7	36.7	28.2	70.288	627 627;246;19	0
9	8	28.7	20.1	20.1	69.334	617 617;585;61	0
5	5	16.6	16.6	16.6	46.637	410 410;208;82	0
1	1	14.4	14.4	14.4	14.888	132 132;155;20	0.001997
1	1	3.5	3.5	3.5	29.652	260 260;401	0.002019
75	76	27.8	27.8	27.8	516.19	4547 4547;4515;	0
2	2	7.5	7.5	7.5	56.289	505 505;514;15	0
0	0	0.8	0.8	0.8	211.1	1894 1894	0.001536
5	5	4.6	4.6	4.6	205.12	1838 1838;234;1	0
15	14	20.9	20.9	20.9	113.08	1014 1014;108;1	0
0	0	2.1	2.1	2.1	66.171	582 582;712	0
6	6	45.2	45.2	36.5	37.497	356 356;64	0
6	5	30.7	22.2	22.2	38.15	361 361;362;31	0
7	6	22.2	22.2	22.2	54.626	505 505;534;49	0

13	12	33.8	33.8	25.6	70.67	636 636;522;59	0
2	2	9.1	9.1	9.1	31.496	296 296;306;96	0
3	2	13.7	5.2	5.2	67.97	615 615;631;64	0
1	2	6.6	6.6	6.6	39.908	351 351;367;40	0
1	1	3.4	3.4	3.4	39.871	350 350;368	0
2	2	6.2	6.2	6.2	48.103	438 438;392;42	0
7	7	26.4	26.4	26.4	43.476	390 390;300;19	0
6	5	19.6	19.6	19.6	64.732	571 571;265;57	0
1	2	12.4	12.4	12.4	42.533	371 371;633;46	0
8	8	28.8	28.8	25.6	56.51	527 527;588;53	0
5	4	23.9	20.1	20.1	49.539	457 457;521;52	0
1	2	4.5	4.5	4.5	85.95	783 783;179;71	0
0	0	6.9	6.9	6.9	17.188	160 160;178	0.003902
1	1	9.4	9.4	9.4	13.466	117 117;122	0
1	0	9.1	9.1	9.1	16.648	154 154	0
1	0	8.8	8.8	8.8	15.598	136 136;134	0
33	35	60.2	60.2	59	74.139	664 664;634;61	0
8	10	29.6	29.6	29.6	55.18	504 504;252;10	0
2	2	2	2	2	105.93	930 930;939;95	0
5	6	10.7	10.7	10.7	106.92	941 941;901	0
12	12	9.3	9.3	9.3	273.6	2335 2335;1012;	0
0	1	3.8	3.8	3.8	37.476	312 312	0
6	4	8.7	8.7	8.7	90.932	795 795	0
1	1	4.9	4.9	4.9	32.992	285 285;307;33	0.001533
1	1	6.3	6.3	6.3	48.506	428 428;505;15	0
5	4	14.6	14.6	14.6	96.557	847 847	0
4	4	7.7	7.7	7.7	91.809	804 804;368	0
4	4	10	10	10	106.06	939 939;1037;1	0
1	1	3.8	3.8	3.8	36.567	340 340	0
11	9	20.8	20.8	20.8	89.301	812 812;845;80	0
1	1	7	7	7	19.492	171 171;191;22	0.002011
10	11	33.1	33.1	22.6	80.253	729 729;731;72	0
7	5	10.5	10.5	10.5	86.604	765 765;796;27	0
0	0	5.5	5.5	5.5	83.515	746 746;585;77	0.000535
6	5	8.2	8.2	8.2	117.46	1032 1032;1031;	0
2	2	7.6	7.6	7.6	45.169	406 406;455	0
9	8	30.3	17.9	17.9	69.086	614 614;535;61	0
1	1	7.6	7.6	7.6	20.342	185 185;375;39	0.009346
2	2	7.2	7.2	7.2	54.416	483 483;187	0
0	0	4.6	4.6	4.6	62.223	564 564;119;15	0
0	1	3.3	2.4	2.4	122.86	1058 1058;1070;	0
0	0	2.8	2.8	2.8	88.907	797 797	0.001531
1	1	18.2	18.2	18.2	8.1336	66 66;163	0.004785
0	1	3	3	3	107.33	960 960	0
4	4	22.7	22.7	22.7	40.684	361 361;306	0
5	5	14	14	14	71.635	622 622;218;13	0
1	2	7.6	7.6	7.6	83.549	727 727;774	0
2	2	3.7	3.7	3.7	81.169	703 703;737;75	0
6	5	13	13	13	84.784	738 738;270;26	0
9	9	70	70	70	15.054	140 140;104;14	0

5	6	10.4	10.4	10.4	96.022	868 868;873;27	0
0	1	4.6	4.6	4.6	50.576	458 458;469	0
2	2	19	19	19	14.45	121 121;189;19	0.000534
12	11	51.1	51.1	51.1	29.804	272 272;246;20	0
15	13	57.2	57.2	57.2	33.296	299 299;298;26	0
6	7	38.3	38.3	38.3	28.768	261 261	0
14	14	49.5	49.5	49.5	43.786	394 394;340;28	0
3	3	14.3	14.3	14.3	58.957	516 516;534;53	0
0	2	7.1	7.1	7.1	60.632	533 533;535	0
3	2	5.9	5.9	5.9	80.699	710 710	0
6	6	17.8	17.8	17.8	58.44	527 527;524;52	0
1	2	11.8	11.8	11.8	17.102	152 152	0
3	3	19.2	19.2	19.2	29.13	265 265;377;18	0
4	2	38.4	38.4	38.4	19.155	164 164;139;16	0
2	1	2.7	2.7	2.7	98.555	879 879	0.000534
6	4	28.9	28.9	28.9	32.895	301 301;329;11	0
1	2	8.8	8.8	8.8	42.153	407 407;368	0
5	4	23.2	23.2	23.2	26.87	233 233;249;25	0
1	1	7.9	7.9	7.9	26.011	228 228;254;23	0.000529
2	3	22.9	22.9	22.9	20.593	179 179;231;25	0
1	1	11.2	11.2	11.2	11.487	107 107;127;26	0.001547
2	1	17.1	17.1	17.1	18.607	164 164;234;23	0
5	5	35	35	35	24.526	220 220;230;23	0
7	6	41.9	41.9	41.9	22.842	203 203;252;24	0
10	10	42.6	42.6	42.6	29.555	263 263;269;23	0
2	3	12.5	12.5	12.5	27.647	248 248;255;36	0
8	7	43.6	43.6	43.6	26.411	241 241;183	0
9	8	51.6	51.6	51.6	27.887	248 248;178;18	0
3	1	12.7	12.7	12.7	30.354	276 276;272;27	0
1	1	7.6	7.6	7.6	13.919	131 131;131;19	0.00053
5	4	30.7	30.7	30.7	26.489	241 241	0
2	2	9	9	9	22.836	201 201;84	0
1	2	21.5	21.5	21.5	12.082	107 107;112;14	0
1	1	15.9	15.9	15.9	29.204	264 264	0
7	6	28.9	28.9	28.9	28.48	263 263;160;11	0
3	3	13	13	13	25.357	239 239;102;21	0
2	1	6.9	6.9	6.9	29.965	277 277;210;14	0.000541
1	2	1.4	1.4	1.4	223.69	2017 2017;1845;	0
2	1	11.4	11.4	11.4	63.132	560 560;55;154	0
5	6	31.7	31.7	31.7	40.548	353 353;325;34	0
2	1	10.4	10.4	10.4	32.311	279 279;576;59	0
1	1	1.2	1.2	1.2	93.532	824 824;855	0.003897
2	1	13.9	13.9	13.9	17	144 144;145;10	0
3	4	23.2	19.8	19.8	29.224	263 263;168;18	0
1	2	19.5	19.5	19.5	13.171	118 118;248	0
3	3	48.8	48.8	48.8	22.079	213 213;258;10	0
1	1	14.6	14.6	14.6	15.771	137 137;139	0
1	1	10.4	10.4	10.4	14.401	135 135;156;17	0
6	5	38.1	38.1	38.1	19.891	189 189;169;16	0
5	5	15.5	15.5	15.5	42.674	375 375;347;34	0

5	5	9.6	9.6	9.6	140.3	1263 1263;1272;	0
17	17	38.4	38.4	38.4	57.116	508 508;464;27	0
15	15	46.7	46.7	37.6	56.782	505 505	0
11	8	24.7	24.7	24.7	72.932	645 645	0
9	8	31.4	31.4	31.4	47.837	437 437;440;44	0
0	0	12.5	12.5	12.5	14.364	128 128;197;19	0
1	1	2.9	2.9	2.9	252.5	2266 2266;2275;	0
7	4	19.8	19.8	19.8	57.548	510 510	0
0	0	12.3	12.3	12.3	21.491	203 203;543	0
1	1	2.8	2.8	2.8	125.56	1141 1141;1213;	0
2	3	21.5	21.5	21.5	16.515	144 144;154;14	0
1	1	11	11	11	9.404	82 82;94;107;;	0.008967
4	4	31.7	31.7	31.7	24.68	227 227;109;15	0
3	3	13	13	13	36.748	324 324;178;63	0
15	14	29	29	29	127.12	1179 1179;906	0
1	1	4.2	4.2	4.2	55.272	518 518;519	0
3	3	11.8	11.8	11.8	37.19	330 330;433	0
1	1	2.1	2.1	2.1	138.49	1214 1214;1258;	0
0	0	1.9	1.9	1.9	63.984	571 571;552;60	0
1	0	6.6	6.6	6.6	18.874	167 167;177;19	0.000541
2	2	2.8	2.8	2.8	116.58	1059 1059;1218;	0
2	2	6	6	6	51.828	451 451;445;48	0
2	2	6.5	6.5	6.5	31.088	293 293;261	0
0	0	2.3	2.3	2.3	68.262	596 596	0
1	1	14.2	14.2	14.2	11.535	106 106;107;14	0
1	2	13.3	13.3	13.3	19.186	173 173;197;13	0
2	2	10.8	10.8	10.8	33	305 305;423;42	0.001572
4	4	11.7	11.7	11.7	63.836	582 582;526;22	0
2	1	30.4	30.4	30.4	11.799	102 102;146;14	0
0	1	8	8	8	16.552	137 137;300	0.008057
0	1	6.2	6.2	6.2	19.125	176 176	0
8	9	39.6	39.6	39.6	42.835	394 394;313;32	0
4	4	5.2	5.2	5.2	103.13	928 928	0
2	0	7.7	7.7	7.7	33.31	284 284;128;22	0
1	1	4	4	4	28.466	247 247	0.000534
2	2	17	17	17	15.911	147 147	0
1	1	6.9	6.9	6.9	31.357	274 274;282;28	0
5	3	14.3	14.3	14.3	59.271	546 546	0
9	8	24.5	24.5	24.5	62.006	560 560;611;63	0
2	1	1.3	1.3	1.3	308.77	2819 2819;2653;	0.004815
6	7	17.8	17.8	17.8	56.084	522 522	0
1	1	11.4	11.4	11.4	18.388	158 158;177;18	0
3	3	4.8	4.8	4.8	208.7	1871 1871	0
2	2	17.6	17.6	17.6	9.681	85 85;90	0
3	3	35.1	35.1	35.1	11.203	97 97	0
4	4	34.3	34.3	34.3	11.74	105 105	0
1	1	11.2	11.2	11.2	11.471	98 98	0.000537
5	4	65.4	65.4	65.4	11.662	104 104	0
2	2	22.3	22.3	22.3	11.801	103 103	0
3	5	27.6	27.6	27.6	11.117	98 98;64;95	0

2	2	10.5	10.5	10.5	29.81	266	266	0
3	4	23.3	23.3	23.3	35.54	322	322;308;32	0
7	7	30.7	30.7	30.7	32.103	277	277;266;26	0
1	3	3.7	3.7	3.7	228.18	2108	2108;2140;	0
1	1	7.9	7.9	7.9	18.967	178	178;274;53	0.00154
1	1	10.6	10.6	10.6	29.497	274	274;521;63	0
4	4	25.4	25.4	25.4	30.921	280	280;284;39	0
2	1	2.7	2.7	2.7	111.98	1042	1042;342;1	0
1	1	1.5	1.5	1.5	96.502	877	877;969;12	0.008984
4	4	8.5	8.5	8.5	52.949	482	482;476;35	0
2	2	37.5	37.5	37.5	9.9743	96	96;42	0
0	0	17.6	17.6	17.6	7.7412	68	68	0
1	1	2.7	2.7	2.7	118.39	1084	1084;929;9	0.00202
1	1	19	19	19	8.7513	79	79;241;293	0
1	1	4.7	4.7	4.7	27.989	257	257;265	0
5	5	23.5	23.5	23.5	30.315	285	285;286;22	0
2	1	3	3	3	164.2	1458	1458;1472;	0
5	3	36.4	36.4	36.4	11.758	107	107;110;11	0
2	5	11.4	11.4	11.4	114.74	1060	1060;1237;	0
1	1	3.6	3.6	3.6	116.07	1069	1069;1072;	0
7	6	34.3	34.3	34.3	32.118	289	289;221;93	0
4	4	25.6	25.6	25.6	26.777	242	242;300;23	0
7	8	10.5	10.5	10.5	102.99	915	915;919;83	0
2	2	6.8	6.8	6.8	53.753	483	483;530;51	0
1	1	6.4	6.4	6.4	17.479	156	156	1
0	1	2.1	2.1	2.1	130.55	1166	1166;1155;	0.004796
9	9	42.9	42.9	27.3	50.184	462	462;462;44	0
1	1	22.8	3.9	3.9	44.348	381	381	0.000534
1	1	9.9	2.2	2.2	58.264	505	505	0
2	3	3.9	3.9	3.9	107.21	947	947;1003;9	0
2	1	7.2	7.2	7.2	42.008	376	376;87	0
0	0	2.7	2.7	2.7	57.215	524	524;472;48	0
0	1	2.5	2.5	2.5	102.13	933	933;913;95	0.00053
2	2	9.2	9.2	9.2	54.223	458	458;458;38	0
0	0	4.2	4.2	4.2	38.155	356	356	0.008975
0	0	8.3	8.3	8.3	12.311	109	109	1
2	2	12.2	12.2	12.2	25.868	246	246;359;32	0
5	4	8.8	8.8	8.8	129.63	1178	1178;298;5	0
3	3	8.9	8.9	8.9	40.188	359	359;390;39	0
2	4	17	17	17	37.514	341	341;341;35	0
1	1	3.9	3.9	3.9	51.459	486	486;501	0.002489
4	4	71.6	71.6	9.4	57.936	531	531;516;45	0
1	1	66.3	4.1	4.1	58.061	531	531;485;28	0.008924
12	12	33.5	33.5	33.5	50.663	445	445;400;26	0
2	3	7.9	7.9	7.9	71.026	632	632;280;11	0
4	4	42.2	42.2	42.2	17.745	161	161;79;99;	0
1	1	25.3	25.3	25.3	8.2153	79	79;90;173;!	0.001538
8	8	24.5	24.5	24.5	63.541	587	587;253;10	0
3	3	27	27	27	23.239	200	200;201;16	0
9	8	26	26	26	52.164	466	466;148;10	0

32	32	30.9	30.9	30.4	189.25	1657 1657;1191;	0
1	2	11.2	11.2	11.2	25.545	224 224;277	0.002491
3	3	49.5	49.5	19.3	21.45	192 192;211;19	0
2	2	42.2	12	12	21.429	192 192;148;18	0
0	1	7	7	7	44.223	399 399;400;24	0.000541
5	5	30.5	25	25	22.541	200 200;203;12	0
9	9	54.1	54.1	50.5	24.488	218 218;179;15	0
12	12	72.6	72.6	72.6	23.897	215 215;181	0
5	7	46.6	46.6	46.6	22.977	206 206;235;16	0
4	4	59.5	59.5	22	22.677	205 205;173;14	0
2	1	63.2	32.8	24.4	22.171	201 201;169;20	0
3	4	23.6	23.6	23.6	24.347	225 225	0
1	1	8.9	5.2	5.2	23.495	213 213	0.008519
1	1	15.5	15.5	15.5	7.8818	71 71;95;136;	0.001556
6	5	37.7	37.7	37.7	23.545	212 212;181;18	0
3	2	29.3	29.3	24.4	24.997	225 225;211;89	0
1	2	15.7	15.7	15.7	21.214	185 185;201;15	0
0	1	5.2	5.2	5.2	23.339	212 212	0.009333
7	7	38.9	38.9	38.9	23.482	216 216;249;16	0
4	4	27.4	27.4	27.4	23.548	208 208;208;71	0
14	15	76.3	76.3	76.3	23.489	207 207;160;13	0
1	1	15.8	10.3	10.3	23.155	203 203;179;42	0.00297
1	1	14.5	5.8	5.8	23.564	207 207;207	0
1	0	18.4	18.4	18.4	22.837	201 201;23;201	0
2	2	29.3	29.3	22.6	18.26	164 164;206	0
2	2	37.6	37.6	17	18.778	165 165;184;15	0
1	1	26.8	26.8	15.3	20.504	183 183	0
1	1	17.9	5.5	5.5	23.48	218 218	0
2	2	23.5	23.5	10.3	23.399	204 204;210;16	0
1	1	28.8	28.8	28.8	5.8998	59 59;79	0.000536
2	2	15.9	15.9	15.9	21.493	189 189;99;122	0
2	1	3.3	3.3	3.3	102.56	935 935;987;99	0
2	3	4.5	4.5	4.5	211.68	1898 1898;1907;	0
3	3	21.1	21.1	21.1	24.462	218 218;229	0
8	7	31.1	31.1	31.1	44.969	421 421;452;37	0
2	3	12	12	12	32.365	284 284;314;10	0
0	1	6.8	6.8	6.8	27.423	251 251;287;47	0.000536
1	1	1.5	1.5	1.5	123.03	1118 1118;1129	0
2	2	5.8	5.8	5.8	89.09	828 828;128	0
2	3	13.8	13.8	13.8	39.157	354 354;320;28	0
2	5	24.6	24.6	24.6	34.756	305 305;356;10	0
2	2	9.2	9.2	9.2	36.877	336 336;303;36	0
1	2	11.3	11.3	11.3	36.104	319 319;340;63	0.001578
3	2	52.4	52.4	52.4	9.1703	82 82;121	0
2	2	9.6	9.6	9.6	29.247	270 270;278;35	0
1	2	3.6	3.6	3.6	68.137	616 616;313	0
7	7	31.1	31.1	31.1	38.89	331 331;280	0
2	3	22.6	22.6	22.6	17.609	155 155;317;33	0
7	7	30.8	30.8	30.8	40.317	373 373;392;11	0
1	1	1.4	1.4	1.4	106.16	928 928	0.001523



2	2	8.7	8.7	8.7	40.251	357 357;273	0
1	2	12.3	12.3	12.3	38.087	341 341;176	0
4	5	23.6	23.6	23.6	35.386	318 318;178;30	0
1	2	7.4	7.4	7.4	36.864	336 336	0.000532
3	3	24.8	24.8	24.8	14.814	129 129;193;23	0
2	2	34.1	34.1	34.1	9.792	88 88;112;158	0
4	4	15.7	15.7	15.7	50.435	439 439;334;19	0
0	1	8.1	8.1	8.1	22.187	197 197;300;30	0.002946
1	1	24.5	24.5	6.4	21.523	188 188;193;16	0
4	4	41.4	35.6	35.6	21.308	191 191	0
8	10	30.4	30.4	30.4	49.973	461 461;199;18	0
2	3	4.7	4.7	4.7	90.069	792 792;570;75	0
4	4	18.3	18.3	18.3	33.789	289 289;374;38	0
2	2	11.3	8.8	8.8	34.834	318 318;218;25	0
3	3	16.7	16.7	14.2	34.769	318 318;321;20	0
1	1	4.8	4.8	4.8	33.108	291 291;717;73	0
10	10	33.7	33.7	33.7	54.972	490 490;430;27	0
4	4	17.6	17.6	17.6	23.134	193 193;194;19	0
1	3	16.7	16.7	16.7	52.839	461 461;45	0
3	3	11.9	11.9	11.9	26.72	244 244;149;21	0
0	1	8.6	8.6	8.6	32.334	280 280	0
3	2	6.3	6.3	6.3	145.81	1282 1282	0
6	4	13.7	13.7	13.7	83.629	746 746;634;21	0
5	3	18.1	18.1	18.1	41.401	353 353	0
3	2	17.5	17.5	17.5	22.653	189 189;260;98	0
2	2	15.8	15.8	15.8	47.707	423 423	0
2	1	7.4	7.4	7.4	41.193	365 365	0
2	1	20.9	20.9	20.9	9.7691	86 86;250;250	0.002002
3	0	24.3	24.3	24.3	24.605	214 214;306;59	0
10	13	16.9	16.9	16.9	152.45	1410 1410;1407;	0
3	2	30	30	30	23.51	210 210;218;26	0
0	0	4.2	4.2	4.2	31.886	285 285;513;60	0.003901
11	10	30.7	30.7	30.7	42.331	391 391;378;29	0
7	5	18.8	18.8	15.2	69.491	669 669;156	0
0	0	19.2	12.1	0	37.034	339 339;118;12	0
3	3	6.4	6.4	6.4	100.18	843 843;243;29	0
0	0	0.9	0.9	0.9	114.54	1027 1027;1060	1
4	4	8.4	8.4	8.4	85.737	759 759;618;20	0
2	1	10.4	10.4	10.4	24.079	211 211;408;22	0
7	6	34.7	34.7	34.7	26.698	245 245;423;50	0
3	2	20.7	20.7	20.7	19.889	174 174;173;10	0
6	5	14.1	14.1	14.1	64.929	618 618;600;65	0
3	3	13.9	9.5	9.5	53.496	527 527;525;52	0
1	1	13.6	13.6	13.6	7.5737	66 66;412	0.005725
1	2	9.5	9.5	9.5	27.924	252 252;136	0
5	4	24.9	24.9	24.9	24.665	237 237;290;30	0
1	1	12.8	12.8	12.8	24.561	211 211;257;28	0
1	2	1.4	1.4	1.4	148.25	1313 1313;2017;	0.001054
4	4	27.9	27.9	27.9	25.308	229 229;244;32	0
1	1	3.1	3.1	3.1	38.638	353 353	0.001518

0	0	3.3	3.3	3.3	34.803	334	334	0
0	1	18	18	18	7.0253	61	61;183;186	0.001541
2	1	3.7	3.7	3.7	132.71	1197	1197;1236;	0
1	1	12.4	12.4	12.4	31.484	282	282	0
10	10	37.9	37.9	37.9	50.227	456	456;386;31	0
11	12	37.3	37.3	37.3	46.306	418	418;463;35	0
5	5	21.5	21.5	21.5	43.66	395	395;299	0
1	2	9.4	9.4	9.4	24.105	213	213;523;21	0
18	16	24.9	24.9	24.9	114.76	1042	1042;997;9	0
3	2	16.4	16.4	7.2	95.18	848	848;915;91	0
1	1	13.2	5	5	107.47	953	953;115	0
1	1	2.5	2.5	2.5	53.847	481	481;499;40	0
0	1	1.6	1.6	1.6	101.05	891	891	0
3	2	9.3	9.3	9.3	72.379	642	642;550;57	0
3	3	9.7	9.7	9.7	46.382	414	414;434;34	0
1	0	13.4	13.4	13.4	13.322	119	119;157;33	0
1	1	6.1	6.1	6.1	36.648	329	329	0
2	2	19	19	19	38.287	347	347;321	0
0	1	5.6	5.6	5.6	22.047	195	195;229	0.008937
1	1	5.7	5.7	5.7	28.048	261	261	0.000533
0	0	8.7	8.7	8.7	14.133	126	126;136;37	0.009777
14	13	53.2	53.2	53.2	47.687	440	440;356;37	0
1	2	9.9	9.9	9.9	41.239	373	373;547	0
14	12	37.5	37.5	34.6	53.454	483	483;504;49	0
2	2	11.3	11.3	11.3	50.494	453	453	0
5	7	21.6	21.6	21.6	52.743	473	473;143	0
2	1	4.1	4.1	4.1	62.924	562	562;407	0
0	0	1.5	1.5	1.5	78.139	681	681;820;91	0.008954
6	7	7	7	7	299.61	2752	2752;2334;	0
6	6	30.4	30.4	30.4	28.329	253	253;248;20	0
1	0	13.4	13.4	13.4	20.913	172	172;165;17	0.002966
1	1	4.4	4.4	4.4	42.316	389	389;483;48	0.004792
5	5	42.1	42.1	42.1	15.371	133	133;221;13	0
3	3	40	40	40	10.32	95	95;124;164	0
2	2	13.4	10	10	30.858	269	269;272;12	0
4	3	15.2	15.2	12.5	38.418	335	335;344;37	0
4	5	42.3	42.3	42.3	15.763	137	137;235;13	0
7	5	33	33	33	25.542	221	221;109;11	0
1	1	8.4	8.4	4.1	40.781	369	369;412;43	0
1	2	4.6	4.6	4.6	78.452	699	699;778;68	0
1	1	3	3	3	51.856	468	468;527	0.000539
4	4	15.8	15.8	15.8	58.042	524	524;181;22	0
1	1	41.5	41.5	41.5	7.3568	65	65;396	0.007615
2	2	5.1	5.1	5.1	51.691	447	447;457;19	0
11	9	22.9	22.9	22.9	65.308	589	589;395;41	0
3	3	17.1	17.1	17.1	30.158	263	263;288;32	0
6	6	33.3	33.3	28.8	35.594	309	309;255;30	0
4	4	21.2	21.2	21.2	28.02	255	255;289;14	0
2	2	31.5	7.3	7.3	32.595	286	286;330;34	0
3	3	31.5	31.5	10.4	37.186	327	327;169;13	0

1	2	6.9	6.9	6.9	47.815	423 423;454;46	0
3	0	26.1	19.2	19.2	23.145	203 203;267;30	0
2	2	30.6	7.9	7.9	34.95	304 304;323;33	0
5	5	22.9	22.9	22.9	38.438	350 350;363;95	0
3	4	9.5	9.5	9.5	61.312	536 536;514	0
1	1	6.9	6.9	6.9	58.182	518 518;588;51	0
4	4	27.9	27.9	27.9	18.885	165 165;400;33	0
13	13	51.2	51.2	51.2	42.1	375 375;231;12	0
6	5	20.8	20.8	20.8	43.024	380 380;395;37	0
11	11	35.2	35.2	35.2	46.44	418 418;295;32	0
2	3	3.7	3.7	3.7	96.221	839 839;871;87	0
0	1	4.7	4.7	4.7	37.98	342 342;354;37	0
1	1	15	15	15	12.999	120 120;230;25	0.00296
2	2	20.5	20.5	20.5	9.3804	88 88;93	0
2	2	6.7	6.7	6.7	40.307	359 359	0
2	1	23.4	23.4	23.4	35.503	321 321;325;32	0
4	5	23.6	23.6	23.6	35.619	322 322;144;17	0
1	2	11.7	11.7	11.7	18.651	163 163;164;17	0.000529
1	3	31.4	31.4	31.4	11.805	102 102;80;169	0
3	4	31.8	31.8	31.8	17.027	157 157;227;25	0
3	1	17.8	17.8	17.8	20.313	180 180	0
2	4	39.1	39.1	39.1	13.058	115 115;136	0
2	2	24.2	24.2	24.2	13.654	120 120;144;10	0
3	4	45.3	45.3	45.3	10.112	86 86;66;82	0
4	3	28	28	28	29.702	271 271;160	0
3	3	6.1	6.1	6.1	66.107	589 589;596;62	0
3	3	6.4	6.4	6.4	74.605	671 671;357;61	0
5	4	9.8	9.8	9.8	83.359	714 714;712;75	0
1	1	3	3	3	44.971	403 403;540	0.002978
1	0	4.1	4.1	4.1	38.37	342 342;525	0.001573
3	4	36.5	36.5	36.5	17.259	148 148;134;13	0
1	1	18.5	18.5	18.5	17.176	162 162;193;19	0
2	2	16	16	16	17.792	162 162;313	0
2	2	24.4	24.4	24.4	9.7251	86 86	0
2	2	20.2	20.2	20.2	13.281	119 119;44;75	0
2	2	36.1	36.1	36.1	12.398	108 108;118;78	0
4	4	50	50	50	13.291	120 120;126;62	0
5	4	30.2	30.2	30.2	17.546	169 169;231;24	0
0	1	1.1	1.1	1.1	318.38	2785 2785	0
2	2	25.3	25.3	25.3	16.645	146 146;101;58	0
2	2	31	31	31	8.1111	71 71;95;135;	0
1	0	13.5	13.5	13.5	20.974	185 185;571;53	0.002981
24	24	31.6	31.6	30.7	113	1023 1023;1023;	0
4	3	15.3	15.3	15.3	34.893	301 301;303;13	0
3	3	12.2	12.2	12.2	31.512	279 279;119;13	0
2	2	4	4	4	56.195	503 503;487	0.002957
2	2	9.5	9.5	9.5	56.025	506 506;406;88	0
3	2	11.4	11.4	11.4	51.457	472 472;163;19	0
0	1	4.7	4.7	4.7	23.531	213 213;679	0.001057
1	1	3.4	3.4	3.4	124.59	1150 1150;1196;	0

3	3	10.4	10.4	10.4	54.083	492	492	0
1	1	4.6	4.6	4.6	54.557	479	479	0.00155
8	6	34.2	34.2	34.2	38.324	357	357;336;11	0
3	3	42.6	42.6	42.6	17.605	155	155;180;18	0
1	0	5.8	5.8	5.8	51.976	469	469	0.000532
0	2	15.7	15.7	15.7	19.73	172	172;172;15	0
2	2	36.2	36.2	36.2	14.766	130	130;162;11	0
8	8	24.9	24.9	24.9	54.178	489	489;558;49	0
2	2	12.1	12.1	12.1	37.523	355	355;601	0
26	25	15.5	15.5	15.5	282.83	2457	2457;2498;	0
15	14	9.9	9.9	9.9	274.83	2366	2366;2364;	0
3	3	20.9	20.9	20.9	18.72	163	163;163;10	0
0	0	3.6	3.6	3.6	94.584	837	837;735;83	0
1	1	19.3	19.3	19.3	14.864	135	135;202;56	0
2	2	28.7	28.7	7.2	48.991	428	428;443;32	0
3	3	7.3	7.3	7.3	59.711	548	548;571;61	0
2	2	5.5	5.5	5.5	88.885	793	793;728;25	0
3	3	12.4	12.4	12.4	58.848	501	501	0
9	7	9.7	9.7	9.7	145.83	1304	1304;37;15	0
5	6	10.6	10.6	10.6	100.23	895	895;273;35	0
7	6	11.3	11.3	11.3	135.58	1217	1217;399;2	0
2	2	20.8	20.8	20.8	14.585	125	125	0
4	3	20	20	20	27.872	240	240;240;24	0
4	4	30.9	30.9	30.9	33.901	307	307;471;47	0
13	14	27.7	27.7	26.6	76.149	707	707;669;22	0
3	1	15	15	15	23.128	207	207	0
9	9	30.7	30.7	30.7	47.285	410	410;417;47	0
0	1	3.1	3.1	3.1	89.04	771	771;927;96	0.009781
1	1	41.3	41.3	41.3	10.353	92	92;96;98;1	0
14	14	37.3	37.3	37.3	61.585	550	550;513;63	0
15	13	23.5	23.5	23.5	102	910	910;231	0
5	3	31.5	31.5	31.5	17.302	149	149;85;174	0
1	1	6	6	6	19.574	168	168;179;18	0.005261
2	2	1.4	1.4	1.4	184.28	1589	1589;1283	0
1	0	2.3	2.3	2.3	70.256	654	654;684;68	0
6	6	22.3	22.3	22.3	41.9	373	373;254	0
4	6	33.2	33.2	33.2	33.409	310	310;356;31	0
1	1	1	1	1	101.16	905	905;920	0.000541
26	25	54.8	54.8	54.8	73.68	679	679;95;163	0
15	14	34.1	34.1	34.1	62.639	543	543;590;51	0
1	1	14.9	14.9	14.9	23.598	221	221	0
1	0	2.5	2.5	2.5	45.263	405	405;512;79	0.002941
4	6	5.4	5.4	5.4	135.65	1197	1197;1099;	0
3	2	5.8	5.8	5.8	141.54	1217	1217	0
4	3	3.8	3.8	3.8	140.86	1211	1211;1233;	0
5	5	6	6	6	144.45	1263	1263;1230;	0
7	7	21.4	21.4	21.4	67.299	616	616;664;58	0
1	1	14.2	14.2	14.2	36.249	346	346;105	0
4	2	11.6	11.6	11.6	48.039	441	441;463;19	0
2	1	13	13	13	46.51	432	432;190;37	0

5	5	15.4	15.4	15.4	56.157	520 520;334;12	0
2	2	12.5	12.5	12.5	33.995	305 305;320;30	0
10	9	33.8	33.8	33.8	49.96	450 450;289;18	0
1	1	10.7	10.7	10.7	22.622	205 205;265;29	0
3	3	41.4	41.4	41.4	7.8891	70 70;137;184	0
0	0	2.8	2.8	2.8	46.772	427 427;634;71	0
2	1	2	2	2	117.8	1042 1042;88	0.002964
3	3	21.4	21.4	21.4	15.936	154 154;135	0
5	5	32.4	32.4	32.4	19.73	176 176;222;11	0
4	4	16.2	16.2	16.2	37.804	333 333;365	0
1	0	6.3	6.3	6.3	23.721	207 207;211	0.002962
1	1	15.7	15.7	15.7	47.144	420 420;520;79	0
0	0	5.6	5.6	5.6	31.978	288 288;300	0.001574
1	1	15.1	15.1	15.1	21.127	186 186;159;26	0
1	1	12.7	12.7	12.7	41.45	361 361	0
0	2	13	13	13	26.711	238 238	0
2	0	5.5	5.5	5.5	136.18	1245 1245;1130;	0
7	7	9	9	8.1	121.9	1052 1052	0
1	1	7.2	7.2	7.2	52.238	456 456;494;48	0.001566
1	2	15.8	15.8	15.8	20.549	177 177;288;39	0
1	1	3.6	3.6	3.6	62.032	527 527;585	0
9	7	37.9	37.9	37.9	41.92	393 393;146;32	0
2	1	10.4	10.4	10.4	18.58	164 164;198;29	0
1	0	10.4	10.4	10.4	26.411	241 241;259	0
1	1	1.5	1.5	1.5	79.145	753 753;977	0.000532
1	1	7.8	7.8	7.8	28.97	258 258	0
0	2	19.7	19.7	19.7	15.62	142 142;149;15	0
1	1	11.6	11.6	11.6	32.461	310 310;169;21	0
2	2	16.3	16.3	16.3	16.545	153 153;198	0
0	1	9.4	9.4	9.4	29.176	255 255	0
2	2	11.7	11.7	11.7	27.4	239 239;261	0
1	1	63.1	63.1	6	32.444	298 298;292;23	0
1	1	63	5.7	5.7	32.316	297 297;318	0
8	8	4.8	4.8	4.8	269.76	2541 2541;1471;	0
1	1	5.1	5.1	5.1	47.606	448 448;466;46	0
6	5	17.1	17.1	17.1	44.739	414 414;243;29	0
3	3	21.4	21.4	17.5	61.557	589 589;592;44	0
6	4	11.2	11.2	11.2	93.609	813 813;563;59	0
1	1	13.7	13.7	13.7	13.735	124 124	0
1	2	5.2	5.2	5.2	77.394	674 674;682;69	0
1	1	3.6	3.6	3.6	54.418	468 468;502;71	0.001558
17	17	40.1	40.1	40.1	60.343	556 556;401;33	0
16	14	36.3	36.3	36.3	57.488	535 535;530;48	0
14	15	35.6	35.6	35.6	54.719	509 509;539	0
10	11	33.5	33.5	33.5	53.848	486 486;541;50	0
8	8	26.3	26.3	26.3	54.804	499 499;543;45	0
14	14	38	38	38	60.533	545 545;500;50	0
17	16	43.4	43.4	43.4	59.62	548 548;529;47	0
9	10	20.5	20.5	20.5	58.024	531 531;486;48	0
2	3	1.8	1.8	1.8	271.69	2446 2446;2472;	0

2	1	2.1	2.1	2.1	129.06	1205 1205;1445;	0
2	2	5.1	5.1	5.1	46.91	412 412;421;79	0.001561
3	1	14	14	14	19.792	178 178;251;25	0
2	2	27.6	27.6	27.6	16.021	145 145;215;21	0
2	3	35.8	35.8	35.8	17.963	165 165;209;22	0
0	1	22	22	22	17.764	159 159;228;22	0
1	1	5.4	5.4	5.4	26.301	241 241	0
1	1	10.3	10.3	10.3	22.147	204 204	0
1	1	3	3	3	78.839	689 689;176;56	0
5	5	51.4	51.4	51.4	11.737	105 105;85	0
1	1	14	14	14	19.206	172 172	0
3	3	26.8	26.8	26.8	13.941	123 123;75;80;!	0
6	6	25.7	25.7	25.7	47.628	432 432;324	0
5	5	19.3	19.3	16.2	53.166	482 482;498;54	0
6	5	39.1	39.1	39.1	25.838	238 238;256	0
5	5	32.9	32.9	32.9	32.251	289 289;281;13	0
2	3	13.9	13.9	13.9	31.791	280 280;105	0
6	5	34.1	34.1	34.1	29.642	258 258;296;84	0
1	1	8.1	8.1	8.1	33.429	297 297;124	0
0	1	0.9	0.9	0.9	169.58	1478 1478;1593	0.00249
5	6	30.4	30.4	30.4	26.888	257 257;264	0
1	0	5.4	5.4	5.4	23.743	204 204	1
15	16	28.6	28.6	28.6	83.434	723 723;756;11	0
9	11	12.7	12.7	12.7	129.38	1170 1170;1085;	0
1	1	10.3	10.3	10.3	15.761	145 145;353	0.000537
0	0	6.7	6.7	6.7	19.786	180 180;187;26	0
2	1	31.8	31.8	31.8	5.0526	44 44	0
6	7	12.4	12.4	12.4	108.66	955 955	0
12	10	46	46	46	50.287	476 476;215	0
9	9	10.5	10.5	10.5	140.73	1249 1249;1157;	0
1	0	6.2	6.2	6.2	20.214	178 178;272	0.002972
5	6	20.3	20.3	20.3	46.172	404 404;188;18	0
2	3	11.2	11.2	11.2	33.067	295 295;238	0
1	1	0	0	0	3014	27118 27118;359!	1
1	3	12.6	12.6	12.6	55.697	492 492;619;54	0
0	0	17.5	17.5	17.5	8.6579	80 80;213;274	0
6	5	14	14	14	67.821	599 599;584;46	0
0	0	3.2	3.2	3.2	42.692	379 379;376	0
7	6	23.4	23.4	23.4	37.54	337 337;318	0
0	1	0.7	0.7	0.7	188.15	1679 1679;1681;	0
5	4	20.9	20.9	20.9	33.935	301 301;301;11	0
2	3	48.3	48.3	48.3	9.9601	89 89;112;96;!	0
3	3	28.3	28.3	28.3	12.527	113 113;140;11	0
2	1	2.2	2.2	2.2	121.69	1077 1077;1098	0.001563
3	2	14.6	14.6	14.6	29.096	246 246;219;21	0
1	1	17.3	17.3	17.3	17.699	162 162;206	0.008958
11	10	22.4	22.4	22.4	88.549	835 835;753;46	0
0	1	7.3	7.3	7.3	82.785	727 727	0
1	1	4.2	4.2	4.2	28.673	263 263;577;59	0.002016
2	2	8.3	8.3	8.3	45.935	411 411;447;44	0

6	5	15.5	15.5	15.5	89.034	808 808;697;51	0
22	22	36.3	36.3	36.3	84.87	760 760;679;81	0
1	1	12.4	12.4	12.4	12.951	113 113;180;18	0
3	2	16.3	16.3	16.3	33.665	288 288;188;10	0
1	1	4.2	4.2	4.2	74.68	683 683;128;36	0
1	1	23.8	6.2	6.2	21.768	193 193	0
10	10	66.3	66.3	66.3	22.391	199 199;220;18	0
2	0	11.7	11.7	11.7	29.541	281 281;379;43	0
20	20	34.4	34.4	34.4	89.321	806 806;115;16	0
17	18	36.8	36.8	36.8	67.877	623 623;631;45	0
7	8	4.1	4.1	4.1	292.75	2671 2671	0
2	2	12.8	12.8	12.8	32.477	297 297	0
6	6	33.5	33.5	33.5	21.525	188 188;197;17	0
3	2	11.1	11.1	11.1	33.435	288 288;343;37	0
2	1	21.2	21.2	21.2	9.8703	85 85;399;101	0
4	4	7	7	7	87.996	760 760	0
1	2	15	15	15	11.896	107 107;169	0.000535
1	1	12.8	12.8	12.8	29.573	265 265;266;29	0
3	3	24.3	24.3	24.3	18.998	173 173;148	0
1	1	12.6	12.6	12.6	20.161	174 174;185;19	0
3	2	5.8	5.8	5.8	66.911	589 589;815;48	0
5	5	15.2	15.2	15.2	75.775	663 663	0
2	3	6.6	6.6	6.6	67.887	589 589;253	0
5	2	11.4	11.4	11.4	72.54	625 625;642	0
1	1	7.1	7.1	7.1	27.079	239 239;169;18	0.002009
1	1	5.7	5.7	5.7	25.206	227 227	0
1	2	15	15	15	16.904	153 153;219	0
1	1	7.8	7.8	7.8	13.631	116 116;166;20	0
0	0	21.3	21.3	13.3	24.069	211 211;227;17	0
1	1	9.6	9.6	9.6	26.005	229 229;120;16	0
2	1	21.3	14	14	27.277	235 235	0
3	2	5.9	5.9	5.9	62.642	560 560;572	0
2	2	9.1	9.1	9.1	26.21	243 243	0
2	2	21.3	21.3	21.3	34.905	324 324;158;26	0
0	1	9.7	9.7	9.7	30.549	267 267;271	0
0	1	11.2	11.2	11.2	9.743	89 89;125;208	1
0	0	10.8	10.8	10.8	13.389	120 120;128;17	0
1	1	7.8	7.8	7.8	72.039	644 644;689;30	0
0	0	68.3	68.3	68.3	3.9694	41 41;68;113	0
2	2	9.9	9.9	9.9	25.223	222 222;247;15	0
3	3	14	14	14	44.875	400 400	0
2	3	17.6	17.6	17.6	36.223	323 323;192;28	0
2	2	8.5	8.5	8.5	56.773	494 494;555;19	0
1	0	14	14	14	20.958	186 186;183;13	0.001053
3	3	6	6	6	101.31	890 890;898;84	0
13	9	12.7	12.7	12.7	144.12	1414 1414;1488;	0
3	3	10	10	10	34.012	311 311;208	0
17	15	32.4	32.4	32.4	82.999	763 763;250;82	0
11	12	31.6	31.6	31.6	48.879	452 452;474;45	0
4	4	5.6	5.6	5.6	107.77	1010 1010;433;1	0

15	15	78.7	78.7	78.7	26.669	249 249;286;16	0
2	1	4.7	4.7	4.7	63.843	570 570;588	0
1	1	12.5	12.5	12.5	44.41	400 400;638	0
12	11	28.4	28.4	28.4	82.392	732 732;767;53	0
2	2	11	11	11	41.729	374 374;384;39	0
5	6	18.8	18.8	18.8	55.21	505 505	0
2	4	15.3	15.3	15.3	39.594	352 352;187;21	0
1	1	29.9	14.4	3.9	32.876	284 284;284;28	0
9	10	56	56	38.7	29.032	248 248;227;23	0
2	1	47.2	6	6	28.521	248 248;110;11	0
1	2	47.5	32.4	8.5	32.722	284 284;179;17	0
5	5	20	20	20	48.851	430 430;471;18	0
0	0	59.9	3.1	0	46.297	416 416;451;45	0
0	0	55.2	55.2	0	50.151	451 451;335;15	0
1	2	48	7.9	7.9	57.73	519 519;449;32	0
4	3	57.5	12.5	12.5	48.328	433 433;448;15	0
2	3	48.4	16.2	12.7	47.766	426 426;444;37	0
1	2	46.5	13.3	13.3	49.906	445 445;445	0
1	1	15.7	2.6	1.5	88.381	797 797;450;37	0
2	2	47.9	47.9	6.5	49.83	445 445;444;15	0
1	1	21.7	9.9	9.9	49.857	446 446;338;96	0
2	2	21.4	7.4	7.4	49.775	444 444;407;41	0
1	1	21.5	21.5	21.5	15.173	135 135;451;45	0
3	2	41.7	41.7	41.7	10.08	84 84;119;108	0
4	3	8.9	8.9	8.9	74.403	644 644	0
1	1	1.4	1.4	1.4	72.66	654 654 0.009795	
1	0	3.6	3.6	3.6	45.083	411 411;440	0
2	2	6.2	6.2	6.2	56.749	501 501;582;58	0
3	3	39.1	39.1	39.1	19.863	184 184;207;22	0
5	5	30.6	30.6	30.6	23.764	222 222;186;20	0
3	3	22.8	22.8	22.8	30.211	272 272;213	0
1	1	1.1	1.1	1.1	213.57	1972 1972;1975;	0
8	7	27.2	27.2	27.2	35.709	323 323	0
2	2	7.4	7.4	7.4	40.282	350 350;59;291	0
1	1	7.5	7.5	7.5	28.882	254 254;1186;3	0
1	1	14.5	14.5	14.5	16.669	152 152;159	0
4	6	10.6	10.6	10.6	170.45	1479 1479;1483	0
3	4	13.4	13.4	13.4	56.033	491 491;512;52	0
7	8	21.1	21.1	21.1	49.966	435 435;362	0
3	3	6.1	6.1	6.1	59.143	528 528;388	0
3	3	12.7	12.7	12.7	32.184	291 291;477	0
5	6	17.6	17.6	17.6	51.556	437 437;428;16	0
1	1	14.8	9.2	9.2	15.945	142 142;148;18 0.003889	
2	2	16.7	16.7	16.7	19.687	180 180;159	0
2	4	21.2	21.2	21.2	28.415	255 255;89;142	0
1	1	8.4	8.4	4.9	25.486	225 225;87;128 0.004817	
3	3	5.3	5.3	5.3	118.23	1028 1028;1029;	0
2	0	15.2	15.2	15.2	21.85	184 184	0
0	0	4.7	4.7	4.7	78.863	681 681	0
3	4	10	10	10	82.004	719 719;771;60	0



2	0	5.2	5.2	5.2	62.003	556 556;143;17	0
2	2	4.4	4.4	4.4	70.193	597 597	0
2	1	8	8	8	51.84	475 475	0
1	1	3.1	3.1	3.1	58.32	521 521;522	0
0	2	5.5	5.5	5.5	56.399	487 487;536;46	0
15	14	9.6	9.6	9.6	244.5	2136 2136;625;5	0
3	3	14.6	14.6	14.6	39.31	357 357;409;12	0
1	1	20	20	20	10.834	95 95	0
1	1	23.9	23.9	23.9	7.3713	67 67;75;77;9	0.002984
3	2	14.1	14.1	8.4	59.219	561 561;589;41	0
0	1	20.6	20.6	20.6	11.422	102 102;172;18	0
0	1	10.9	10.9	10.9	12.383	110 110;798;80	0.002935
1	2	3	3	3	93.307	835 835;858;13	0.005717
6	6	35.7	35.7	35.7	26.182	230 230;194;22	0
8	7	25	25	25	51.086	448 448;459;48	0
2	2	16.1	16.1	16.1	25.335	218 218;258;35	0.000538
2	1	8.1	8.1	8.1	34.5	307 307;343;13	0
4	4	22.4	22.4	22.4	28.05	241 241;272;27	0
7	7	50.6	50.6	50.6	17.965	156 156;93;106	0
4	2	6.5	6.5	6.5	113.63	1079 1079;976;9	0
2	2	27.9	27.9	27.9	15.765	140 140;150;17	0
3	3	21.5	21.5	21.5	22.406	200 200;123;14	0
1	1	11.7	11.7	11.7	17.875	154 154;122;15	0
3	4	32.9	32.9	32.9	17.138	152 152;87;105	0
1	1	10.5	10.5	5.1	42.208	370 370;147;17	0
2	1	20.7	6.9	6.9	16.363	145 145	0.005728
1	1	18.5	18.5	18.5	8.5507	81 81;85	0
20	19	28.8	28.8	28.8	113.8	1018 1018;1058;	0
2	1	24.7	24.7	24.7	8.5468	73 73;36	0.000531
0	1	5	5	5	27.015	238 238;290;29	0.001542
3	2	13.6	13.6	13.6	56.777	508 508	0
7	9	29.4	29.4	29.4	55.023	494 494;427;39	0
6	5	9.3	9.3	9.3	174.97	1531 1531;1555;	0
3	2	9	9	9	50.527	443 443;532;18	0
4	4	32.1	32.1	32.1	22.222	196 196;169;14	0
1	1	3.3	3.3	3.3	34.723	302 302;325	0.004819
1	1	3.8	3.8	3.8	32.544	291 291	0.008933
2	2	17.2	17.2	17.2	21.883	192 192;194;16	0
16	16	20.3	20.3	20.3	128.48	1107 1107;1078;	0
11	11	14.8	14.8	14.8	118.99	1039 1039;1044;	0
3	3	3.4	3.4	3.4	127.06	1108 1108;187;1	0
1	1	2.4	2.4	2.4	145.01	1253 1253;1294;	0
1	0	7	7	7	24.992	229 229;242	0.001537
1	1	12.4	12.4	12.4	14.726	129 129;193;24	0
1	1	6.9	6.9	6.9	28.487	261 261;208;21	0
1	2	43.1	43.1	43.1	6.4575	58 58	0
2	3	14.2	14.2	14.2	42.495	388 388;480;34	0
3	2	24.3	24.3	24.3	15.621	144 144;146;17	0
1	1	6.4	6.4	6.4	24.884	218 218;201;26	0
1	1	8.3	8.3	8.3	21.458	193 193;228;29	0.001551

1	1	5.8	5.8	5.8	16.276	139 139;124;13	0.00895
3	2	8.3	8.3	8.3	56.967	508 508;517;49	0
8	8	23	23	23	43.171	409 409;337;11	0
0	0	11.9	11.9	11.9	11.354	101 101	0
2	2	14.4	14.4	14.4	38.169	327 327;226;25	0
1	1	71.4	71.4	71.4	3.9415	35 35;53;161;	0
5	5	11.8	11.8	11.8	91.706	796 796;41;46;	0
1	0	5.6	5.6	5.6	49.301	444 444;428;43	0
2	1	6.8	6.8	6.8	31.102	280 280;307;24	0.001576
5	5	6	6	6	131.83	1183 1183;1264;	0
0	1	3.1	3.1	3.1	59.747	522 522;524	0
18	16	42.4	42.4	42.4	70.389	655 655;678;63	0
0	0	3.9	3.9	3.9	28.368	254 254	0.000537
5	5	21.3	21.3	21.3	43.159	362 362;400;33	0
3	2	12.3	12.3	12.3	30.361	276 276;312;16	0
2	3	10.4	10.4	10.4	36.034	308 308;131;10	0
1	0	9.3	9.3	9.3	11.756	108 108;160	0.001056
3	3	52	52	52	11.309	100 100;68;72;	0
1	1	33	33	33	11.438	100 100;99;74	0
1	1	12.4	7.6	7.6	27.893	249 249	0
3	4	25.5	25.5	20.6	27.228	243 243;71;99;	0
1	0	1.6	1.6	1.6	82.091	739 739;644;74	0.007597
0	1	32.4	32.4	32.4	8.1425	71 71;99;101;	0
3	3	20	20	20	24.593	215 215;79	0
1	1	15.7	15.7	15.7	40.228	356 356;191;32	0
7	7	8.8	8.8	8.8	141.44	1268 1268;1268;	0
15	17	25.5	25.5	25.5	116.72	1066 1066;1134;	0
0	0	9.3	9.3	9.3	53.341	474 474;475;34	0
1	1	5.7	5.7	5.7	19.835	176 176;177	0.005736
15	15	71.4	71.4	71.4	30.772	283 283;183	0
14	15	70.4	70.4	70.4	31.566	294 294;282;28	0
6	5	36.7	36.7	36.7	30.658	283 283;284;10	0
1	1	3.3	3.3	3.3	94.198	810 810	0.000531
0	1	11.6	11.6	11.6	15.736	155 155	0.004826
4	5	16.6	16.6	16.6	64.735	584 584;617;18	0
0	1	16.2	16.2	16.2	8.0792	68 68;93;130;	0.001546
6	7	20	20	20	56.5	511 511;496;51	0
1	0	36.4	36.4	36.4	4.7434	44 44;119;179	0
3	1	11.7	11.7	11.7	44.659	392 392;351;23	0
3	4	20.8	20.8	20.8	26.145	226 226;196;20	0
2	2	33.9	33.9	33.9	13.757	118 118;99;78;	0
4	5	17.2	17.2	17.2	51.57	443 443;465;48	0
6	6	22.4	22.4	22.4	66.193	606 606;245;46	0
4	4	18	18	18	43.237	394 394;429;43	0
1	2	3.9	3.9	3.9	99.365	895 895;951	0
2	1	6.6	6.6	6.6	74.89	677 677;147;18	0
1	1	11.6	11.6	1.8	68.07	610 610;322	0
1	1	4.5	4.5	4.5	36.588	334 334	0
1	1	33.3	33.3	33.3	5.4821	48 48;189;294	0.00484
1	1	7.6	7.6	7.6	36.405	328 328;385;38	0.00054

0	0	2.2	2.2	2.2	94.498	830 830;89;97	0.000531
1	0	3.6	3.6	3.6	73.918	631 631;696	0.002012
16	15	29.8	29.8	29.8	82.704	732 732;131;19	0
13	12	25.8	25.8	25.8	69.842	609 609;559;56	0
3	3	43.9	32	32	31.947	303 303;342;37	0
2	2	4.3	4.3	4.3	56.877	529 529;579;53	0.002951
2	2	6	6	6	72.531	652 652;810	0
1	1	13	13	13	18.947	162 162;426	0
4	3	7.2	7.2	7.2	114.08	1024 1024;624;6	0
1	1	8.7	8.7	8.7	34.114	310 310;53;109	0
2	2	3.1	3.1	3.1	117.01	1074 1074	0
2	2	4.3	4.3	4.3	87.563	786 786;826;15	0
2	1	28.7	28.7	28.7	9.8382	87 87;376	0
1	1	5.8	5.8	5.8	21.844	206 206;240;32	0
1	1	12.9	12.9	12.9	17	155 155;481;49	0
0	0	8	8	8	40.14	377 377	0
3	3	9.8	9.8	9.8	57.643	540 540;572;41	0

Table S2 Proteomic results

Score	Identificati	Identificati	Identificati	Identificati	Identificati	Identificati	Identificati	Identificati
38.42	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
23.623	By MS/MS	By MS/MS	By MS/MS	By matchin	By matchin	By MS/MS	By MS/MS	By MS/MS
6.8435	By matchin	By matchin	By matchin	By matchin	By matchin	By MS/MS	By MS/MS	By MS/MS
48.221	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
114.83	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
29.681	By matchin	By matchin	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
30.744	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
138.41	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
38.927	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
130.44	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
2.8474	By matching		By matchin	By matchin	By matchin	By matchin	By MS/MS	By MS/MS
5.2437	By matchin	By matchin	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By matching	
4.3317	By matchin	By MS/MS			By matching			
70.802	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
7.7474	By MS/MS	By matching			By matchin	By MS/MS	By MS/MS	By MS/MS
30.939	By MS/MS	By MS/MS	By matchin	By matchin	By matchin	By MS/MS	By MS/MS	By MS/MS
15.057	By MS/MS	By MS/MS	By matchin	By MS/MS	By matchin	By MS/MS	By MS/MS	By MS/MS
16.383	By MS/MS	By MS/MS	By MS/MS	By matchin	By MS/MS	By MS/MS	By MS/MS	By MS/MS
4.6271	By matchin	By MS/MS	By matchin	By matchin	By matchin	By MS/MS	By matchin	By MS/MS
40.616	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
26.327	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By matchin	By MS/MS	By MS/MS	By MS/MS
10.253	By matchin	By matchin	By matchin	By matchin	By matchin	By MS/MS	By MS/MS	By MS/MS
2.4303	By matchin	By matching		By matching		By matchin	By MS/MS	By MS/MS
16.444	By matchin	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
11.065	By matchin	By MS/MS	By MS/MS	By MS/MS	By matchin	By MS/MS	By MS/MS	By MS/MS
16.988	By matchin	By matchin	By matchin	By matchin	By matchin	By MS/MS	By MS/MS	By MS/MS
2.0492	By MS/MS	By matchin	By matchin	By matching		By matchin	By MS/MS	By MS/MS
33.961	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
8.2739	By MS/MS	By MS/MS	By MS/MS	By matchin	By MS/MS	By MS/MS	By MS/MS	By MS/MS
3.047				By matching		By MS/MS		By MS/MS
9.4403					By matchin	By matchin	By MS/MS	By MS/MS
3.3453	By matchin	By matchin	By matchin	By matchin	By matchin	By matchin	By MS/MS	By MS/MS
5.3949	By matchin	By matchin	By matchin	By matchin	By MS/MS	By MS/MS	By MS/MS	By MS/MS
8.9226			By matchin	By matchin	By matchin	By matchin	By MS/MS	By MS/MS
3.9098	By MS/MS	By MS/MS	By matchin	By matchin	By MS/MS	By matchin	By matchin	By matchin
6.4657	By matchin	By MS/MS	By matchin	By matchin	By MS/MS	By matchin	By matchin	By matchin
10.205	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
18.459	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
4.5992	By MS/MS	By matchin	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By matchin	By MS/MS
2.0157	By MS/MS	By MS/MS	By matching		By matchin	By matchin	By matching	
7.2971	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By matchin	By MS/MS	By matchin
3.3786	By matchin	By MS/MS	By MS/MS	By MS/MS	By matchin	By MS/MS	By MS/MS	By matchin
4.9234	By MS/MS	By MS/MS	By matchin	By matchin	By MS/MS	By matchin	By matchin	By matchin
7.4621	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By matchin	By MS/MS		By matchin
2.353	By MS/MS		By MS/MS	By MS/MS	By matchin	By matchin	By matching	
4.4329	By matchin	By matchin	By matchin	By MS/MS	By MS/MS	By MS/MS	By matching	
2.3893	By matchin	By MS/MS	By MS/MS	By MS/MS	By matchin	By matchin	By matchin	By matchin
1.679	By matchin	By MS/MS	By matchin	By matching		By MS/MS	By matchin	By matchin

5.2893 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By matchin By matchin  
3.5068 By matchin By MS/MS By matchin By matching By MS/MS By matchin By matchin  
39.672 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
1.6032 By MS/MS By matchin By MS/MS By matchin By MS/MS By matchin By matchin By matchin  
8.1001 By matchin By matchin By MS/MS By MS/MS By MS/MS By matchin By matchin By matchin  
14.532 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
4.6085 By MS/MS By MS/MS By matchin By matchin By MS/MS By MS/MS  
4.8001 By matchin By MS/MS By MS/MS By MS/MS By MS/MS By matching By matchin  
17.582 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By matchin By MS/MS  
2.7637 By MS/MS By MS/MS By MS/MS By matchin By matchin By matchin By matchin By matchin  
4.8256 By matchin By MS/MS By matchin By matchin By MS/MS  
1.9918 By MS/MS By matchin By matchin By MS/MS By MS/MS By matchin By MS/MS By MS/MS  
3.7219 By MS/MS By matchin By matchin By MS/MS By matchin By matchin By matchin By matchin  
1.6085 By MS/MS By matching  
4.9141 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By matchin By matching  
3.696 By MS/MS By MS/MS By matchin By matchin By MS/MS By MS/MS By matchin By matchin  
16.076 By MS/MS By matchin By matchin By matchin By MS/MS By matching  
3.943 By MS/MS By MS/MS By matchin By matchin By MS/MS By matchin By MS/MS By matchin  
3.4486 By MS/MS By MS/MS By MS/MS By matching By matchin By matching  
3.6271 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By matchin By matchin  
1.7948 By MS/MS By MS/MS By MS/MS By matching By matchin By matchin By matchin  
8.8327 By MS/MS By MS/MS By matchin By matchin By MS/MS By MS/MS By MS/MS By MS/MS  
37.221 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
3.7107 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By matchin By matchin By matchin  
3.2468 By MS/MS By matchin By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
1.5272 By matching By MS/MS By MS/MS By MS/MS By MS/MS By matchin By MS/MS  
16.674 By MS/MS By MS/MS By matchin By MS/MS By MS/MS By MS/MS By MS/MS  
51.215 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
29.813 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
12.258 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
48.667 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
8.7874 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
8.8125 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
29.615 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
13.042 By MS/MS By MS/MS By MS/MS By MS/MS By matchin By MS/MS By MS/MS By MS/MS  
16.204 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
28.609 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
10.469 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
12.616 By matchin By matchin By MS/MS By matchin By matchin By MS/MS By MS/MS By MS/MS  
5.6077 By MS/MS By MS/MS By MS/MS By MS/MS By matchin By MS/MS By MS/MS By MS/MS  
10.52 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
5.585 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
4.8962 By MS/MS By MS/MS By MS/MS By matchin By matchin By MS/MS By MS/MS By MS/MS  
11.325 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
36.183 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
2.8134 By MS/MS By matchin By matchin By MS/MS By matchin By MS/MS By MS/MS  
34.572 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
2.2138 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
25.885 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS  
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4.8971 By matchin By MS/MS By MS/MS By MS/MS By matching  
4.5914 By matchin By matchin By matchin By matchin By MS/MS By MS/MS

Sequence c	Sequence c	Sequence c	Sequence c	Sequence c	Sequence c	Sequence c	Sequence c	Intensity
68.6	68.6	56.9	56.9	56.9	56.9	61.8	68.6	1.01E+08
10	11.5	10.7	6.4	9.7	11.5	11.3	11.3	9426100
9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	1429000
36.9	36.9	34	34	36.9	34	36.9	36.9	35065000
51	39.2	51.8	51.4	54.5	58.4	61.2	54.5	73396000
34.1	30.5	45.1	41.1	39.8	45.1	43.9	43.1	18080000
27.1	23.5	29.1	28.7	31.6	32.4	31.6	27.5	28981000
66.7	63.9	60.6	52.8	67.1	63.9	67.1	71.3	2.43E+08
40.8	40.8	38	38	40.8	38	40.8	45.7	34360000
42	40	44.9	49.8	47.8	49.4	47.3	47.3	1.06E+08
1	0	1	1	1	2	2	2.1	556860
6.3	6.3	6.3	6.3	6.3	6.3	6.3	0	1998800
6.5	6.5	0	0	6.5	0	0	0	610700
23.3	26.4	26.4	26.4	26.4	26.4	19	23.6	16519000
4	2.3	0	0	1.3	2.3	3.7	3.7	1052600
26.8	26.8	20.6	17.6	6.7	23.8	23.8	23.6	9018600
16.9	16.9	7.9	14.4	5.4	20.2	20.2	20.2	6197800
15.4	15.4	15.4	11.6	11.3	15.4	18.4	14.4	5644200
18.9	18.9	5.4	5.4	16.5	18.9	8	16.5	2762500
24.9	19.2	19.4	23.8	13.4	28.9	31.6	31.6	11123000
19	14.4	9.5	19	10.3	19	23.6	19	5347500
4.2	5.9	0.9	3.1	2.8	5.4	5.4	10.7	3130900
11.9	11.9	0	11.9	0	17.3	17.3	17.3	1035100
17.5	12.6	9	9	6.2	19.4	28.9	25.8	7285000
4.1	9.2	2.1	2.1	4.8	14	14	8.5	3713700
8	8	10.9	8	10.9	17.2	19.8	22.3	4552300
4.2	4.2	4.2	4.2	0	4.2	4.2	4.2	835590
10.5	15.5	9.1	9.1	5.7	9.4	12.3	12.3	10713000
14.9	12.4	14.9	12.4	6.5	14.9	14.9	14.9	4560300
0	0	0	2.6	0	2.6	0	4.7	444720
0	0	0	0	3.1	3.1	10	9.7	659460
4	17.5	13.6	17.5	17.5	23.2	23.2	23.2	1828000
10.5	10.5	10.5	10.5	10.5	10.5	10.5	17.6	1102400
0	0	6.1	6.1	13.3	13.3	22.1	17.7	3580900
15	15	15	15	15	15	15	15	1139400
18.2	18.2	18.2	18.2	18.2	18.2	18.2	18.2	2236500
22.5	29.5	29.5	29.5	22.5	29.5	22.5	29.5	4155300
15.1	23.6	23.6	23.6	23.6	23.6	23.6	15.9	6692600
9.8	9.8	9.8	9.8	3.7	9.8	9.8	9.8	2403700
16.1	16.1	16.1	0	16.1	16.1	16.1	0	705820
11.9	8.5	11.9	7.2	8.5	8.5	8.5	3.8	2206000
6.6	6.6	13.2	6.6	6.6	6.6	6.6	6.6	838480
24.3	24.3	11.6	7.5	19.1	24.3	19.1	7.5	2888100
12	12	12	12	8	4	0	4	1530100
10.2	0	10.2	10.2	10.2	4.8	4.8	0	759050
29.1	29.1	29.1	29.1	29.1	29.1	17.5	0	1216900
3.3	3.3	3.3	3.3	3.3	3.3	3.3	3.3	915050
10.4	10.4	10.4	10.4	0	10.4	10.4	10.4	991220

19.8	19.8	19.8	19.8	13.4	19.8	13.4	7	3646100
4	6.8	4	4	0	6.8	2.8	6.8	972770
16.3	19.6	21.8	20.8	15.7	16.6	15.5	10.7	22405000
5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	970750
12.7	12.7	23.5	23.5	7.2	18.1	7.2	23.5	2356600
15.4	7.7	10.2	7.7	13.6	10.4	10.4	10.4	3896300
53.2	53.2	53.2	21.3	53.2	53.2	0	0	915350
15	12.8	12.8	15	15	12.8	0	7.2	1479800
11.1	0	11.1	11.1	11.1	11.1	11.1	11.1	2292100
11.8	11.8	11.8	11.8	5.7	11.8	5.7	5.7	1069000
11.1	17.1	11.1	11.1	11.1	0	0	0	1099600
6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	928410
8.4	2.6	8.4	8.4	8.4	8.4	5.8	5.8	1561400
0	5.1	0	5.1	0	0	0	0	443630
15	15	15	15	15	15	15	0	813950
14.9	14.9	14.9	14.9	14.9	14.9	7.4	7.4	2305400
5.7	5.7	5.7	5.7	5.7	5.7	0	0	595410
13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	913760
14.8	23	14.8	14.8	0	14.8	8.1	0	1084400
11.6	11.6	11.6	11.6	20.5	11.6	11.6	11.6	1093300
3.7	3.7	3.7	3.7	0	3.7	3.7	3.7	705420
16.5	16.5	9.6	4.3	9.6	9.6	11.3	16.5	19303000
35.2	41.8	41.8	48.7	42.9	48.7	54	28.4	32519000
8.6	8.6	8.6	8.6	8.6	4.8	3.9	8.6	2150500
5.4	5.4	5.4	5.4	5.4	5.4	0	5.4	1646600
3.1	0	3.1	3.1	3.1	3.1	3.1	3.1	2674500
9.7	9.7	5.5	18.8	0	18.8	18.8	27.9	5850500
48.1	48.1	48.1	41.1	41.1	41.8	53.2	43	36741000
53.8	53.8	53.8	46.2	53.8	46.2	53.8	53.8	28972000
43	37.1	37.1	22.5	19.2	29.1	37.1	37.1	18051000
37.7	38.4	31.8	30.5	31.8	31.1	37.7	38.4	46066000
40	33	33	33	24	40	47	47	16204000
33.6	28.1	25.3	25.3	19.9	39	39	33.6	20350000
51.9	45.2	48.9	42.2	28.9	48.9	48.9	48.1	23555000
32.9	32.9	32.9	32.9	27.6	32.9	32.9	32.9	36391000
43.4	29.7	42.8	42.8	22.8	42.8	42.8	36.6	22246000
27	29.4	29.4	24.2	26.6	26.6	31.7	31.7	42332000
22.7	22.7	22.7	22.7	22.7	19.3	22.7	22.7	8200700
34.6	23.5	40.7	23.5	12.3	42	42	46.9	8296900
28.7	28.7	23.1	28.7	23.1	28.7	28.7	28.7	12464000
17.6	17.6	17.6	17.6	17.6	17.6	26.7	26.7	9131500
15.2	15.2	15.2	15.2	8	22.4	15.2	22.4	10712000
31.3	31.3	31.3	20.9	20.9	31.3	31.3	20.9	13999000
39.3	39.3	38.1	38.1	38.1	39.3	39.3	39.3	22209000
17.4	33.3	33.3	33.3	17.4	33.3	33.3	33.3	24747000
12.5	12.5	12.5	12.5	12.5	12.5	32.1	0	2060700
51.4	51	47.7	37.4	31.7	42.8	47.7	45.7	75349000
10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	5821100
40.9	47.3	39.4	35.6	33	40.9	43.6	47.3	50478000
35.7	41.4	27.8	27	27.8	30.8	40.3	40.3	50438000



35	35	35	13.5	18.5	28	28.5	28.5	20623000
22.9	26.1	18.9	22.9	18.1	22.9	18.9	26.1	49899000
12.9	24.2	12.9	8.8	8.8	8.8	24.2	12.9	17974000
50	50	50	43.8	39.9	43.8	49.5	50	82760000
37.6	37.6	34	34	26.3	37.6	37.6	38.7	52763000
40.7	40.7	34.2	30.4	28.5	40.7	40.7	37.6	56848000
48.2	46.5	46.3	44.4	38.4	45.4	48.4	47.6	3.08E+08
2.7	2.7	2.7	2.7	2.7	2.7	2.7	1.4	1363900
4.4	2.5	4.4	4.4	2.5	2.5	2.5	1.9	718560
51.7	55.7	55.7	51.7	55.7	51.7	55.7	55.7	5.33E+08
27.5	38.9	38.9	41.7	26.3	41.7	41.7	38.9	59692000
28.9	28.9	28.9	28.9	14.9	28.9	28.9	28.9	20113000
79.1	79.1	78.3	78.3	71.3	47	79.1	47	67609000
36.5	40.5	35.5	31	31	34.5	40	35.5	48632000
33.6	33.6	27.2	31.3	27.2	30.9	33.6	36.9	28764000
23	23	19.1	23	18.5	18.5	23	16.3	34762000
22.6	22.6	18.6	22.6	18.1	18.1	22.6	16.4	494060
45.5	54.5	45.5	45.5	45.5	45.5	54.5	54.5	60744000
25.1	29.9	25.1	25.1	20.4	29.4	25.1	29.9	42617000
27.6	33.5	27.6	27.6	27.6	27.6	33.5	30	25268000
36.3	36.3	36.3	36.3	36.3	26.6	36.3	36.3	27297000
25	25	25	25	25	25	25	25	38857000
34.3	34.3	34.3	18.9	18.9	8.3	39.6	44.4	17867000
27.4	27.4	27.4	27.4	27.4	27.4	27.4	27.4	42542000
37.6	31.9	37.6	37.6	37.6	37.6	37.6	37.6	33305000
29.9	17.2	29.9	17.2	29.9	17.2	29.9	29.9	8741300
51.1	51.1	51.1	51.1	51.1	51.1	51.1	51.1	28258000
37.9	37.9	37.9	37.9	27.1	37.9	37.9	37.9	34178000
21.5	26.6	20.3	26.6	14.6	20.3	26.6	26.6	20866000
28.9	28.9	28.9	28.9	28.9	21.5	29.8	28.9	24355000
23.4	29	17.9	17.9	11.7	17.9	29	29	30945000
30.1	36	30.1	14.7	6.6	36	36	36	20292000
30.6	30.6	30.6	30.6	21.3	30.6	30.6	38	25411000
35.7	35.7	35.7	35.7	35.7	35.7	35.7	42	25276000
0	14.5	14.5	14.5	14.5	14.5	14.5	14.5	7241700
34.2	39.7	27.8	25.1	27.8	27.8	38	36.2	72703000
45.2	59.1	59.1	48.7	59.1	48.7	59.1	45.2	33280000
44.4	44.4	37	37	37	15.7	23.1	44.4	17216000
33.1	33.1	33.1	33.1	33.1	33.1	33.1	38.3	20762000
35.9	36.8	36.8	36.8	35.9	29.1	36.8	29.1	28445000
24	24	24	10.4	10.4	24	24	24	10288000
35.1	35.1	35.1	35.1	44.7	44.7	44.7	35.1	19591000
28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	21966000
15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15492000
29.4	55.9	55.9	11.8	11.8	29.4	55.9	51.5	10511000
15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6	2270100
34.2	34.2	31.9	30.2	28.3	30.2	32.3	32.8	91580000
27.9	38	32	24.6	17.5	38	38	38	40237000
26	26	29.5	26	23.3	29.5	29.5	26.7	47588000
33.2	33.2	33.2	33.2	22.6	33.2	27.4	33.2	42718000

40.2	44	44	44	24.8	44	43.6	37.2	67566000
5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	1148200
22.6	22.2	22.2	22.2	22.2	24.9	25.3	22.6	37192000
35.4	28.1	28.1	20.8	15.1	28.1	35.4	35.4	15463000
0	9.1	0	0	0	9.1	9.1	17.3	1634200
11.5	15.1	17.4	13.8	10.2	24	28.5	30.9	21744000
0	0	0	8.9	8.9	8.9	8.4	8.4	678190
0	7.7	7.7	16	7.7	7.7	7.7	16	613610
45.1	46.3	44.6	43.9	43.6	46.8	46.5	46.5	3.92E+08
12.8	12.8	12.8	14.3	7.8	12.4	10.9	9.1	22183000
3.5	0	0	0	0	3.5	3.5	3.5	1530500
0.8	0.8	1.9	1.3	1.3	1.3	1.9	1.3	998090
0	4	4	0	4	0	4	0	774980
5	6.8	6.8	0	6.8	11.8	11.8	5	3042800
21.1	21.1	21.1	21.1	21.1	21.1	21.1	21.1	13141000
1	1	1	0	1	1	1	1	1214500
9	0	15.3	9	0	27.7	27.7	27.7	8504000
8.2	0	8.2	8.2	0	13.8	13.8	13.8	2937600
11.4	13.9	9.6	9.6	10.7	11.4	13	15	12072000
69.6	69.6	69.6	61.6	61.6	69.6	69.6	69.6	20226000
69.6	69.6	69.6	61.6	61.6	69.6	69.6	69.6	1.82E+09
26.6	26.6	26.6	26.6	26.6	26.6	26.6	26.6	2.23E+08
12.8	12.1	11	12.8	12.8	12.8	19.8	19.8	6739900
0	6.6	3	6.3	6.3	9.9	14.7	12.7	3589800
10.2	5.6	5.6	5.6	5.6	8.1	16.4	11.8	2972100
3.3	8	8	3	6.3	14	14	9.3	2754200
0	0	0	0	0	0	13.1	0	357350
26.5	26.5	19.5	19.5	30.1	26.5	37.2	37.2	4487300
25.9	25.9	25.9	25.9	25.9	25.9	25.9	25.9	2058600
0	7.8	7.8	7.8	0	7.8	7.8	7.8	770810
18.2	13.2	17.9	18.2	13.4	23.2	23.2	23.2	10460000
26	26	26	26	26	26	26	26	7974000
3.1	7.3	7.6	10.8	7.6	17.7	33	25.3	6137500
0	0	0	0	9.6	0	0	0	234580
14.7	14.7	9	5.8	9	14.7	14.7	9	1479600
1.6	1.6	2.8	2.8	2.8	2.8	2.8	2.8	19306000
11.3	11.3	11.3	11.3	7.2	11.3	11.3	11.3	9311800
10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10525000
20.6	28.9	28.9	28.9	37.1	28.9	45.4	28.9	14463000
10.3	10.3	10.3	10.3	10.3	10.3	0	0	1070800
18.7	18.7	18.7	18.7	18.7	18.7	11	7.7	1592700
19	19	19	19	19	19	19	19	11606000
6.6	14.5	19.3	19.3	4.8	11.4	11.4	11.4	3384100
15.9	15.9	15.9	11	15.9	15.9	15.9	15.9	1634400
13.8	13.8	13.8	0	0	13.8	0	13.8	930880
38.1	58.7	17.5	0	17.5	58.7	58.7	58.7	2408100
4	4	4	0	4	7.7	4	4	1759100
9.8	0	0	0	0	9.8	9.8	9.8	752800
26.6	28.9	30.3	22.2	16.2	32.2	39.1	39.6	28207000
24.6	16.4	15.1	14.2	18.5	15.1	22	19.8	5006100

4	4	9	9	9	9	9	0	2201100
10	16.2	20.5	10	20.5	32.4	32.4	32.4	3691200
0	0	0	0	3.1	5.8	5.8	8.9	683560
0	0	7	9.2	0	15.4	15.4	12.3	4049100
16.9	18.6	22.2	22.2	16.7	24.3	24.3	26.4	23862000
20.1	29.4	20.1	20.1	13.8	29.4	17	20.1	15238000
0	0	0	18.4	0	18.4	18.4	18.4	823160
42.6	42.6	42.3	43	32.9	42.6	40.3	39.6	1.61E+08
42.3	42.3	42.3	42.3	32.6	42.3	39.9	42.3	17010000
7.7	10.9	10.9	10.9	6.2	7.9	10.9	7.9	2976900
29.8	30.4	38.1	30.4	13.8	38.1	43.6	43.6	24659000
33.1	33.1	33.1	33.1	16.5	33.1	33.1	33.1	3977200
31.3	31.3	21.3	31.3	14	38	38	38	1132400
24.6	24.6	24.6	24.6	12.6	24.6	12.6	24.6	3748900
10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	3474100
0	0	13.3	8.3	13.3	13.3	13.3	20.6	1078500
1.3	2.3	2.3	2.3	2.3	2.3	1.3	2.3	1505000
3.6	3.6	3.6	3.6	3.1	2.8	3.6	3.6	4457300
0	4.2	4.2	4.2	4.2	4.2	4.2	4.2	1004700
0	0	6.8	0	0	6.8	0	6.8	0
6.4	6.4	6.4	6.4	0	6.4	6.4	6.4	1112200
9.4	9.4	8	4.2	5.7	9	7.7	7.7	4942100
0	0	4.6	10.8	8.3	9.2	9.2	9.2	1844000
4.5	7	7	7	4.5	7	9.4	14.2	2653100
28.1	27.5	26	21.3	26.2	29.1	35.2	33.6	28633000
5.8	5.8	5.8	8.1	8.1	7.4	3.1	5.8	1543400
26.9	35.9	26	18.9	18.9	39.9	36.5	33.7	48850000
26.6	33.3	29	21.2	17.8	44.1	34	31	5442900
14.6	23.5	11.8	5	5	13.6	26.3	19.5	1561800
6	6	6	9.5	9.5	9.5	18.7	18.7	4094900
24	24	24	21.6	14	21.6	19.8	16	20032000
3.7	3.7	3.7	3.7	0	0	0	0	728740
0	0	0	1.5	1.5	1.5	1.5	1.5	1155800
7.3	4.5	4.5	4.5	2.8	7.3	4.5	0	1153000
22	26.3	29.1	29.4	20.3	41.6	46.3	43	54444000
16.4	22.5	28	26	16.8	37.8	43.6	42.7	23709000
14.2	6.5	14.2	11.9	3.5	19.8	12.1	19.8	3844000
5.4	5.4	0	0	5.4	5.4	5.4	5.4	1758100
0	0	14.3	0	0	0	0	14.3	454260
35.5	40.8	42.9	36.4	42.9	49.8	60.1	48.2	3.07E+08
2.1	1.1	2.1	2.1	2.1	2.1	0	1.1	873650
0	0	0	0	3	0	0	3	2839100
14.8	18.8	22.7	17.6	17.6	24.6	14.5	15.6	4046500
3.5	3.5	0	3.5	3.5	3.5	3.5	3.5	393600
9.9	9.9	9.9	9.9	7.8	9.9	9.9	9.9	5422400
18.6	18.6	10.3	10.3	6.4	18.6	18.6	18.6	7256700
11.9	17.2	11.9	11.9	11.9	13.1	17.2	17.2	6755800
6.9	4.3	8.7	8.7	6.9	8.8	10.6	8.8	3024600
5.7	5.7	5.7	5.7	5.7	2.7	5.7	5.7	2812200
11.2	13.4	13.4	14.7	14.7	12.3	14.7	10.1	12880000

[illegible]

23.6	47.3	47.3	23.6	0	23.6	47.3	0	5558100
31.6	51.3	31.6	51.3	17.1	31.6	31.6	31.6	9552700
33.3	33.3	26.6	29.6	17.5	26.6	23.9	30.3	28448000
27.2	46.5	37.6	20.7	10.3	34.3	40.8	40.8	26723000
45.4	45.4	45.4	45.4	32.4	32.4	45.4	45.4	17342000
11.1	9.6	11.1	11.1	9.7	7.7	5.8	9.2	7684000
5.3	5.3	5.3	5.3	5.3	0	0	5.3	449570
4.4	4.4	4.4	4.4	4.4	2.3	2.3	2.3	1472100
3.7	2	2	3.2	2	9.5	9.5	6.3	1867200
4.7	4.7	0	2.5	0	4.7	4.7	4.7	1269300
2.2	2.2	2.2	2.2	0	2.2	2.2	2.2	1177900
1.6	1.6	0	0	1.6	1.6	1.6	1.6	481630
7.7	9.1	13.6	13.6	11.9	18.7	20.8	25.1	40591000
7.8	7.8	6.7	6.7	6.7	6.7	7.8	7.8	2982800
6.5	5.5	0	0	3.1	4.3	5.5	5.5	1219300
22.2	19.4	19.6	16.8	12.6	18.4	22.2	20.7	18282000
9.8	8.2	8.2	6.2	9.8	6.2	6.2	6.2	2685100
22.1	22.1	22.1	22.1	14.2	7.9	7.9	0	2874800
1.7	3.4	1.7	3.4	0	5.1	3.4	3.4	1476400
19.5	18.9	17.3	14.8	12.4	18.9	20.6	23.6	48721000
4.2	11.2	8	6.4	6.7	16.1	18.8	13.4	5712100
11	13	12.8	14.3	9.4	14.5	11.5	14.3	12171000
3.4	3.4	0	3.4	3.4	3.4	7.2	7.2	699630
4.5	6.6	12.9	8.9	13	6.6	6.6	4.5	12333000
13.3	16.2	5.9	5.6	0	16.2	21.8	19	1442100
18	22.5	12.2	15.6	12	18.3	22.2	17	16640000
0	0	0	0	0	0	3	3	294950
8.9	6.1	8.9	8.9	6.2	6.1	4.7	8.6	2914500
4.1	4.1	4.1	4.1	4.1	2	2	2	1127400
0	0	20.3	20.3	20.3	0	20.3	0	279150
5.2	0	5.2	5.2	0	5.2	5.2	5.2	1199800
5	4.7	4.7	2.3	4.7	4.7	7.5	7.5	2653400
1.8	1.8	0	0	0	1.2	3.1	1.2	541080
27	27	27	27	27	27	27	27	21815000
0	0.3	0	0	0	0	0	0	313070
2.5	2.8	2.5	2.5	0	11.3	11.3	11.3	2086700
0	0	3.3	3.3	6.9	13.9	6.9	10.2	1373900
46.3	46.3	47.8	47.8	47.8	47.8	36.1	42.9	20941000
9.3	9.3	13.4	13.4	19.5	19.5	15.4	13	11423000
22.2	22.2	0	22.2	22.2	0	22.2	22.2	682650
13.3	13.3	13.3	13.3	13.3	13.3	13.3	8.6	7165800
11.1	8	11.1	11.1	11.1	8	11.1	8.7	3920900
35.3	35.3	16.8	16.8	16.8	16.8	35.3	35.3	12454000
2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	919460
0	4	0	0	0	0	4	4	437420
10.1	7.6	10.1	3.8	3.8	3.8	10.1	10.1	1331300
0	0	12.3	0	5.6	26.7	26.7	12.3	1739000
4.8	6.7	4.8	2.1	2.7	6.7	6.7	4.1	1415100
17.9	15.7	16.1	9.6	14.6	15.1	19	19.1	26267000
14.1	9.3	4.8	0	4.8	4.8	4.8	0	945780

14.9	17.9	15.1	15.7	12	31.6	31.6	31.6	12641000
0.3	0.3	0.3	0.3	0.3	0.3	0	0.3	949020
10.5	0	10.5	16.4	16.4	16.4	16.4	10.5	2380600
16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.3	1912100
9.2	8.8	12.9	12.9	9.2	12.9	12.9	9.2	3695500
0	0	0	0	0	0	4.6	4.6	178230
5.5	13.4	7.9	0	0	13.4	5.5	13.4	1536700
6.8	14.3	14.3	14.3	6.8	14.3	14.3	6.8	2877300
0	1.3	0	0	0	0	0.5	1.8	2397500
3.7	0	0	4.6	14.8	17.8	17.8	17.8	1560300
4.9	4.9	0	4.9	0	4.9	4.9	0	216470
2.6	2.4	2.6	6.7	6.7	7.7	9.3	9.3	3314300
18.8	17.6	15.8	13.7	11.1	18.8	17.9	15	18255000
10.5	10.5	10.5	10.5	10.5	10.5	10.5	8.2	11459000
6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	578800
10	12.3	7.5	6.9	5.9	8	10.9	10.6	18134000
1.8	0	1.8	3.1	3.1	3.1	1.8	1.8	2579300
8	8	8	8	8	6.6	6.6	8	6854000
16.4	16.4	16.4	24.6	10.3	16.4	16.4	6.2	3372900
2.2	0	0	2.2	2.2	2.2	2.2	0	2648600
23.4	25.9	24.7	23	17.3	25.9	26.1	20	49784000
14	15.7	14	14	9.4	14	10.5	12.2	8313500
8.9	9.2	10.8	8.9	9	10.8	9.2	9.2	20609000
45.4	45.4	40.5	29.7	28.6	45.4	45.4	45.4	9259700
31.2	30.9	25.5	27.5	21.6	28.7	28.2	27.7	1.22E+08
23.3	23.3	38	23.3	14.1	38	38	38	7088200
2.5	7.1	5.9	7.7	4.2	7.3	10.4	11.2	6194700
10	11.4	7.4	5.9	1.4	11.4	11.4	11.4	4518400
0	0	0	7.3	13.7	12.8	11.8	17.3	1994400
9.1	4.7	12.8	12.8	9.1	16.4	31.2	28.2	6129000
47	47	45.1	45.1	41.7	45.1	47	47	1.53E+08
7.1	0	12.9	12.9	5.8	12.9	7.1	12.9	2436100
10	4.5	7.1	10	7.1	5.5	7.3	4.5	4548700
10	10	10	10	10	10	10	10	750130
3.5	3.5	3.5	5.6	3.5	5.6	7.3	7.3	4587600
11.2	15.8	15.8	19.2	11.2	19.2	19.2	15.8	9911200
10.1	10.5	30	30	31	53.8	54.5	58.8	10277000
7.7	6.7	8.8	5.5	8.6	7.4	5.5	5.3	5297000
12.4	14	14	14	11.4	12.7	11.6	9.9	13100000
7.9	6.1	7.9	6.1	4.9	6.1	1.4	6.4	2433700
8.9	13.6	8.9	3.8	3.8	3.8	8.5	13.6	2637800
4.7	4.7	4.7	0	0	0	0	9.9	647940
11	11	4.8	4.8	0	11	11	6.1	2061100
6.2	2.4	2.4	2.4	2.4	2.4	6.2	2.4	850040
4.8	4.8	0	3.6	4.8	3.6	3.6	0	476000
11.8	14	12.7	16.3	16.7	14	10.4	13.7	6754900
21.7	21.7	21.7	6.8	0	6.8	41.6	38.9	5650300
21.3	19.2	17.8	24.2	16.2	21	26.4	27	24447000
6.8	8.1	9.7	10.1	8.5	11.4	4.9	11.4	4194900
16.2	20.1	17.2	15.9	18.9	17.4	21.5	17.6	18985000

9.1	9.6	17	11.6	9.9	17	10.1	17	4153400
11.2	11.2	11.2	7.9	7.9	7.9	8.3	11.2	6819900
2.5	1.8	3.6	3.6	2.9	2.4	2.5	2.5	6935000
51.1	51.1	51.1	51.1	41	46.6	46.6	51.1	55693000
0.9	0.9	2.3	2.3	1.4	2.3	2.3	0.9	1101900
3.1	3.1	3.1	3.1	1.2	1.2	0	0.6	1076500
15.7	13.1	15.7	13.1	13.1	13.1	13.1	13.1	6389700
10.3	10.3	10.3	10.3	6.7	10.3	10.3	10.3	4714700
26.7	31.6	21.8	22.8	27.7	26.7	31.6	31.6	30236000
29.6	29.6	22.2	29.6	29.6	29.6	29.6	29.6	8933100
17.4	13.2	17.4	17.4	4.1	17.4	13.2	17.4	2316600
6.3	3.6	6.3	6.3	2.3	3.6	2.3	5	2606800
42.6	42.6	42.6	42.6	0	42.6	42.6	42.6	2145300
4.6	4.6	4.6	4.6	8.9	4.6	4.6	4.6	1189600
3.7	3.7	4.3	1.1	0	2.2	2.6	6.9	1969000
11.5	22.5	20.9	20.9	9.9	15.2	26.7	22.5	7659800
5	1.2	0	3.5	3.5	6.2	6.2	7.4	1251700
3.4	3.7	7.1	7.1	3.4	7.1	7.1	7.1	1812300
8.2	12.9	20.6	12.9	12.9	29.4	29.4	36.5	8029300
0	0	0	0	0	0	2.6	0	0
16.1	28	16.1	28	28	16.1	16.1	16.1	1335400
41.6	41.6	41.6	41.6	14.3	27.3	41.6	27.3	2318100
6.3	6.3	6.3	6.3	0	6.3	6.3	6.3	572520
25.9	25.9	25.9	25.9	22.8	25.9	25.9	25.9	7313500
25.3	43.6	39.8	39.8	20.3	48.5	52.3	52.3	27309000
4.3	4.3	6	6	4	4.3	4.3	4.3	2756200
0	0	0	1.7	1.7	0	1.7	1.7	494400
3.9	3.9	3.9	3.9	0	3.9	3.9	0	818040
15.3	15.3	15.3	15.3	0	15.3	0	15.3	1454100
17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	1595600
23	23	14.2	23	36.1	23.5	30.1	36.1	14522000
1.7	1.7	0.6	0.6	1.7	1.7	1.7	1.7	1669800
18.1	20.5	20.5	20.5	14.1	18.1	12.8	15	38479000
22.9	25.4	23	19.5	12.7	29.2	32.6	32.2	82461000
13.8	9.6	13.8	13.8	13.8	13.3	13.3	13.3	5553400
3.3	3.8	7.1	7.1	7.1	7.1	7.1	3.3	1272100
25.6	25.6	25.6	13.2	13.2	13.2	13.2	13.2	2653400
19	19	14.7	19	11.4	19	19	19	12320000
6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	3252000
12.9	12.9	12.9	12.9	12.9	12.9	12.9	12.9	6832300
7.9	14.5	14.5	7.9	0	14.5	14.5	14.5	2975500
11.9	9	6.1	6.1	6.1	11.9	9	5.6	2417400
0	5.4	0	0	0	0	5.4	5.4	287520
0	4.9	4.9	4.9	4.9	4.9	4.9	4.9	527130
8.5	2.2	8.4	10	9.9	8.5	7	7.2	3285500
6.5	10.8	10.8	10.8	10.8	10.8	7.9	3.5	1867900
0	1.1	0	1.1	0	0	1.1	3.1	481180
25.4	25.4	31	38.7	31	38.7	38.7	43.7	18114000
11.6	11.6	11.6	11.6	11.6	0	0	0	362110
6.9	5.2	6.9	3.6	3.3	8.2	9.3	8.7	7792900

3	3	3	3	3	4.6	3	2.4	2216100
14.8	10.4	9.5	9.5	11.7	9.5	13.8	14.5	11742000
8.8	10.8	8.8	8.8	8.8	9	11	10.2	3335200
13	13	2.7	2.7	2.7	13	13	13	2046600
1.9	1.9	1.9	0	3	3.2	3.2	5.7	2540400
63.9	59.6	54.8	54.8	46.4	59.6	63.9	59.6	1.1E+08
0	0	2.2	0	2.2	0	0	0	170090
13.5	13.5	7.9	7.9	7.9	7.9	12.1	13.5	6779700
7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	1061600
8.5	8.5	8.5	8.5	0	8.5	8.5	0	516860
0	26.1	0	26.1	26.1	0	26.1	26.1	375100
31.1	24.5	31.1	31.1	31.1	31.1	24.5	31.1	4945500
3.8	3.8	3.8	3.8	1.6	5.5	7.8	6.8	2537100
5.8	8.6	8.6	7.3	10	5.8	8.2	4.1	17056000
33.3	28	28	23	28.7	33.3	33.3	28	64927000
0	0	0	0	0	0	0	1	187230
1.8	4	1.6	3.7	2.3	4.8	5.8	7.1	1615800
1.4	1.2	1.4	1.4	1.4	2.6	2.6	2.3	775930
7.2	0	0	7.2	0	7.2	0	0	3995500
7.6	10.3	8.7	8.7	9.3	10.3	10.3	11.6	6412700
3.2	0	3.2	3.2	3.2	0	5.7	3.2	616150
0	0	0	3.8	0	3.8	3.8	6.7	514910
12.1	12.1	12.1	12.1	12.1	12.1	20.8	12.1	1073300
24.4	24.4	19.7	18.8	11.7	16.4	22	22	24916000
4.2	4.2	4.2	4.2	0	1.6	1.6	1.6	5818900
26.8	27.4	26.8	26.8	26.8	29.3	29	27.4	36828000
17.8	17.8	17.8	17.8	17.8	17.8	17.8	0	1417600
7.6	0	7.6	7.6	7.6	7.6	7.6	7.6	1502000
6.8	8.2	11	9.3	9.3	11	15.2	13.5	7717800
2.3	2.3	2.3	2.3	2.3	2.3	0	2.3	329170
0	0	0	0	0	0	23.9	23.9	699390
11.3	11.3	11.3	11.3	11.3	11.3	11.3	9.9	2117200
0	9.8	5	0	6	14.9	14.9	8.9	1674200
0	0	5.9	9.9	9.9	5.9	5.9	9.9	1146900
0	0	10.2	0	0	10.2	10.2	10.2	4056700
7.6	7.6	3.9	0	7.6	7.6	7.6	7.6	1665400
10.3	12.4	8.6	7.6	8.6	12.4	12.4	12.4	7118700
2.6	2.6	1.2	3.5	3.7	1.2	1.2	3.5	1141700
0	2.5	0	0	0	2.5	2.5	2.5	588420
0	0	0	0	1.3	1.3	1.3	1.3	315890
0	0	2.6	3.3	2.4	7.6	6.1	6.6	3838000
8.1	11.4	10.8	10.8	11.4	14.1	11.4	14.1	2771000
14.1	9.5	14.1	9.5	14.1	17.2	22.4	22.4	4672300
0	0	0	0	18.4	18.4	18.4	18.4	736250
36.7	12.2	36.7	36.7	36.7	36.7	49	49	5529400
11.6	11.6	11.6	0	11.6	0	11.6	0	427690
16.1	24.9	24.9	32.6	21.2	41.5	41.5	46.6	6632200
9	4.5	9	9	9	9	9	9	2724600
10.3	10.3	10.3	10.3	10.3	10.3	10.3	0	495570
4.8	3.7	3.7	4.8	4.8	4.8	3.7	3.7	2608400





[illegible]

5.5	4.1	7.5	5.5	5.5	5.5	7.5	7.5	6747300
0	0	0	0	0	0	0	4.2	284720
13.2	13.2	13.2	13.2	13.2	9.4	9.4	13.2	4235600
23.9	13	23.9	23.9	23.9	23.9	23.9	23.9	4789100
17.8	17.8	11.8	11.8	9.3	15.3	15.3	15.3	17929000
36.2	39.2	34.9	34.3	32.1	28.7	40.4	33.6	80028000
27.4	27.4	27.4	21.7	17.9	23.8	26.1	27.9	42254000
47.1	37.6	47.1	47.1	47.1	47.1	37.6	37.6	15837000
5.8	7.1	5.8	5.8	5.8	5.8	3.3	5.8	10674000
2.7	2.7	1.6	2.7	1.6	1.1	0	0	1506500
4.1	0	0	4.1	0	4.1	0	4.1	518550
2.8	6.1	6.1	6.1	2.8	6.1	6.1	6.1	1470000
1.9	2.1	1.3	1.3	0.8	2.1	1.3	1.5	1129200
4.7	4.7	4.7	4.7	4.7	4.7	0	0	889890
11.1	11.1	11.1	11.1	11.1	7.5	6.7	3.1	2501100
0	0	0	0	0	3.3	3.3	3.3	377100
0	0	0	0	0	0	0	8.8	175710
4.4	12.3	4.4	4.4	8.8	8.8	8.8	4.4	735180
2.9	1	2.9	2.9	0	2.9	2.9	1	1190400
0	0	1.7	1.7	1.7	3.1	5.6	5.6	1191300
4.4	4.4	2.6	0	1.8	3.3	3.3	3.3	1367500
0.3	0.3	0.3	0.3	0	0.3	0	0	697580
37.1	37.1	24.7	24.7	24.7	37.1	37.1	49.4	6413900
37.1	37.1	24.7	24.7	24.7	37.1	37.1	49.4	3209800
0	0	0	0	12.5	16.7	38.5	29.2	1562000
0	0	0	0	0	0	0	1.5	138380
4.5	4.5	4.5	4.5	4.5	4.5	3.2	0	3571300
10.5	11.1	10.9	10.4	9.8	9.1	8.5	8.7	20108000
4.6	4.6	4.6	4.6	4.6	6.5	14.1	14.1	3327500
6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	1342300
0.3	0.5	0.8	0.6	1.2	1.5	1.4	0.8	3184300
6.3	12.8	12.8	12.8	8.5	8.5	8.5	10.6	7846200
8.1	8.1	8.1	8.1	8.1	8.1	0	8.1	499180
10.2	10.2	5.1	5.1	5.1	10.2	10.2	10.2	1008100
4.3	4.3	1.5	1.5	1.5	1.5	3.5	2.9	1421800
12.5	26.7	29.6	29.6	15	33.8	33.8	33.8	6038700
8.7	4.9	8.7	8.7	8.7	8.7	8.7	8.7	2581300
0	4.9	8.5	8.5	4.9	8.5	3.6	8.5	1368900
11.8	6.8	9.8	5	6.8	11.8	11.8	13.3	5258200
21.5	9.2	17.5	14.7	9.2	21.5	21.8	25.8	10216000
22.8	22.8	22.8	28.4	22.8	18.7	14.9	19.4	16633000
32.5	37.6	41.6	37.6	41.6	36.5	36.1	41.6	23151000
15.6	15.6	15.6	14	11.4	20.7	20.7	20.7	616200
38.7	30.7	38.7	24.4	24.4	38.7	38.7	38.7	35034000
32.2	32.2	22.2	37.2	27.6	31.8	37.2	46.4	37559000
23.3	23.3	13.2	36.6	26.8	31.1	36.6	45.9	605880
20.1	25.9	23.8	23.6	18.5	27.7	32.5	29.5	81190000
37.3	35.3	27.6	26.9	25.2	39.4	38.7	40.8	1.87E+08
10.7	8.6	7.4	5.9	4.4	5.4	7.1	5.4	4225000
17.5	9.2	9.2	17.5	12.3	12.3	17.5	12.3	6269100

38.9	42.5	35.4	37.6	29.9	36.9	46	38.5	88720000
5	5	5	5	5	5	5	5	2883600
5	5	5	5	5	5	5	5	1746300
2.2	2.2	2.2	2.2	2.2	2.2	2.2	2.2	902720
22.8	22.8	14.6	17.7	13.8	22.8	17.7	19.7	8540000
9.8	9.8	9.8	9.8	9.8	7.2	7.2	7.2	3728600
0	0	0	0	10.2	10.2	0	10.2	381190
7.5	6.5	9.5	9.5	5.7	9.5	6.2	6.2	5952700
5.1	5.1	5.1	5.1	3.9	3.4	3.4	3.4	2671700
27.6	26.8	27.6	27.6	27.6	27.6	31.4	26.8	28994000
13.8	13.8	13.8	16.7	13.8	16.7	6.7	10.1	23185000
15.3	15.3	15.3	6.7	15.3	4.3	12.9	12.9	2554800
36.7	34.6	33.9	27.9	28.6	32.5	34.9	34.5	1.18E+08
0	0	0	0	0	12.9	12.9	12.9	461620
10.6	37.5	37.5	37.5	26.9	37.5	37.5	21.2	19497000
15.1	18.6	18.6	18.6	12.3	15.1	14	16.1	18472000
16.2	16.2	16.2	12.1	7.4	7.4	9.9	11.5	3879900
28.6	34.5	28.6	28.6	23.8	28.6	34.5	21.4	18155000
5.2	5.2	5.2	5.2	5.2	0	0	0	592250
29.3	27.9	29.6	27.4	22.2	26.4	32.1	26.5	89194000
21.3	40.2	40.2	21.3	21.3	32	32	40.2	5468100
24	22.5	22.5	22.5	20.2	26.3	22.5	22.5	37699000
5.2	3	0	3	3	3	3	3	1069200
12.5	12.5	12.5	8.6	10.3	12.5	10.3	15.6	6704800
2.2	0	2.2	2.2	2.2	2.2	2.2	2.2	1439400
8.6	8.6	5	8.6	0	5	5	8.6	7661300
3.1	0	1.8	0	0.7	1.8	0	1.3	878430
8.4	8.4	11.8	8.4	7.4	11.8	11.8	11.8	3767900
0	0	17.9	0	17.9	0	17.9	17.9	280650
8.1	3.8	3.8	3.8	0	8.1	4.3	3.8	1032500
15.9	15.9	12.4	15.9	15.9	15.9	12.4	10.4	2729100
17.2	21.6	18	21.6	17.2	21.6	13.6	7.1	9444000
17.7	29.1	28.2	28.2	17.5	28.2	29.1	29.1	29609000
25.5	25.5	25.5	0	25.5	18.2	18.2	18.2	2629000
0	1.5	1.5	1.5	0	0	0	1.5	287790
5.7	5.7	5.7	5.7	5.7	5.7	0	0	353760
29.8	53.4	32.8	28.8	19.7	46.3	51.5	53.7	58839000
11.2	11.2	9.5	13.4	10.5	11.7	16.5	16.8	5977500
7.4	11.5	8.8	4.9	3	10.1	13.2	12.9	4320400
0	0	3.1	5.2	0	10.6	13.7	14.4	3390200
14	14	7.3	7.3	7.3	14	14	0	914250
0	0	0	0	0	33.1	19.8	33.1	1220900
0	0	6.9	13.9	6.9	21.5	21.5	14.6	2088300
7	6.3	14.9	11.7	9.2	19.7	19.7	9.5	5017500
9.9	19.5	15.9	15.9	15.9	23.1	26.7	26.7	9719100
9.1	10.8	10.6	10.6	9.1	16.9	16.9	17.8	7975900
0	0	4.2	0	4.2	11.4	11.4	11.4	667480
2	2.8	2	3.3	3.8	8.5	8.2	8.2	6678400
6.3	5.7	3.7	2.6	1.5	10.1	11.2	11.2	6074900
6.1	2.2	4.3	4.3	3.2	7.5	7.5	8.2	5000900

16.2	15	13.4	8.4	11	11.2	22.8	20.2	7257300
17.5	17.5	17.5	13	9.2	19.6	19.6	17.5	7806300
5.3	5.3	5.3	5.3	5.3	8.4	8.4	8.4	2561700
8.4	0	0	3.4	3.4	5	14.5	11.5	1632200
7.7	10.3	7.7	5.4	0	7.7	13.2	4.9	2143800
20.3	20.6	18.2	15.4	18.8	22.5	32.9	33.8	7044000
0	11.3	18.9	18.9	0	18.9	18.9	18.9	1087200
0	10.2	10.2	10.2	10.2	10.2	10.2	10.2	1180400
4.9	3.3	9.9	9.9	7.6	13.7	15	13.3	4448100
0	0	13.5	0	0	13.5	13.5	0	419870
9.7	8.9	6.2	8.6	10.8	14.1	14.1	12.9	16044000
3.4	0	3.4	0	0	5.4	2	5.4	557030
0	0	4.9	7	4.7	9.6	7	6.8	4235800
6.1	19.3	19.3	22.8	19.3	28.5	34.6	34.6	9787800
2.3	0	0	2.3	0	6.5	6.5	6.5	1294800
29.5	29.5	24	24	29.5	29.5	32.2	32.2	28823000
3.8	5.1	2.9	1.7	1.7	4.6	7.1	5.6	3590800
22.9	29	11.4	11.4	11.4	25.7	33.1	33.1	8737200
11.5	11.5	11.5	11.5	11.5	11.5	11.5	11.5	598050
20.2	20.2	5.9	20.2	9.2	20.2	20.2	23.5	1841500
0	0	0	5.7	0	5.7	5.7	5.7	310470
7.6	12.4	7.6	7.6	7.6	7.6	7.6	12.4	1661900
7.9	5.2	0	0	2.7	7.9	7.9	7.9	931280
1.8	0.8	3.2	0.8	5.3	6.9	6.4	5.6	3778500
7.1	5.4	7.8	9	8	13	11.7	13	30012000
2.2	2.2	1.2	1.2	1.2	2.2	1.2	2.2	764030
10.5	13.1	11.7	11.2	7.5	11.5	10.4	10.7	12636000
10.6	10.4	15.4	12.3	14.7	16.9	20.1	22.4	10743000
6.8	7.8	6.7	6.7	6.1	9.7	9.9	12.8	12129000
17.9	14.5	16.4	14.2	12	15.7	15.7	15.7	14643000
33.9	39.5	39.5	32.5	29	36	30.4	33.9	13924000
15	15	15	15	16.4	11.5	24.5	32.9	3826900
22.1	23.9	28.3	28.3	18.4	33.1	33.1	30.1	13298000
0	1.2	7.4	8.9	4	17.9	22.4	19.9	7495500
12.4	11.5	9.8	12.8	7.2	25.9	25.5	27.1	13470000
17.5	20.1	16.6	9.3	4.2	18.7	23.3	24.1	7519500
5.1	5.1	5.1	7.9	5.1	7.9	11.3	11.3	3223400
22.2	20.2	22.2	14.2	20.2	18.2	12.1	14.2	8044200
32.3	32	28.4	31.2	29.6	35.1	44.4	41	51955000
20.4	18.5	16.5	14.3	12.4	21.6	22.3	22.2	65658000
0	0	22.2	22.2	37	32.6	47.4	47.4	4983000
11.3	11.3	11.3	11.3	7.5	7.5	7.5	7.5	1618000
12	15	18.6	11.5	14.8	11.5	12	18.6	15913000
8.3	5.2	6.7	8.3	5.2	5.2	8.8	8.3	1928800
35.5	31.7	35.5	35.5	35.5	35.5	27.3	27.3	17299000
0	0	0	0	0.5	0	0	0	30630
40.1	39.4	37.5	39	37.2	41.6	44.6	44	3E+08
19	19.1	20.4	21.7	21.8	23.8	26.4	23.9	56583000
5.8	0	5.8	0	5.8	5.8	12.3	12.3	680540
18.4	21.6	20.8	10	12.4	26.8	26.8	22.6	11290000

0	9.2	16	15	4.9	29.1	29.1	32.5	2927500
15.3	15.3	15.3	15.3	12.4	15.3	15.3	15.3	5651100
13.6	15.4	15.4	15	10.5	12.4	12.1	15.4	4838100
6.2	0	6.2	6.2	6.2	2.3	6.2	6.2	1279700
8.6	8.6	8.6	5.6	9.5	8.6	9.5	8.6	5888400
22.2	22.2	22.2	22.2	22.2	22.2	11.1	22.2	2034500
2.7	2.7	2.7	2.7	2.7	2.7	0	0	386780
48.9	44.5	52.7	49.2	48.1	57.1	63.2	62.9	1.89E+08
16.5	14	18.7	11	16.8	18.7	19	18.7	12757000
25.9	27.6	22.3	22.3	16.1	22.9	24.4	24.6	24252000
16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	5553300
15.2	15.2	15.2	15.2	18.6	15.5	15.5	15.5	3159600
58.5	71.9	71.9	64.4	54.1	71.9	58.5	71.9	81018000
0	4.4	0	0	0	9.6	9.6	9.6	699140
8.5	6.2	8.5	4.4	8.5	8.5	6.2	8.5	3772700
18.8	18.8	18.8	18.8	18.8	18.8	18.8	12.8	1756600
0	10.6	21.3	33	21.3	33	33	22.3	2501500
13.4	13.7	15.3	13.8	12	13.5	12	12.5	13719000
7.5	7.5	7.5	7.5	7.5	4.9	4.9	4.9	1594500
20.1	21.3	17	10.9	10	9.7	9.7	8.1	15006000
1.2	1.2	0	0	0	0	1.2	1.2	503820
10.9	10.8	5.9	7.6	7.6	8.8	8	10.1	6706600
0	0	1.9	2.9	1.9	2.9	2.9	1.9	538860
0	0	0	0	0	0	15.3	15.3	233400
0	0	2.7	2.7	2.7	2.7	2.7	4.2	424310
0	0	0	0	0	9.7	9.7	9.7	180450
0	5.1	5.1	8.4	8.4	20.7	10.5	24.9	2336500
19.4	20.6	13.6	12.8	8.9	26.6	30.9	32.8	17051000
8.6	8.6	10.1	10.1	5.4	18.3	20.2	14.1	22418000
37.9	37.6	37.6	36.4	31.2	35.3	28.2	33.5	78085000
37.3	37.3	31.9	34.1	34.4	36	30.3	30.3	66980000
0	0	0	0	1.8	1.8	1.8	3.3	361540
0	0	0	0	0	5.2	5.2	5.2	378860
0	0	0	0	0	3.6	8.7	2	600190
20.9	22.6	18.1	18.1	12.7	20.1	20.1	22.6	10111000
9	9	7.3	9	7	9	6.9	9	3293300
9.3	8.8	7.5	5.6	5.4	10.7	8.8	7.3	3372500
0	0	4.2	4.2	4.2	7.8	7.8	7.8	1518400
0	8.9	8.9	8.9	8.9	8.9	8.9	8.9	1810600
4.9	6.4	11.3	10.2	4.9	10.2	14.1	14.1	2625200
8.4	8.4	8.4	8.4	20	12.6	8.4	8.4	3907600
0	5.8	12.9	9.5	9.5	20.7	19.9	20.3	2804100
21.4	26.7	36.2	36.2	21.9	49	52.9	50.5	68356000
52.9	51.5	52.9	46.8	44.4	44	53.2	56	4.34E+08
2.8	2.8	2.8	2.8	0	2.8	2.8	0	460300
12.5	14.4	13.1	13.1	13.1	11.7	11.7	11.4	12011000
30	10	30	30	30	30	30	10	4253000
5	2.8	3.7	7.6	3.7	5.4	3.9	7	3550300
5.7	5.7	5.7	5.7	5.7	5.7	5.7	0	897140
0	0	0	7.3	0	7.3	7.3	7.3	301560

0	0	6.6	4.6	4.6	6.6	6.6	6.6	1707900
0	6.7	6.7	6.7	6.7	6.7	6.7	6.7	1257000
12.5	16.5	18.3	15.1	10.8	10.6	10.8	13.1	5597400
7.6	7.6	5.6	7.7	5.9	11.1	12.5	14.1	13680000
6.7	6.7	5.2	4.7	6	5.2	6.7	2	4995500
4.9	3.3	1.9	1.9	3.3	1.9	1.9	1.9	1132200
5	5	5	5	5	10.4	5.4	5	1295400
9.6	7.3	12.8	14.8	2.1	12.8	12.8	7.3	3503700
2.5	2.5	2.5	0	2.5	2.5	2.5	2.5	506210
16	16	16	16	16	16	16	0	1159500
5.3	6.9	8.7	6.9	6.9	1.9	1.9	5.3	1755300
11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.2	1512200
0	0	0	7.3	0	0	0	0	32450
5.6	3.3	0	3.3	5.6	0	3.3	0	1483300
7.2	7.2	7.2	7.2	4.8	0	0	0	1148000
3.2	3.2	0	0	0	0	0	3.2	269260
24.9	28.6	17.1	17.1	17.1	17.1	28.6	12.9	4717800
9.6	9.6	9.6	9.6	9.6	0	9.6	9.6	1002400
12.2	6.4	12.2	12.2	12.2	12.2	12.2	12.2	1906200
22.7	18.5	27.5	25.8	25.8	27.5	23.2	15.9	43544000
20.3	20.3	20.3	0	20.3	20.3	20.3	0	832880
10.4	10.4	10.4	10.4	0	10.4	10.4	0	1265200
2.3	4.3	2.3	2.3	4.3	4.3	4.3	4.3	1044300
19.5	22.3	19.5	12.1	11	27.1	22.3	21.2	2336300
23.4	23.4	23.4	19.7	19.4	28.2	28.2	17.5	6869500
69.4	69.4	59.7	69.4	59.7	69.4	59.7	25	6585900
23.2	19.1	19.1	23.2	23.2	18.8	22.1	23.2	6773300
27.1	26.8	27.1	27.1	27.1	25	30.3	23.2	33720000
21.8	21.8	21.8	15.8	19.5	24.3	22.3	20.6	13363000
7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.2	1502400
11.3	11.3	11.3	11.3	11.3	9	11.3	9	3797900
7	7	7	7	7	7	3.1	7	636200
4.3	0	0	4.3	0	0	0	0	98521
46.4	57.7	50.5	33.8	28.4	50.5	68.1	64.4	62096000
1.9	6.3	6.3	6.3	6.3	1.9	6.3	6.3	2040400
0	0	0	1.2	1.2	0	0	0	133450
14.6	14.6	14.6	14.6	10.1	14.6	14.6	14.6	4636600
24.8	24.8	24.8	23.5	31.4	24.8	24.8	23.5	7973700
8	13.4	10.9	10.5	8.9	13.4	5.8	10.5	5631000
5.3	5.9	5.9	4.3	3.1	4.3	2.1	4.1	5856200
2.2	2.2	2.2	2.2	2.2	2.2	0	2.2	5093200
34.4	41	36	31.2	27.4	38.9	52.5	47.2	2.97E+08
10.7	16.5	19.9	23.2	12.7	30.7	25.6	26.4	23160000
15.1	15.1	15.1	15.1	13.7	15.1	15.4	15.4	1.01E+08
44.1	40.6	37	42.1	34.8	46.7	48.3	43.7	2.51E+08
32.9	32.9	32.9	32.9	32.9	32.9	32.9	32.9	2207000
15.1	22.5	22.5	20.4	19	27.1	29.5	34	43785000
21.8	20.3	19	17.7	14.4	21	20.1	16.3	28664000
62.9	72.2	72.2	72.2	59	72.2	72.2	72.2	2.25E+08
31.1	33.7	35.9	33.7	27.9	35.9	45.2	43.7	1.08E+08

44.8	40.1	49.3	45.6	37.3	49.2	50.6	52.2	5.02E+08
13.8	14.2	14.2	15.8	14.4	15.8	15	15	386650
0	0	37.5	37.5	31.7	54.8	54.8	54.8	3696400
0	0	0	0	14.8	27	27	14.8	644860
15.5	15.5	5.1	8.9	5.1	8.9	5.1	11.7	2264000
0	0	12.9	12.9	12.9	12.9	12.9	12.9	474800
48.6	48.6	21.8	21.8	21.8	21.8	32.4	38	25171000
6.1	6.1	6.1	27.9	0	6.1	6.1	6.1	560130
7.7	7.7	4.4	4.4	4.4	7.7	7.7	4.4	2299900
4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	1173300
0	0	11.2	19.6	14.6	30	30	34.2	5864600
14.6	8.7	18.2	13.8	22.1	18.2	18.2	18.2	4968000
2.5	7.1	13.9	12.1	9.6	16.4	13.9	16.4	11568000
23.6	16.7	16.7	11.5	6.6	16.7	23.6	23.6	15372000
6.8	12.7	14	16.9	13.7	21.5	40.7	30.3	36423000
20.2	11.2	9.3	15.4	13.5	21.9	28.1	17.7	21056000
15.7	6.7	11.4	20.5	11.4	13.8	30	38.6	20981000
4.1	8.5	4.4	4.4	4.4	8.5	10.7	8.5	2381600
33	33	28.4	28	28.2	30.1	37.3	30.6	40228000
33.6	33.6	29.1	29.1	29.1	29.1	31.9	33.6	47193000
23.6	23.6	23.6	23.6	23.6	23.6	19.6	27.8	7279800
29	29	17.5	18.7	12.4	22.7	29	13.6	13528000
31.1	36.4	23.9	20.7	28.2	35.5	43.2	41.1	75005000
27.2	26.1	13.4	11.2	23.4	22.8	35.7	33.4	34482000
36.5	36.2	33	29.4	17.2	36	40.1	40.5	51675000
19.9	23	18	17.3	19.7	33.6	33.2	22.2	29890000
24.2	25.6	17.4	21.2	17.2	21.5	25.6	25.6	18494000
25.3	28.7	21.8	18.3	19.3	24.6	29.6	28.6	1.25E+08
4.1	4.1	4.1	5.6	5.6	5.6	4.1	5.6	1705600
21.2	19.7	18.3	17.8	15.4	18.5	17.4	19.1	13837000
27.5	26.1	32	38.2	31.2	48.2	56.4	36.3	1.42E+08
42	44.7	46.6	37	31.3	41.2	42	40.8	46662000
10.5	10.9	10	11.6	5.5	7.1	5.8	9.2	4003400
16.9	19.4	19.4	15.7	10.1	18.2	14	14.8	19925000
2.9	2.9	2.9	2.9	2.9	1.6	1.6	2.9	2317400
29.7	29.7	29.7	11.4	0	29.7	37.3	37.3	12959000
0	10.4	0	10.4	0	0	19.4	9	400430
0	0	0	0	0	8.5	8.5	8.5	584220
15	22.4	23.4	23.4	23.4	23.4	23.4	15.9	9871300
0	0	23.2	0	23.2	0	0	23.2	246320
21.4	12.7	5.6	12.7	12.7	19.8	35.7	35.7	3720900
5.5	5.5	5.5	5.5	10.5	5.5	0	0	574300
0	0	3.9	0	0	3.9	3.9	3.9	442100
5.2	9.4	9.4	9.4	5.2	9.4	11.4	6.8	5028100
9.8	17	17	17	11.9	16.5	12.4	16.5	15140000
20.2	31.9	31.9	31.9	31.9	27.7	27.7	31.9	2.78E+08
26.9	26.9	26.9	26.9	26.9	31.1	26.9	31.1	10799000
25.7	26.1	26.1	26.1	25.7	26.1	21.7	26.1	89649000
5.6	5.6	5.6	5.6	5.6	5.6	10.3	10.3	1600500
27.2								



31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.2	26236000
3.7	3.7	3.7	3.7	14.5	14.5	0	14.5	380270
21.7	21.7	21.7	21.7	21.7	21.7	16.8	21.7	10265000
53.2	47.6	53.2	46.8	35.7	53.2	46.8	53.2	13227000
46.8	52.4	52.4	46	40.5	52.4	40.5	52.4	9275500
52.4	41.3	52.4	40.5	40.5	52.4	40.5	46.8	2589000
36.1	40.4	40.4	35.5	31.3	40.4	31.3	40.4	9.76E+08
26.5	19.9	26.5	26.5	19.9	19.9	18.4	18.4	1.86E+08
52.4	52.4	52.4	52.4	52.4	51.5	44.7	52.4	1.07E+09
12.4	8.5	14.1	15.4	12.2	17.3	17.3	20.2	12731000
12.2	12.2	6.6	4.9	5.6	10.6	17.9	14.1	2477000
43	33.7	35.9	35.9	35.1	39.2	39.2	35.9	8157100
43	33.7	35.9	35.9	39.7	39.2	39.2	40.5	64100000
6.8	6.8	6.8	6.8	3.8	6.8	6.8	6.8	1862800
25.7	25.7	22.4	22.4	22.4	25.7	25.7	23.2	9447800
30.3	26.5	23.2	23.2	27	26.5	30.3	30.3	18412000
23.1	22.6	19.4	19.4	23.1	22.6	26.3	26.3	2130800
15.7	15.7	19	19	13.3	20.9	20.9	20.9	11314000
12.7	12.7	12.7	16.4	12.7	26.7	18.8	14.3	8531000
8	8	8	8	8	8	8	8	1371600
14.8	14.8	14.8	12.3	11.9	10.7	10.7	7.9	8988700
4.3	8	8	8	0	8	3.7	4.3	1243600
9	4.8	9	16.2	9.2	13.5	15.8	18.5	9630700
20.6	20.6	20.6	20.6	20.6	20.6	14.5	12.5	11936000
5.5	0	10.1	28	16.1	28	28	28	4520200
12.5	12.5	13.6	10	8.8	11.3	11.3	11.3	9757000
29	29	29	29	0	29	29	29	3319900
18.1	20.2	16.6	16.3	15.5	21.7	22.5	20.8	13159000
19.4	13.1	15.7	13.1	13.1	13.1	22.1	16.5	6856300
1.9	1.9	4.6	1.9	1.9	1.9	4.6	4.6	994670
2.6	4.6	2.6	2.6	0	4.6	2.6	2.6	1416100
16.1	19.2	15.5	15.5	10.4	18.4	20	19.1	29775000
2.5	0	4.7	0.9	2.5	10.4	10.9	13.3	5132500
1.3	1.3	1.3	1.3	1.3	2.8	4.4	6.5	2451300
0.9	0	0	0	0.9	1.9	1.1	0	880950
1	2.2	2.2	2.2	2.2	2.2	2.2	1.3	591470
6.9	6.9	6.9	6.9	3.4	3.4	6.9	6.9	1086700
6.6	6.6	6.6	6.6	3.4	6.6	3.2	6.6	1876300
1.2	1.2	3.1	3.1	3.1	0	1.2	1.9	605310
0	1.3	4.5	4.5	3.2	4.5	1.3	0	640680
27.7	27.7	20.4	28	22.5	40.8	47.4	45	17097000
9.6	0	0	9.6	9.6	9.6	18.6	18.6	1093500
25.3	31.9	23.6	17.9	23.6	26	31.9	28.9	20208000
3.8	3.8	3.3	3.3	3.8	3.1	1.5	1.8	5882900
10	10	7.3	2.8	10	10	10	10	2687500
14.7	14.7	14.7	14.7	14.7	7.9	7.9	18.8	14775000
2.6	2.6	2.6	2.6	2.6	2.6	2.6	0	3359600
15.1	16.6	15.4	13	11.7	14	17.1	12.6	30330000
5	4.1	4.1	4.1	4.1	3.1	4.1	3.1	5402600
28.4	28.2	27.5	21.1	21.9	24	24.1	23.1	31883000

8.2	8.2	6.3	8.2	6.3	4.2	2.9	4.2	5862200
3.5	3.5	3.5	3.5	3.5	3.5	3.5	3.5	5117100
19.5	20.8	19.5	20.8	19.3	18.2	18.2	16.5	62654000
23.8	25.9	24.9	26.5	24.3	24.1	25.8	24.4	71654000
5.3	5.3	5.3	5.3	2.6	5.3	5.3	5.3	1300700
6.5	6.5	6.5	6.5	8.8	6.5	4.9	6.5	1989600
0	0	4.3	4.3	0	9.8	9.8	10.5	749410
0	0	21.6	21.6	0	21.6	21.6	21.6	1991200
8.9	10.3	10.3	5.1	6	10.3	8.7	10.3	3624600
13.1	23	23	19.9	13.4	26.4	23.6	32.7	14736000
9.7	15.4	17.2	16.6	17	22.1	29.2	27.6	26268000
0	0.9	0.9	0	0	0	0	0.9	496590
0	0	0	0	0	5.9	5.9	5.9	197260
21.8	21.8	19.3	21.8	22.4	12.4	19.9	19.3	12164000
8.7	8.7	16.5	10.7	8.7	16.5	8.7	16.5	5836800
18.4	18.4	16.9	22	13.8	22.7	34.8	29.2	11540000
8.8	9.3	6.2	5.2	4.6	7.4	9.8	9.8	8511600
7.5	8.7	8.7	8.7	7.2	8.7	7.6	7.6	7492100
25.8	25.8	25.8	25.8	25.8	25.8	25.8	25.8	1290300
28.9	32.6	31.9	32.3	27.8	30.9	35.4	35.3	55681000
33.4	24.4	27.4	35.8	35.8	27.4	30.1	27.4	18586000
9.4	9.4	9.4	9.4	9.4	9.4	9.4	9.4	2064400
6.4	8.9	7.4	7.3	7.8	12	8.8	6.9	1512000
60.3	60.3	60.3	49.3	49.1	47.8	46.1	49.8	3.06E+08
31.6	30.3	27.4	30.3	27.2	28.3	30.3	25	9767000
55.1	53.5	53	55.1	56.3	55.1	55.1	55.1	2.93E+08
73.8	78.8	77	75.8	76.2	75.5	78.8	54.8	7.39E+08
1.1	1.1	9.5	9.5	9.1	1.1	11.4	8.3	1457800
6.4	8.9	8.2	10.4	6.4	8.2	9	8.2	2944300
7.4	7.4	7.4	7.4	5.6	9	9.6	8.2	179150
42.5	45.1	42.5	40.7	38.1	40.5	44.2	43.9	1.82E+08
29.4	41.1	38.1	38.1	34.2	33.3	34.4	29.1	20034000
23	33	31.7	31.7	27.8	27	26.2	22.7	739340
61.8	59.7	61.8	61.4	61.6	63.1	61.4	64.4	1.59E+09
61.1	61.5	61.1	59.6	52	59.6	54	54.2	5.26E+08
5.7	5.7	2.4	2.4	0	9.1	9.1	9.1	4481200
0	0	0.8	0.8	0.9	3.5	1.8	4.2	1652400
7.2	8.3	4.2	3.9	7.2	7.2	8.3	8.3	3933100
1.1	1.1	1.1	1.1	1.1	1.1	0	0	401300
4.7	7.7	7.7	7.7	6.3	4.8	6.1	6.1	4242200
3.7	3.7	0	3.7	3.7	0	0	0	1017800
32.7	32.7	32.7	18.8	32.7	32.7	18.8	12.9	28881000
0	0	0	0	0	2.4	2.4	0	223630
5.9	5.9	16	0	5.9	16	16	16	2495700
12.2	16.9	16.9	16.9	16.9	16.9	18.1	12.6	7665800
19.9	19.9	19.9	15.4	15.4	20.7	16.7	16.7	3504000
32.8	32.8	32.8	32.8	32.8	35.7	32.8	33	28398000
3.1	7.5	7.5	4.4	7.5	6.2	7.5	3.1	5647000
44.9	50.2	49	47.8	52.4	44.2	47.8	46.1	1.03E+08
46	43.2	43.1	43.2	40.3	36.9	37.1	26.6	62583000

1.9	1.9	1.9	1.9	0	0	0	1.9	791950
1.1	1.4	0.5	0.5	0.5	0	0	0	509610
6.7	6.7	6.7	6.7	4.5	6	6	3.2	5097100
5.2	5.2	5.2	4.4	5.2	4.1	3.6	2.5	2585900
9.8	7.3	9.8	9.8	7.7	6.1	7.7	6.6	4050200
0	0	14.6	14.6	0	14.6	14.6	14.6	273480
7.1	14.1	9.4	7.1	7.1	11.8	14.1	11.2	7047800
5.4	5.4	5.4	5.4	5.4	3.6	0	3.6	1829900
9.9	9.9	9.9	9.5	9.9	9.5	9.5	9.9	55184000
0	0	0	0	0	2.5	1	3.7	631510
14.5	14.5	14.5	6	6	6	6	14.5	1731000
11.9	11.9	11.9	6.5	6.5	6.5	6.5	6.5	914190
11.1	11.1	11.1	7.4	9.2	9.2	6.9	9.2	4563200
23.3	23.7	24.2	22	17.6	23.2	23.2	23.5	67890000
4	2.1	2.1	4	3.3	8.4	6.8	5.2	1666000
1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1890600
3.1	3.1	3.1	3.1	6.7	5.1	0	8.7	1523600
28	28	28	28	15.6	28	29	32.2	31091000
5.3	3.8	2.6	3.8	3.8	5.3	5.3	6.1	2562400
1.2	3.1	4.4	3.1	3.1	1.9	0	0	1054600
2.9	0	7.9	7.9	5.5	13.2	13.2	13.2	3502700
9.6	9.6	9.6	9.6	9.6	9.6	6.8	9.6	19407000
2.1	2.8	7.9	10.6	6.5	12.6	12.6	10.6	4505600
15.7	16.9	19.5	21.8	14.6	24.5	24.5	38.3	12102000
10	6.7	15.9	19.9	17.9	21.4	25.6	18.9	13222000
4.2	4.2	4.2	4.2	6.7	2.3	0	1.8	1047900
21.1	28	22.3	19.6	19	42.2	42.2	42.2	1.38E+08
15.3	7.2	16.8	19.8	14.7	28.4	28.4	32.9	11547000
11	9.4	11	11	11	7.7	4.7	6.3	6018800
9.5	9.5	9.5	5.8	5.8	8.2	7	4.4	2092500
22.1	22.1	19.9	19.9	19.9	19.9	20.7	22.2	30014000
10.1	8.2	8.2	8.2	8.2	6	8.2	8.2	1818100
7.6	13.3	0	7.6	0	20.3	20.3	20.3	1158200
5.6	4.1	5.6	6.8	6.8	5.6	2.3	4.1	5955200
2.9	0	2.9	2.9	2.9	0	0	0	506270
3.7	6.5	3.7	3.7	3.7	6.5	8.8	5.1	1295900
0	0	2.7	2.7	0	5.4	10.8	7.6	3570300
0	20	20	20	20	20	20	20	385110
12.1	12.1	12.1	12.1	12.1	12.6	14.9	14.9	9720700
8.8	8.8	8.8	8.8	3.5	8.8	8.8	8.8	3085600
4.3	9.4	9.4	9.4	4.3	9.4	0	4.3	1391000
1.5	5.3	1.5	1.5	2.2	0	0	0	552570
2.5	2.5	2.5	2.5	2.5	2.5	2.5	0	1003000
10.3	13.3	10.3	10.3	13.3	10.3	13.3	10.3	7597800
9.4	9.4	9.4	9.4	9.4	9.4	0	0	612090
8.6	6.7	8.6	8.6	8.6	8.6	8.6	8.6	32971000
4.1	4.1	4.1	4.1	0	4.1	4.1	4.1	5772500
17.9	17.9	17.9	8.2	8.2	17.9	17.9	9.7	931300
17.4	7.8	17.4	17.4	17.4	17.4	17.4	17.4	24398000
3.9	3.9	7.5	14.1	11.1	14.1	14.1	14.1	3323800

9	9	9	9	6.3	5.2	6.3	6.3	2545000
8	6	4	4	9.8	4	0	2	1298400
0	2.5	2.5	2.5	0	2.5	0	2.5	188510
5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	3292400
8	4.8	8	8	8	8	8	8	3093300
12.2	10.9	15	16	13.5	15	12.8	16	10358000
8.1	13.8	18.1	25.7	25.7	25.7	35.2	39	10738000
65.7	65.7	59.2	59.2	53.6	59.2	55.9	62.7	2.96E+08
19.2	19.2	14.7	19.2	14.7	15.1	15.1	4.5	3686600
0	0	0	0	0	11.2	11.2	11.2	625810
0	0	0	0	0	0	0	3.3	66671
19.2	19.2	19.2	19.2	38.5	19.2	19.2	19.2	1123800
6.7	6.7	6.6	3	6.6	6.2	1.6	5.7	3386600
0	0	0	0	0	6.9	6.9	0	233430
0	0	0	6.7	0	6.7	6.7	14.4	1264200
20.4	22	15.2	11.2	9.3	16.4	21.4	22	28523000
8.4	5.5	6.7	5	5	3.3	3.8	8.4	5580200
4.8	7.5	8.6	9.2	11	6.5	6.5	3.9	4538600
0	0	0	0	6.3	0	0	0	50231
3.4	6.5	6.5	3.4	3.4	6.5	3.4	3.4	1765900
0	1.4	3.1	1.4	3.5	0	0	0	308650
18.3	18.3	18.3	18.3	18.3	18.3	18.3	18.3	3028300
26.2	26.2	26.2	26.2	26.2	26.2	26.2	26.2	5918700
16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	4531000
18.4	18.4	18.4	0	18.4	0	0	0	423540
22.2	26.5	26.5	26.5	16.8	26.5	26.5	17.3	4337000
5	2.6	2.6	2.6	5	5	5	5	1364400
19.7	19.7	19.7	19.7	19.7	19.7	32.8	19.7	4681900
5.5	4	7.8	7.8	3.9	6.3	3.9	4	4332400
15.5	12.3	12.3	15.5	15.5	12.3	12.3	7.9	2383100
13.1	13.1	13.1	13.1	13.1	13.1	13.1	8.3	2861800
0	0	6.6	6.6	0	6.6	6.6	6.6	388910
11.1	11.1	11.1	11.1	11.1	11.1	11.1	8.3	2770000
0	0	4.3	7	7	11.3	11.3	11.3	984070
5.3	6.8	5.3	5.3	4.1	6.9	8.6	9.7	5227700
0	5.8	5.8	0	5.8	5.8	5.8	5.8	376340
9.7	6.3	9.7	9.7	6.3	9.7	6.3	2.5	2747300
3	3	3	3	3	3	3	3	850890
0	5.4	5.4	5.4	5.4	0	5.4	5.4	702880
18.6	18.6	18.6	18.6	18.6	18.6	0	0	942180
7.8	11.3	7.8	11.3	0	11.3	11.3	11.3	1155100
11.3	24.2	24.2	24.2	24.2	24.2	0	11.3	1216900
25	21.6	18.5	18.1	14.7	16.8	21.6	11.2	7449000
17.1	17.1	17.1	17.1	17.1	17.1	0	17.1	579220
24.8	27.3	22.8	24.9	24.8	24.9	16.3	16.5	36673000
18.2	18.2	18.2	18.2	18.2	18.2	18.2	18.2	2371700
13.3	18.1	13.3	18.1	13.3	18.1	13.3	13.3	1735700
0	0	0	0	0	0.6	0.6	0	242270
0	6.3	10.1	10.4	23.1	27.2	37.3	45.1	6412600
0	3.2	3.2	3.2	3.2	5.6	9.3	9.3	1325600

23.7	23.7	23.7	23.7	23.7	7.6	23.7	0	947520
3	0	0	3	0	3	3	3	380710
10.7	10.7	10.7	10.7	10.7	13.4	13.4	13.4	23884000
2	2	2	2	2	2	2	2	631180
21.3	21.3	21.3	21.3	5.4	21.3	21.3	21.3	6206800
9.3	9.3	9.3	9.3	3.3	12.5	12.5	3.5	1873800
10.2	10.2	10.2	10.2	8.1	10.2	6.1	7.4	3483600
7.3	19.5	15.2	9.9	13.9	15.2	19.5	22.1	4097700
11.8	11.8	12.2	8.4	5.6	8.4	11.8	8.4	242070
8.6	16.4	8.6	8.6	8.6	8.6	16.4	16.4	2817900
4.8	7.3	7.3	7.3	7.3	4.8	4.8	4.8	1621900
26.3	26.3	0	0	0	14.7	14.7	14.7	1944700
13.7	11.1	16.2	16.2	13.7	13.1	10.2	10.8	5193200
7	7	7	7	7	7	7	7	1342200
22.7	22.7	22.7	22.7	11.3	22.7	22.7	22.7	1998100
25	25	25	25	0	25	25	25	1163900
65.5	65.5	65.5	65.5	65.5	65.5	65.5	65.5	22516000
14.2	10.7	5.8	14.2	10.7	17.2	9.4	14.2	2556100
39.6	32.1	27.1	39.6	26	39.3	27.1	29.9	30797000
16.6	17.9	16.6	16.6	12.5	17.9	12.2	13.5	11113000
0	10.7	0	0	0	0	10.7	10.7	260270
1.3	1.3	1.3	1.3	1.3	0	0	1.3	439190
16	16	16	16	7.7	16	16	16	4410800
5.1	5.1	9.5	9.5	9.9	3.6	3.6	3.6	3743100
9.4	7	9.4	3.3	5.3	4.7	2.2	10.8	2667400
0	0	0	0	0	2.5	8.5	8.5	632460
20.9	18	20.9	20.9	18	20.9	20.9	20.9	5538000
2.4	2.4	2.4	2.4	2.4	2.2	4.6	2.4	693760
14.3	14.3	14.3	14.3	14.3	14.3	14.3	14.3	5559400
15.9	9	20.8	21.8	19.4	30.3	34.7	34	28228000
4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	6675500
4.6	4.6	4.6	2.7	2.7	2.7	1.6	2.7	2341700
6.1	6.1	6.1	6.1	6.1	6.1	6.1	11.3	879870
25.3	25.3	25.3	33.6	33.6	21.7	25.3	25.3	6062900
10.9	10.9	16.3	16.3	10.9	16.3	10.9	11.7	3538900
0	3.2	3.2	3.2	3.2	3.2	0	0	345470
17.3	17.3	17.3	17.3	17.3	17.3	17.3	0	1251100
16	7.7	7	10.2	7	15.3	22.3	15.3	7591600
8.6	8.6	0	2.6	2.6	8.6	8.6	2.6	741480
11.2	15	14.4	13.5	12	15.7	13.6	15.2	23702000
7.8	7.8	7.8	4.9	7.8	7.8	4.9	4.9	1547300
24.8	23.4	33.8	14.5	14.5	24.8	14.5	24.8	3563100
6	6	6	6	6	0	0	6	1858200
22.6	22.6	22.6	22.6	15.8	22.6	22.6	22.6	1148800
26.8	27.4	26.1	25.6	20	26.5	27.1	26.8	97891000
8	8	0	8	8	8	0	8	583370
51.7	43.4	38.6	43.4	35.9	43.4	54.5	46.9	72637000
1.8	3	3	1.8	3	1.8	0	1.2	788890
50.3	60.5	44.1	44.1	28.2	50.3	60.5	60.5	43159000
6.7	6.7	5.3	4.4	3.3	5.8	6.7	6.4	6908800

5.6	6	5.2	5.2	5.2	5.6	5.6	5.2	6188400
4.7	4.7	3.1	3.1	3.7	4.7	4	4	10237000
49.7	46.6	38.7	35.8	36.4	44.1	44.6	44.7	5.43E+08
0	0	32.7	51.9	51.9	51.9	51.9	51.9	2239700
30.4	30.4	30.7	34	25.6	35.2	35.2	35.2	36064000
0	0	0	0	0	7.8	7.8	7.8	664100
4.6	4.6	4.6	4.6	4.6	0	2.1	2.4	1112200
14.1	11.9	11.4	13.8	6.1	11.6	12.5	8.5	11177000
5.4	4.4	3.3	2.1	0	3.3	4.4	3.2	1333300
2.8	2.8	1.2	1.9	3.7	2.1	1.2	1.2	2084700
16.8	7.9	12.9	19.3	15.3	23.3	23.3	23.3	16093000
8.8	8.8	8.8	6	6.7	8.8	6.9	6	3401700
6	6	6	6	6	6	6	6	931080
12.9	12.9	12.9	12.9	12.9	12.9	0	0	579440
14.7	14.7	0	0	0	0	14.7	0	422290
6.8	6.8	6.8	6.8	6.8	6.8	6.8	13.7	1306300
13.1	13.1	13.1	13.1	13.1	5.2	0	7.9	1082800
0	1.8	4.4	4.4	0	0	0	4.4	645280
4.9	4.9	4.9	4.9	4.9	4.9	0	0	946160
4.9	4.9	4.9	4.9	0	4.9	4.9	4.9	658460
23.4	23.4	23.4	23.4	16.5	21.9	21.9	20.9	11169000
0	0	0	0	0	2.2	2.2	0	137130
5	2.1	7.1	7.1	7.1	4.8	2.1	2.7	1351500
8.3	6.4	6.9	6.9	6.9	3.4	4.7	6.4	4357500
7.7	0	7.7	7.7	0	7.7	16.7	16.7	680980
20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	5865000
0	0	0	1.2	1.2	0	0	1.2	497000
8.1	0	0	0	0	8.1	0	0	213880
22.6	22.6	13	22.6	22.6	22.6	22.6	13	7858600
0	0	0	0	11.5	15.8	15.8	10.4	1883300
15.1	6.4	15.1	15.1	15.1	0	6.4	0	1340900
37.8	39.8	42.5	42.3	39.8	40.6	40.2	42.6	3.65E+08
2.7	0	2.7	0	0	0	2.7	2.7	403300
11.3	14.9	14.9	11.3	14.9	11.3	11.3	11.3	2754100
29	29	21.9	17.7	13.7	24.9	28.1	27.8	82941000
28.2	28.2	21.2	17.1	13.1	24.1	27.2	26.9	2526700
7.1	7.1	7.1	7.1	7.1	7.1	5.1	5.1	1653900
20	20	20	20	9.1	18.1	13.9	16.5	25410000
11.8	11.8	11.8	9.1	11.8	11.8	11.8	8.2	5320100
32	32	32	32	26.5	32	32	32	30288000
2.4	2.4	2.4	2.4	2.4	2.4	2.4	0	1126800
18.2	25.8	25.8	25.8	18.2	25.8	25.8	25.8	8934900
1.4	0	0	3.7	0	4.6	4.6	4.6	1868400
5.7	5.7	5.7	3.2	7.1	4.1	0	1.6	1636300
7.7	7.9	9.8	9.8	5.1	18.7	16.9	20.2	9591600
0	0	0	2.3	0	2.3	2.3	2.3	279660
1.2	1.2	1.2	1.2	1.2	0	0	0	1495100
5.5	5.5	5.5	5.5	5.5	4.7	5.5	4.7	8020200
0	0	0	0	28.9	0	13.3	23.3	2292800
22.9	27.8	23.1	16.6	17.4	30.6	30.6	32.1	24296000

29.3	21.4	29.3	29.3	16.4	29.3	29.3	29.3	6626200
2	1.6	1.6	1.6	1.6	3.6	1.6	6	663480
0	0	11.4	14.6	16.5	19.7	24.3	24.3	4753200
10.3	10.3	10.3	10.3	10.3	10.3	10.3	0	690480
0	0	0	4.6	4.6	21.1	21.1	21.1	1186600
4.1	4.1	1.4	4.1	4.1	4.1	5.4	7	2208300
0	0	20.4	20.4	20.4	20.4	20.4	20.4	520980
0	11.6	11.6	0	11.6	11.6	11.6	11.6	800320
4.6	6.5	6.5	3	4.6	4.6	6.5	6.5	1966400
7.3	10.9	10.9	10.9	10.9	16.9	13.3	9.7	4202100
22.2	20.8	25.5	23.3	24.5	20.3	19	23.8	1.09E+08
9.2	8.2	9.9	8.5	7.7	6.7	3.1	4.9	4331900
7	5.8	5.2	5.2	5.2	6.6	5.8	4.6	4520800
3.4	4.3	4.3	4.2	3.6	4.2	1.9	2.7	3044900
11.7	10.2	12.7	11.8	10.9	11.7	11.2	11.2	13829000
4.4	4.6	4.3	4.3	3.6	5.3	3.4	3	3268600
4.6	3.5	4.5	3.5	2.9	5.4	3.2	4.9	6881800
2.4	4.8	4.8	4.8	5.7	4.8	4.8	3.9	2722800
3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	924110
4.4	4.4	4.4	4.4	4.4	2	0	4.4	930090
12.4	12.4	12.4	12.4	12.4	12.4	9.6	9.6	6258000
13.4	13.4	8.9	9.8	7.5	13.4	13.4	13.4	16831000
3.4	2.9	3.4	2.5	3.4	2.3	2.2	1.2	4354000
6.5	6.5	6.5	9.2	4.6	6.5	6.5	6.5	3371500
2.5	3.3	2.8	2	2	2.8	0	0	2127700
0	0	0	0	0	0	1.6	1.6	162200
15.3	11.1	11.1	13.2	13.2	15.3	7.3	7.2	6534700
11	22.8	22.8	11.8	16.5	22.8	56.7	38.6	5423200
0	0	8.2	0	11.5	11.9	11.9	11.9	1513800
2.3	2.3	2.3	2.3	2.3	2.3	0	2.3	540990
29.3	36.4	42.3	39.8	42.6	42.3	42.3	39.8	63787000
6.1	6.1	0	3.9	6.1	0	3.9	3.9	1083100
2.7	1.3	6.2	2.7	4.4	2.7	2.7	4.2	4548600
1.5	2.7	4	5.6	4	4	1.5	1.5	2036000
0	0	0	0	1.9	0	0	0	389110
9.5	12.8	13.2	11.5	9.6	13.2	6.8	15	8019600
0	0	0.7	0.7	0	0	0	0	51649
3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	1574300
0	1.8	1.8	1.8	0	1.8	1.8	1.8	340350
0	14.7	14.7	14.7	0	14.7	0	0	566490
15.2	16.5	19.4	19.4	14.8	16.8	19.4	15.5	21823000
22.1	23.8	23.8	20.8	16.4	20.8	23.8	23.8	23070000
2.4	2.4	1.4	2.4	2.4	1.4	1.4	1.4	874330
24.9	23.8	24.6	25.7	21.5	23.6	25.2	29.2	49501000
3.8	3.8	5.2	5.2	5.2	5.2	1.6	3.8	3079100
21.1	24.1	19.7	22.1	23.7	23.4	30.7	24.8	85732000
0	0	0	0	0	0	11.4	0	167920
33.7	36.4	38.8	38.8	39.5	38.8	38.8	38.8	2.19E+08
5.3	5.3	5.3	5.3	5.3	5.3	0	0	696850
10.5	10.5	7.9	10.5	2.6	10.5	10.5	3.7	1678100

20.1	20.1	24.3	20.1	24.3	20.1	24.3	14.2	5376900
9.6	9.6	14.1	14.1	14.1	14.1	9.6	5.5	1803000
21.4	21.4	10	16.1	19.2	16.1	16.1	21.4	3839500
6.3	5.5	6.1	5.7	7.4	6.9	5.9	7.5	10354000
0	20	0	20	0	20	20	20	537250
5.9	25	17.1	17.1	17.1	34.2	40.8	31.6	486650
12.7	32.5	20.9	24.3	24.3	36	45.9	36.3	29044000
23.2	23.2	23.2	14.1	14.1	23.2	23.2	23.2	13501000
20.1	6.5	19.8	23.7	19.8	23.7	23.7	19.8	3849800
0	0	0	0	2.2	4.4	4.4	2.2	607260
8.3	8.3	8.3	8.3	8.3	8.3	8.3	8.3	411800
9.5	0	9.5	9.5	0	9.5	9.5	9.5	750540
17.5	17.5	17.5	17.5	17.5	12.3	11.7	11.7	5826100
14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	2994400
33.7	33.3	33.3	33.3	37.3	33.3	30.8	37.3	7653300
5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.3	1074700
13.9	13.9	0	0	0	0	0	13.9	418610
11.6	11.6	11.6	11.6	0	0	0	0	212750
26.7	26.4	24.4	24.4	18.7	23.5	23	26.7	33205000
0	0	11.7	0	11.7	11.7	0	11.7	810790
13	13	11	6.8	8.6	11	13	10.6	2511500
0	0	2.3	2.3	2.3	0	0	0	306620
7.4	7.4	7.4	3	3	5.6	4.4	7.4	1940000
17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	860420
5.8	5.8	5.8	5.8	0	5.8	5.8	5.8	727740
2.8	0	0	2.8	2.8	10.7	10.7	10.7	1849600
8.2	8.2	23.1	23.1	19.8	20.7	38.6	38	15999000
4.2	4.2	4.2	4.2	4.2	7.5	4.2	4.2	575470
4.6	1.7	4.6	4.6	4.6	4.6	2.9	2.9	1331900
78.1	78.1	78.1	52.4	43.8	78.1	78.1	78.1	1574700
60	60	58.2	41.8	41.8	58.2	60	70.9	4.1E+08
41.2	44.9	38	41.2	19.9	36.1	39.8	38.9	73943000
6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	1150000
0	0	4.3	4.3	21.7	0	0	3.4	1862000
0	13	13	13	25	25	40.7	40.7	7712000
9.9	9.9	18.3	18.3	18.3	18.3	18.3	18.3	5847700
0	0	4.9	4.9	0	14.7	14.7	14.7	1858800
11.5	18.7	13.7	23.3	23.3	24.4	30.1	26.6	11753000
6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.2	1390200
10.2	0	0	8.4	10.2	8.4	10.2	10.2	724870
0	0	0	0	0	0	0	2.8	70840
23.3	23.3	23.3	23.3	10.6	23.3	23.3	23.3	3949600
2.2	0	0	2.2	2.2	2.2	0	2.2	226320
7.8	11.1	26.5	24.9	19.7	23.2	26.5	21.6	8318800
6.5	4.5	3.8	2.1	1.7	1.7	4.5	1.7	1883600
55.3	55.3	46.2	49.7	49.7	60.8	72.9	66.8	1.42E+08
24.7	24.7	28.8	24.7	28.8	32.3	53.5	49.5	10840000
50.9	46.1	40.6	21.8	32.1	42.1	46.1	43.9	17370000
48.1	48.1	48.1	48.1	38.3	48.1	48.1	48.1	30821000
29.5	33	36.2	36.2	36.2	40.2	40.2	36.2	27706000



28.2	28.2	28.2	28.2	28.2	28.2	28.2	0	983890
0	2.5	2.5	0	0	0	0	0	135400
2.7	6.3	2.7	6.3	6.3	2.7	0	2.7	648700
30.7	28.7	32.2	30.7	26.6	28.7	24.3	27.3	30059000
4.6	4.6	4.6	4.6	0	4.6	0	4.6	286520
5.3	9.6	8.9	5.4	13.5	7	7.7	6	2875900
38.2	38.2	38.2	38.2	38.2	38.2	0	0	5338900
26.4	26.4	26.4	11.8	11.8	26.4	26.4	26.4	2057700
2	3.8	3.8	2	3.8	2	4.4	6.2	1378800
5.3	5.3	3.4	3.4	6.6	13.6	15.1	14.9	4117800
0	0.7	1.4	1.4	1.4	0.7	0.7	1.4	673900
20.2	20.5	15.8	15.8	15.8	22.4	22.4	19.9	46354000
4.3	4.3	4.3	4.3	4.3	4.3	0	4.3	563900
0	0	17.6	8	22.5	22.5	54.5	54.5	8539500
14.3	14.3	14.3	0	14.3	0	0	14.3	1103800
7.7	7.7	7.7	7.7	13.3	13.3	16.6	16.2	2426700
4.5	4.2	8.3	10.3	8	10.3	12.5	12.5	2711700
4	4	0	4	0	4	4	4	981490
8.3	8.3	8.3	8.3	7.8	8.3	8.3	6.1	2802500
0	0	5.5	4.6	5.5	11	15.5	13.5	2834500
0	0	8.2	8.2	8.2	8.2	8.2	8.2	1001000
38.3	47.8	43.4	38.8	38.6	47.6	49.9	47.6	49671000
26.8	22.8	31.1	31.1	31.1	37.4	40.6	49.2	46206000
4.5	2.4	2.4	2.4	2.4	4.5	0	4.5	801620
4.2	4.2	7.4	7.4	3.2	4.2	4.2	4.2	1301300
0	8	8	0	0	8	8	8	393430
5.7	5.7	8.4	14.9	6.2	18.1	26.5	23.8	6609300
0	0	0	7	7	7	7	7	395890
6.1	6.1	6.1	6.1	6.1	6.1	6.1	3.8	4104500
0	0	0	0	0	0	0	3.1	435090
3.3	5.2	5.2	3.3	0	0	5.2	5.2	817320
2.4	2.4	2.4	2.4	3.7	2.4	3.7	1.3	709190
6.5	14.9	14.9	14.9	12.3	10.2	12.2	10.7	7686600
3.8	3.8	3.8	3.8	3.8	2.8	2.4	0.9	1898800
8.9	10.2	20.9	23.7	23.7	26	30.8	37.4	25209000
8.4	8.4	6	13	2.4	18.8	18.8	16.4	9447200
13.6	12.9	19.5	23.3	15.3	31.7	33.3	36.7	31498000
10.2	9.6	9.6	13.3	13.3	26.4	27.1	24.8	9969300
8.8	9.8	14.9	16.6	12.7	16.6	16.6	16.6	4092800
0	0	0	0	0	0	14.4	14.4	278780
3.5	3.5	3.5	3.5	3.5	3.5	3.5	3.5	889960
23.7	24.2	24.3	21.6	19	20.5	20.8	20.9	1.39E+08
2.2	0	7.5	7.5	7.5	2.2	7.5	7.5	1452600
0.8	0.8	0.8	0.8	0.8	0.8	0	0	379040
4.6	4.1	4.6	4.1	3.4	4.1	3.8	3.9	3176600
17.6	18.2	15.3	14.3	15.5	16.6	19.1	17.9	39277000
2.1	2.1	2.1	2.1	2.1	0	0	0	467170
25.3	36.2	18.8	21.9	18.3	34.8	34.8	38.8	39022000
19.4	23.8	20.8	23.8	15.5	23.8	30.7	27.4	14542000
6.3	6.1	20.8	20.8	17	20.2	20.2	17	5731700

29.6	31.1	23.6	24.2	18.9	25.8	32.5	32.2	40955000
3.7	3.7	3.7	9.1	9.1	9.1	9.1	9.1	1742600
7.8	10.2	6.3	8.8	6.3	11.7	13.7	11.7	1804000
0	0	0	0	0	6.6	3.1	6.6	409640
3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	1098800
6.2	3.2	3.2	3	3	6.2	6.2	6.2	580050
21	24.4	26.2	22.8	17.9	22.8	22.3	20.3	38498000
18.2	17	17	17	14	13.8	13.5	11.7	8365200
12.4	9.7	12.4	12.4	8.9	12.4	3.5	9.7	2122800
18.2	21.3	21.3	17.5	8.2	25	28.8	28.8	34937000
19.5	19.5	13.3	9	6.8	14.4	21.2	16	5686400
4.5	3.3	3.3	1.3	2.4	1.3	1.3	3.3	1511000
6.9	6.9	6.9	6.9	6.9	6.9	0	0	932480
0	0	0	9.4	9.4	9.4	9.4	9.4	533400
0	0	0	0	0	0	9.1	0	0
0	0	0	0	0	8.8	8.8	0	282780
52.7	57.1	54.5	52.1	51.8	56	57.1	58.6	2.5E+08
15.5	21.8	21.8	21.8	24.8	21.8	26.6	29.6	24315000
2	2	1	1	2	2	2	2	1102100
4.4	8	4.4	5.8	5.8	4.6	5.5	7	3970500
6.3	6.6	6.3	5.1	3.8	6.9	6.8	6.8	11193000
0	3.8	3.8	0	3.8	3.8	0	3.8	305710
7.2	7.2	7.2	7.2	4.7	7.2	8.7	6	4606800
4.9	0	0	0	0	4.9	4.9	4.9	246830
3.7	2.6	3.7	3.7	6.3	2.6	3.7	2.6	2389300
8.3	11.1	13	14.6	14.6	11.1	9.9	7.3	10945000
7.7	7.7	1.6	0	0	7.7	7.7	7.7	2342700
10	8.7	8.6	8.3	6.9	10	7.3	6.6	7861400
3.8	0	3.8	3.8	0	3.8	3.8	3.8	504570
15.1	13.3	19.7	20.8	17.2	15.9	16.3	14.3	19692000
7	7	7	7	7	7	7	7	1.96E+08
28.5	30	25.5	23	21.8	29.8	31.4	33.1	36487000
4.4	6.3	10.5	8.8	10.5	9.2	10.5	7.5	6886600
3.2	5.5	3.2	5.5	2.3	0	0	0	708550
8.2	7.2	4.1	1.8	1.9	6.6	7.2	6.3	3009800
7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	1942000
26.2	25.1	16.9	20.7	15.3	25.2	28	26.2	17250000
0	7.6	7.6	7.6	7.6	7.6	7.6	7.6	1010600
7.2	5	7.2	7.2	5	7.2	7.2	7.2	2317200
2.3	2.3	4.6	2.3	4.6	2.3	0	0	1104200
2.4	3.3	2.4	0.9	3.3	2.4	0.9	2.4	758930
0	0	0	0	2.8	0	0	0	630090
18.2	18.2	18.2	18.2	18.2	18.2	18.2	18.2	1220300
3	1.4	3	3	3	3	0	1.7	944460
8.6	14.7	14.7	16.9	14.1	11.4	14.1	15	6092500
14	11.6	11.6	14	12.5	12.7	10	8.4	10737000
6.1	4.5	6.1	7.6	6.1	6.1	2.1	4.5	4590800
3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	1435000
13	10.8	10.7	10.8	6.5	9.5	11.7	9.5	10548000
59.3	59.3	59.3	69.3	63.6	70	60	60	1.63E+08

6.5	8.2	8.1	8.1	6.5	9.2	8.2	8.8	6695400
0	0	0	0	0	0	0	4.6	295450
0	19	8.3	0	0	19	19	19	1054000
48.2	44.5	44.5	46	38.6	47.8	47.8	44.5	80336000
41.8	47.5	45.2	43.1	29.1	32.8	51.2	46.2	64651000
23	13	38.3	30.3	33.3	31	33.3	38.3	21763000
19	23.4	18.3	18.8	10.7	35	45.2	41.1	24992000
14.3	11.8	12	12.4	9.3	7.6	7.6	7.6	7880500
4.9	4.5	2.3	2.3	2.3	2.3	0	4.9	1204500
4.1	2.4	4.1	2.4	2.4	4.1	5.9	4.1	1393900
10.4	10.4	7.4	5.9	5.7	5.7	14.2	14.2	5297400
11.8	11.8	11.8	11.8	6.6	11.8	5.3	11.8	21095000
19.2	19.2	19.2	19.2	5.3	19.2	19.2	19.2	4980400
33.5	24.4	0	7.9	7.9	18.9	29.3	15.2	12789000
1.6	2.7	2.7	1.6	1.6	2.7	2.7	1.6	1047000
6.3	0	17.9	3.7	10	21.3	28.9	21.9	2977900
8.8	8.8	8.8	3.9	3.9	3.9	3.9	8.8	1661800
0	0	20.2	15.5	10.7	20.2	23.2	18.5	3596300
3.9	0	3.9	7.9	3.9	7.9	3.9	3.9	1557300
0	0	0	0	0	22.9	14.5	22.9	2001200
0	11.2	11.2	11.2	0	11.2	11.2	11.2	495850
0	12.8	17.1	0	0	17.1	17.1	12.8	2519400
26.4	22.7	22.7	22.7	19.1	26.4	35	35	6916700
11.8	26.1	36.9	31	31	36.9	41.9	36.9	11676000
17.9	23.6	23.6	19	16	23.6	39.9	39.9	10341000
0	0	4.8	4.8	8.5	12.5	8.9	12.5	3052000
25.3	30.3	19.9	15.8	29.5	28.6	43.6	42.7	13224000
31	25	31	25.4	16.9	31	51.6	48.4	14539000
0	0	3.6	3.6	0	7.6	12.7	3.6	855830
0	0	7.6	7.6	0	7.6	7.6	7.6	572520
27	27	30.7	27	21.2	30.7	30.7	24.9	10628000
0	0	0	0	0	9	9	9	1257700
8.4	21.5	21.5	21.5	8.4	21.5	8.4	21.5	2565100
0	0	7.6	7.6	7.6	7.6	7.6	8.3	1694500
13.7	8	8	12.9	13.7	28.9	28.9	28.5	4315100
13	8.8	13	13	8.8	13	13	13	5643300
3.2	3.2	3.2	3.2	3.2	6.9	6.9	3.2	1531000
0	0	0	0	0	0.8	0.8	1.4	955020
3	0	8.9	3	11.4	5.5	8.9	3	1256400
21	23.2	24.1	21	24.1	31.7	18.7	27.5	8600700
10.4	10.4	10.4	10.4	7.2	10.4	10.4	7.2	1499800
0	0	0	0	1.2	1.2	1.2	1.2	264330
7.6	0	7.6	7.6	7.6	7.6	13.9	7.6	829540
18.3	12.5	12.5	17.5	14.1	12.5	18.3	23.2	6889100
19.5	10.2	19.5	19.5	10.2	19.5	10.2	19.5	1427600
0	0	25.8	48.8	48.8	48.8	48.8	48.8	5168700
14.6	14.6	14.6	14.6	0	14.6	14.6	14.6	3449300
0	0	10.4	10.4	10.4	10.4	10.4	10.4	912490
29.6	29.6	29.6	34.4	29.6	34.4	38.1	38.1	14085000
12.8	12	15.5	15.5	9.3	15.5	15.5	15.5	10303000

0	1.8	1.3	1.1	4	5.1	5.6	5.9	4302300
36.8	36.8	32.1	35.2	22	35.2	30.5	28.7	1.08E+08
42	42	37.2	37	33.1	41.6	46.5	44.8	1.91E+08
23.6	20.2	23.4	24.5	21.1	17.4	20.8	16.3	31065000
29.3	22	28.4	25.6	25.2	24.5	24.5	21.7	84720000
12.5	0	12.5	12.5	12.5	0	0	0	515750
1.7	1.7	2.9	2.9	2.3	0.6	1.1	1.1	2390900
17.8	15.7	16.3	17.8	13.7	14.7	16.3	10.4	21658000
12.3	0	12.3	12.3	12.3	0	0	0	502000
1.8	1.8	1.8	2.8	1.8	1.8	1.8	1.8	2697500
21.5	21.5	19.4	19.4	19.4	19.4	19.4	21.5	6954000
11	11	0	11	11	0	11	11	7510000
12.8	24.7	21.1	12.8	20.7	24.7	21.1	19.8	7782200
0	4	13	0	4	13	13	13	2107700
25.1	26.4	23.9	24.3	22.9	25.4	19.8	17.3	32733000
4.2	4.2	0	0	0	4.2	4.2	4.2	568520
7.6	7.6	3.6	7.6	7.6	7.6	11.8	11.8	1418700
2.1	1.2	2.1	1	1.2	1	1	1	833300
0	0	1.9	1.9	0	0	0	0	423070
6.6	0	0	0	6.6	6.6	6.6	0	376210
2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.8	1529900
3.5	0	0	0	3.5	6	6	6	606390
3.4	6.5	6.5	6.5	3.4	6.5	6.5	6.5	2148800
2.3	2.3	2.3	2.3	2.3	0	0	0	2166500
14.2	14.2	14.2	14.2	14.2	13.2	13.2	13.2	4749200
0	0	0	7.5	13.3	0	7.5	13.3	630870
2.6	10.8	10.8	10.8	10.8	10.8	10.8	10.8	1017700
6.7	9.8	11.7	11.7	9.6	11.7	8.6	9.8	9725600
30.4	30.4	19.6	19.6	30.4	30.4	30.4	10.8	5459900
8	0	0	0	8	0	0	8	270620
6.2	6.2	6.2	6.2	6.2	6.2	0	6.2	2756600
20.1	17.8	22.3	17.8	14	30.5	39.6	39.6	10972000
0	1.1	1.5	2.7	1.5	5.2	5.2	5.2	2771100
0	7.7	2.8	4.9	0	4.9	7.7	0	945620
4	4	4	4	4	4	4	4	1681200
17	0	17	17	17	17	17	17	1914800
0	0	0	0	0	0	6.9	6.9	1088700
2	2	2	4.9	4	12.1	14.3	7.1	3312300
19.5	20.5	18.2	20.5	24.5	18.2	18.9	18.6	13174000
0.6	0	0.6	0	0	1.3	1.3	0.6	400360
12.8	10.3	11.1	11.1	12.8	15.7	15.7	17.8	5256800
11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.4	3210400
2.8	2.8	2.2	4	4.8	2.2	2.2	2.8	3682100
9.4	9.4	9.4	17.6	17.6	17.6	17.6	17.6	25104000
17.5	35.1	17.5	17.5	17.5	17.5	35.1	35.1	27511000
34.3	34.3	34.3	34.3	23.8	34.3	34.3	34.3	65928000
0	0	0	11.2	0	11.2	11.2	11.2	810730
54.8	65.4	65.4	44.2	14.4	54.8	65.4	54.8	8085700
11.7	22.3	22.3	22.3	10.7	22.3	22.3	22.3	4148900
27.6	27.6	27.6	17.3	17.3	26.5	27.6	27.6	28664000

10.5	10.5	10.5	10.5	6.8	10.5	10.5	10.5	1311200
23.3	19.9	15.2	23.3	23.3	23.3	19.9	23.3	7780400
5.1	0	11.6	19.9	19.9	29.2	30.7	29.2	32131000
3	2.4	3.1	3.7	3	1	1	2.7	2440100
7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.9	563830
7.7	10.6	10.6	7.7	7.7	7.7	7.7	7.7	2556300
22.5	13.9	22.5	16.8	22.5	16.8	25.4	25.4	6670500
2.7	1.4	2.7	2.7	2.7	2.7	2.7	1.2	1023300
0	1.5	1.5	0	1.5	1.5	1.5	1.5	324220
8.5	8.5	8.5	8.5	8.5	6.2	8.5	8.5	11893000
37.5	37.5	37.5	37.5	37.5	26	26	26	18401000
17.6	17.6	17.6	17.6	17.6	17.6	0	0	4299900
2.7	2.7	0	0	0	0	2.7	2.7	551070
19	19	19	19	19	19	19	19	1601500
0	4.7	0	0	4.7	4.7	4.7	4.7	704950
16.5	16.5	16.5	20.4	23.5	23.5	23.5	23.5	4239300
3	3	2.1	2.1	2.1	2.1	2.1	1.4	1388100
0	0	25.2	27.1	26.2	36.4	36.4	22.4	29695000
11.4	7.4	7.2	11.4	9.7	9.7	4.3	9.1	5457100
3.6	3.6	3.6	2.3	1.1	2.4	1.2	1.1	1031200
0	0	6.2	12.1	6.2	15.6	34.3	28.4	3598600
14.5	7.4	14.5	7.4	14.5	25.6	25.6	25.6	3949000
2.6	2.6	7.1	7.1	2.6	9.5	9.5	10.5	4958100
4.3	4.3	4.3	0	0	6.8	6.8	6.8	926820
0	0	0	0	0	6.4	6.4	6.4	547390
2.1	2.1	2.1	2.1	2.1	2.1	0	2.1	1012500
42.9	42.9	39.6	35.3	30.1	42.9	40.9	36.8	7.91E+08
14.2	18.9	18.9	18.9	15.2	18.9	22.8	22.8	1769900
6.1	6.5	6.5	6.5	4.4	6.5	9.9	9.9	498250
2.3	2.3	1.3	1.3	3.9	2.3	2.3	3.9	1404900
7.2	7.2	7.2	3.5	7.2	7.2	7.2	3.5	1357300
0	0	2.7	2.7	2.7	2.7	0	0	465650
2.5	0	0	0	2.5	0	0	1.3	115480
3.3	5.9	5.9	5.9	9.2	9.2	5.9	5.9	1603600
4.2	4.2	4.2	4.2	4.2	0	0	0	271190
8.3	8.3	0	0	8.3	8.3	0	0	126010
12.2	12.2	6.9	6.9	6.9	12.2	12.2	12.2	1812400
7.6	5.6	8.1	6.9	6.6	5.6	5.6	5.1	6997800
8.9	8.9	8.9	8.9	6.4	8.9	8.9	8.9	3846300
17	8.8	12.3	17	17	12.3	5.6	13.5	6861000
0	0	3.9	3.9	3.9	0	3.9	3.9	806170
54.2	59.3	52.5	52.4	54.8	59.3	64.2	71.2	6.43E+08
47.8	52.9	46.1	46	48.4	57.1	58.9	65.9	290240
18.4	13.9	26.5	22.9	15.1	33.5	31.2	30.8	18575000
7.9	7.9	7.9	7.9	7.9	5.4	5.4	7.9	3804300
42.2	42.2	42.2	41.6	23	42.2	42.2	42.2	9986300
25.3	25.3	25.3	25.3	25.3	25.3	25.3	25.3	1406200
13.1	13.1	15.5	16.7	12.9	18.1	17.5	17.2	24225000
22.5	22.5	22.5	27	22.5	27	27	27	13485000
0	11.2	9.9	12.2	8.8	15.2	26	23.2	12609000

17.1	17.1	19.8	21.5	16.1	28.1	27.7	28.5	49582000
0	0	7.6	7.6	0	7.6	7.6	11.2	607060
23.4	38	29.2	40.1	33.3	30.2	47.4	49.5	22027000
23.4	38	17.2	40.1	33.3	30.2	40.1	42.2	4104800
3.5	3.5	0	0	3.5	3.5	0	3.5	636850
27	27	30.5	30.5	30.5	30.5	30.5	30.5	17119000
44	45	48.2	44	30.7	47.2	50.9	47.2	38319000
72.6	72.6	72.6	22.8	53	61.9	68.8	68.8	40919000
39.8	37.4	46.6	30.6	29.1	39.8	30.6	46.6	11819000
59.5	53.7	59.5	59.5	56.1	55.6	59.5	59.5	75766000
50.7	50.7	50.7	50.7	54.7	46.8	50.7	43.3	8000900
23.6	23.6	23.6	16	23.6	16	16.9	23.6	7150300
8.9	8.9	8.9	8.9	8.9	5.2	8.9	5.2	556210
15.5	15.5	15.5	15.5	15.5	15.5	15.5	15.5	828410
37.7	37.7	32.1	25.9	27.4	32.1	32.5	29.2	20645000
24.9	29.3	29.3	29.3	29.3	29.3	24.9	15.6	6617400
15.7	15.7	8.1	8.1	0	15.7	7.6	15.7	4087500
5.2	0	5.2	5.2	5.2	5.2	0	5.2	352100
38.9	38.9	38.9	34.3	27.8	32.4	38.9	38.9	34666000
17.3	27.4	21.6	21.6	21.6	21.6	21.6	21.6	43434000
64.7	76.3	71.5	65.2	63.8	73.4	74.9	76.3	1.07E+08
10.8	10.3	10.3	10.3	10.8	10.3	10.3	10.3	625990
8.7	8.7	14.5	8.7	14.5	8.7	14.5	14.5	350430
12.9	18.4	18.4	18.4	18.4	11.4	5.5	0	2143400
24.4	24.4	29.3	24.4	24.4	24.4	24.4	24.4	9136100
30.3	30.3	30.3	30.3	30.3	30.3	37.6	23.6	10369000
20.2	26.8	20.2	20.2	20.2	20.2	20.2	8.7	3609700
17.9	17.9	17.9	17.9	12.4	17.9	17.9	17.9	1014600
23.5	23.5	23.5	23.5	19.1	23.5	23.5	23.5	5906800
28.8	28.8	28.8	28.8	28.8	28.8	28.8	28.8	2833000
15.9	15.9	15.9	15.9	11.1	11.1	11.1	11.1	7464800
3.3	1.7	3.3	3.3	3.3	3.3	3.3	1.7	1451800
3.4	2.3	2.3	2.3	3.4	2.3	2.3	3	4142400
21.1	21.1	21.1	21.1	9.2	15.6	15.6	15.6	7301000
16.4	28	24	20.9	16.4	31.1	31.1	26.6	13809000
12	7.4	7.4	7.4	12	12	7.4	12	2887100
6.8	6.8	6.8	6.8	6.8	6.8	0	6.8	484420
1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	559340
5.8	5.8	5.8	5.8	2.8	5.8	5.8	5.8	1632500
8.5	8.5	8.5	8.5	8.5	8.5	8.5	13.8	2485300
24.6	24.6	22	15.1	9.2	17.7	11.5	24.6	2983700
9.2	9.2	0	6	3.3	6	9.2	9.2	1451200
4.7	4.7	4.7	4.7	0	4.7	4.7	11.3	800370
0	40.2	19.5	19.5	12.2	31.7	52.4	40.2	1562300
0	0	0	4.4	4.4	9.6	9.6	9.6	843560
1.6	0	1.6	1.6	0	1.6	1.6	3.6	957060
29	31.1	14.2	14.2	6.3	14.2	29	29	13883000
12.9	12.9	21.9	21.9	12.9	21.9	22.6	22.6	3327100
16.9	27.1	23.3	27.1	20.6	20.6	30.8	30.8	46293000
1.4	1.4	0	0	0	1.4	1.4	1.4	333470

8.7	8.7	8.7	8.7	3.6	8.7	8.7	8.7	4195400
12.3	7	7.9	12.3	7	7.9	5.3	7.9	1727900
23.6	23.6	23.6	23.6	14.5	23.6	17.3	23.6	9789200
3.6	7.4	7.4	3.6	7.4	7.4	3.9	7.4	582270
24	24.8	24	24	24	24	24.8	24.8	8819900
14.8	14.8	34.1	34.1	14.8	34.1	34.1	34.1	1644100
1.8	4.6	4.6	9.1	1.8	11.6	13.2	13.2	4385400
0	0	0	0	0	0	0	8.1	1560200
24.5	24.5	24.5	17	17	24.5	24.5	24.5	14147000
26.7	32.5	32.5	32.5	41.4	35.6	32.5	32.5	3910900
17.8	15.2	17.8	16.7	16.7	28.9	24.3	30.4	9602300
0	0	1.6	0	0	2.8	2.8	4.7	781030
5.2	9	9	3.8	8.3	13.8	18.3	18.3	2093100
4.1	8.8	4.7	4.7	4.7	8.8	8.8	11.3	1295300
10.1	10.1	4.7	4.7	4.7	10.1	14.2	16.7	2410900
0	0	0	0	0	4.8	4.8	4.8	350670
19	19.6	23.3	23.3	28	21.8	17.8	21	36323000
13	13	17.6	14	14	14	17.6	17.6	23159000
14.1	14.1	14.1	14.1	16.7	12.1	2.8	12.1	5024400
8.6	8.6	11.9	11.9	11.9	11.9	11.9	11.9	2221900
0	8.6	8.6	8.6	8.6	8.6	0	8.6	1223600
4.4	2.7	5.5	5.5	5.5	1.9	3.6	1.9	2297200
9.5	7.6	9.5	6.4	10.6	6.2	10.6	5.8	8512000
3.1	12.5	4	3.1	3.1	5.4	14.2	9.1	3734900
17.5	17.5	17.5	12.2	17.5	17.5	17.5	12.2	2891600
15.8	11.8	11.8	15.8	13.5	11.8	9.5	9.5	5357600
7.4	7.4	7.4	7.4	7.4	7.4	7.4	3.3	3041200
0	0	11.6	20.9	9.3	20.9	20.9	9.3	684590
11.7	19.6	11.7	11.7	11.7	11.7	19.6	0	2132100
4	5.8	11.6	13.2	13	13.3	10.3	13	11389000
22.9	30	30	30	22.4	22.9	17.1	13.3	8004800
4.2	4.2	0	0	0	0	0	0	290010
14.3	10.7	25.1	25.1	26.6	28.6	30.7	28.6	28285000
17.3	17	17	17	17	15.5	17	14.3	17622000
19.2	19.2	19.2	19.2	19.2	19.2	19.2	19.2	3351900
6.4	6.4	3.8	6.4	6.4	6.4	6.4	6.4	3781300
0	0	0	0.9	0	0	0	0	0
6.9	8.4	8.4	8.4	6.7	8.4	7.2	7.2	4229400
0	6.2	10.4	10.4	10.4	10.4	10.4	6.2	1103400
24.9	29	24.9	18	24.9	29	34.7	30.6	9218000
10.9	15.5	20.7	20.7	20.7	20.7	20.7	15.5	6831000
3.9	3.1	8.4	7	8.6	11.7	14.1	11.7	8088600
1.7	4.4	13.9	13.9	13.9	13.9	13.9	13.9	6485400
13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	375650
3.2	9.5	9.5	9.5	9.5	9.5	6.3	9.5	1016200
17.7	21.1	21.1	16	5.1	24.9	24.9	21.1	5085500
12.8	12.8	7.1	7.1	7.1	7.1	5.7	7.1	2593100
0.6	1.4	1.4	1.4	1.4	1.4	0.6	1.4	1532100
27.9	27.9	27.9	27.9	27.9	22.3	22.7	22.7	22484000
3.1	3.1	3.1	3.1	0	3.1	3.1	3.1	328070

3.3	3.3	3.3	3.3	3.3	3.3	0	0	3026500
18	18	18	18	18	18	0	18	577720
0	1.8	1.8	1.8	2.8	1.8	2	1.2	1926200
3.9	7.8	7.8	7.8	8.5	3.9	3.9	3.9	1594800
26.3	27.4	27.4	26.5	17.1	36.2	32.5	29.4	22745000
23	28.5	23.7	18.4	26.1	19.4	29.7	33.5	11797000
6.6	15.7	6.6	11.9	6.6	21.5	21.5	21.5	5983000
0	0	0	0	0	9.4	4.7	9.4	956140
23.9	23.2	23	23	22.3	20.6	21.4	19.7	72875000
9.6	14.6	15	14.9	15	16.3	8.5	13.1	12681000
6.3	8.2	11.6	11.5	13.2	11.5	4	9.4	849950
2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2747400
1.6	1.6	1.6	0	0	1.6	0	1.6	356750
0	0	9.3	9.3	4.8	9.3	6.7	4.2	2867700
0	3.1	3.9	9.7	9.7	9.7	9.7	9.7	1896400
13.4	13.4	13.4	13.4	13.4	13.4	13.4	0	1403500
6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	2803800
19	14.4	14.4	19	19	19	9.8	10.4	3957300
0	0	0	0	0	0	0	5.6	140050
0	0	0	0	0	5.7	5.7	5.7	216180
0	0	8.7	8.7	8.7	8.7	0	0	217360
53	53.2	53.2	49.8	50.9	48.6	53.2	53	3.57E+08
4	9.9	4	4	4	4	4	9.9	1355000
37.5	33.1	30.8	33.1	28.6	30.4	37.5	32.9	40162000
5.5	2.6	9.3	6.6	6.6	8.6	5.7	4.9	2753800
21.6	18.6	21.6	15	21.6	17.1	14.2	21.6	17486000
2	4.1	4.1	4.1	2	4.1	4.1	2.1	1328300
0	0	0	0	1.5	0	0	0	0
4.8	4.3	5.7	5	4.8	5.7	3.7	4.2	9462700
26.9	30.4	30.4	30.4	16.6	30.4	26.9	26.9	18141000
13.4	13.4	7	7	7	0	7	0	919030
4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	993400
42.1	36.1	42.1	42.1	36.1	42.1	42.1	42.1	12764000
32.6	32.6	32.6	32.6	32.6	17.9	40	40	10707000
13.4	13.4	13.4	13.4	7.8	13.4	13.4	10	3079600
12.5	12.5	12.5	15.2	15.2	12.5	15.2	9.9	10195000
30.7	42.3	37.2	32.1	30.7	15.3	35.8	42.3	16978000
23.1	28.5	21.3	33	21.3	22.2	33	21.3	8865600
4.3	8.4	8.4	4.1	4.3	8.4	8.4	4.1	1275500
3	4.6	4.6	4.6	4.6	3	3	4.6	972280
3	0	0	0	0	3	3	3	483590
0	1.7	7.6	13.9	8.4	15.8	13.4	12	3073600
41.5	0	41.5	41.5	41.5	41.5	41.5	41.5	1131700
5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	1785000
10.7	12.2	14.4	16.5	11	18.3	22.9	19.4	12268000
0	0	0	0	0	8.7	17.1	17.1	1012500
23.9	29.8	18.4	24.3	19.7	33.3	33.3	33.3	11162000
16.5	21.2	16.5	16.5	8.6	16.5	16.5	21.2	4514100
17.5	21	18.5	9.1	3.1	21.7	31.5	31.5	1805300
25.7	28.7	18.7	11.3	5.8	22.9	31.5	31.5	16024000



4	4	4	4	0	6.9	2.8	6.9	1713400
11.3	6.9	6.9	4.4	6.9	11.3	26.1	6.9	1121100
19.7	23	21.4	13.5	6.2	21.4	30.6	30.6	1216800
14.9	18.3	9.7	14	14.9	18.6	22.9	22.9	4562200
4.3	5.4	4.3	2.6	4.3	9.5	7.1	9.5	1907700
6.9	6.9	6.9	6.9	3.5	6.9	3.5	3.5	1564100
11.5	7.3	11.5	11.5	0	15.8	27.9	27.9	2453600
16.3	26.9	25.1	28	21.9	35.7	46.1	48	29638000
0	3.9	11.1	9.5	3.9	20.8	20.8	17.6	4974800
35.2	35.2	35.2	32.1	23.2	35.2	32.3	28.9	66101000
2.4	1.2	2.4	1.2	1.2	3.7	2.5	3.7	1984800
4.7	4.7	4.7	4.7	4.7	4.7	0	4.7	2028200
0	0	15	0	0	0	15	15	529600
0	11.4	20.5	20.5	20.5	20.5	20.5	20.5	5960500
0	0	6.7	6.7	2.8	6.7	6.7	6.7	1309400
11.5	11.5	19	19	23.4	6.9	8.7	4	5995800
23.6	20.5	20.5	17.7	17.7	17.7	17.7	20.5	11098000
4.9	11.7	11.7	4.9	0	4.9	4.9	11.7	642360
31.4	31.4	31.4	14.7	26.5	26.5	14.7	31.4	5698900
31.8	17.8	31.8	31.8	31.8	17.8	31.8	31.8	6030300
17.8	17.8	11.7	11.7	5	11.7	17.8	5	7585200
8.7	20.9	8.7	20.9	15.7	20.9	20.9	39.1	3366100
0	0	0	11.7	11.7	24.2	24.2	24.2	1281900
9.3	9.3	32.6	22.1	32.6	36	34.9	45.3	7196300
24.4	24.4	24.4	24.4	24.4	28	19.6	12.5	7550300
6.1	3.9	1.7	2.2	1.7	6.1	6.1	6.1	2001500
4	1.9	1.9	1.9	1.9	4.3	6.4	6.4	2428500
5.6	5	7.3	7.3	3.4	7.3	9.8	8.1	3399700
0	3	3	0	0	3	3	3	525810
0	4.1	4.1	4.1	4.1	4.1	4.1	0	642280
36.5	36.5	36.5	36.5	36.5	27.7	27.7	36.5	13327000
18.5	18.5	18.5	18.5	18.5	18.5	18.5	18.5	1248900
0	8	8	8	16	16	16	16	1074800
15.1	15.1	15.1	15.1	15.1	24.4	24.4	24.4	4891100
10.9	10.9	0	0	10.9	20.2	20.2	20.2	1114000
0	9.3	9.3	9.3	26.9	36.1	26.9	18.5	6075200
50	50	32.5	32.5	32.5	50	50	50	11469000
21.9	13	13	17.2	0	21.9	30.2	26	3136700
0.4	0.8	0.8	0.4	0.4	0.4	0	0.4	1269000
19.2	19.2	25.3	19.2	25.3	19.2	19.2	19.2	2660100
0	0	31	31	31	31	31	31	8713900
0	0	0	0	0	0	13.5	0	224980
27.6	31.6	30.8	28.2	28.8	26.7	28.7	28.3	97953000
15.3	15.3	15.3	15.3	13.6	15.3	15.3	11.6	7378700
12.2	9.3	8.2	8.2	5.4	5.4	12.2	12.2	7937000
1.8	2.2	1.8	4	0	4	4	4	1196900
7.3	7.3	9.5	7.3	4.2	7.3	7.3	7.3	26247000
8.7	8.7	8.7	8.7	9.3	8.7	8.7	6.6	5033800
4.7	4.7	4.7	4.7	4.7	4.7	0	4.7	1279800
0	3.4	3.4	3.4	3.4	3.4	1	1	1054600

10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	18494000
4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	1268600
12.3	11.2	12.3	20.7	12.9	19.3	34.2	26.1	5043200
14.8	42.6	14.8	22.6	14.8	22.6	22.6	22.6	5809000
3.4	2.3	2.3	3.4	0	0	3.4	0	711940
0	0	8.1	8.1	7.6	8.1	0	15.7	2779300
36.2	10.8	10.8	10.8	0	36.2	36.2	36.2	1576700
16.2	24.9	22.3	19.8	19.8	22.3	20.4	20.7	8787100
0	7.9	12.1	12.1	12.1	12.1	12.1	12.1	1105800
3.7	4.4	10.8	11.6	11.2	13	14.2	13.8	21800000
1.6	2.4	7.5	5.5	6.1	8.3	8.7	8.2	10197000
13.5	20.9	20.9	15.3	15.3	20.9	20.9	20.9	4907100
0	2	1.6	3.6	0	0	0	0	409550
19.3	19.3	19.3	19.3	11.1	19.3	11.1	11.1	1369600
11.2	14	3.7	5.6	0	16.8	26.9	24.1	15727000
4.7	1.8	4.7	4.7	4.7	7.3	7.3	7.1	2718900
0	0	3.9	1	0	5.5	3.9	3.9	1090400
0	0	12.4	6.6	10.6	12.4	8.4	8.2	2468300
3.6	7.9	7.8	9.7	9	8.9	9.7	7.8	9192600
1	4	7.8	7.8	2.7	10.6	9.3	10.6	5121700
6.5	5.2	5.2	6.1	5.9	6.4	7.3	7.1	6852900
9.6	20.8	20.8	20.8	0	20.8	20.8	20.8	2087100
20	20	12.5	12.5	7.1	12.5	20	16.7	6694900
23.1	22.5	22.5	17.3	16.3	22.5	22.5	17.9	15723000
14	7.9	16.8	13.4	14.3	22.5	23.2	23.8	36402000
15	15	15	15	10.1	10.1	15	4.8	2119600
17.8	28	18.8	14.1	9.8	27.3	28	28	20582000
0	0	0	0	0	0	0	3.1	105210
26.1	41.3	26.1	41.3	0	26.1	15.2	15.2	4613000
26.4	24.9	28.9	29.8	31.6	30.7	34.7	33.8	17176000
17.5	14.9	12.6	12.6	15.5	22.5	20.9	19.5	19742000
0	0	0	8.1	18.1	31.5	31.5	26.2	2967100
0	0	0	0	0	6	6	6	2240600
0.8	1.4	0.6	0	0	1.4	1.4	1.4	643940
2.3	2.3	2.3	2.3	2.3	2.3	2.3	0	45841000
20.4	20.4	15.5	22.3	15.5	15.5	22.3	22.3	7701000
29	29	25.8	32.6	24.2	32.6	17.4	29	14790000
1	1	1	1	1	1	1	1	8113400
49.2	54.8	54.8	52.4	44.9	52.1	46.5	45.2	2.48E+08
21.9	20.1	24.9	23.4	21.9	30.8	32.8	29.7	30948000
9	14.9	14.9	9	9	9	9	9	1084400
2.5	2.5	2.5	2.5	2.5	2.5	2.5	0	464440
2.8	2.8	2.8	2.8	1.9	3.7	3.7	5.4	3006900
1	0	2.1	2.1	2.6	4.8	3.2	2	1347700
0.8	0	1.7	1.7	1.7	1.7	3.8	3	1200200
6	4.4	3.4	2.6	4.2	3.4	5.1	5.1	7979800
21.4	21.4	16.7	16.7	19.6	21.4	19.6	19.6	11250000
11.6	9	9	11.6	14.2	9	4.6	4.6	7105200
9.3	9.5	11.6	11.6	9.3	9.3	9.3	4.8	6786600
13	13	13	13	13	13	4.9	2.3	3885800

10.2	15.4	15.4	13.3	15.4	15.4	10.2	10.2	8080300
12.5	8.5	8.5	12.5	12.5	8.9	8.5	8.9	3318700
33.8	33.8	33.8	22.9	16.2	27.1	28	27.6	19950000
0	0	0	0	0	0	10.7	10.7	513210
40	14.3	14.3	14.3	40	40	41.4	41.4	3383600
2.8	2.8	2.8	2.8	2.8	2.8	0	0	651920
1.3	1.3	1.3	1.3	1.3	1.3	2	1.3	2045300
9.1	9.1	9.1	16.9	9.1	21.4	21.4	21.4	5426600
24.4	32.4	24.4	24.4	20.5	24.4	32.4	32.4	21568000
8.7	4.5	13.2	4.2	8.7	16.2	16.2	16.2	2125800
0	0	0	0	0	0	6.3	0	0
8.8	2.9	14	14	15.7	11.7	8.8	8.8	4002800
5.6	5.6	5.6	5.6	5.6	5.6	0	0	946360
15.1	5.4	5.4	15.1	5.4	5.4	5.4	5.4	5382800
6.6	9.7	6.6	6.6	12.7	6.6	3	6.6	2909300
0	8.8	0	8.8	0	8.8	0	13	482490
2.6	1.2	4.3	5.5	4.3	2.9	3.8	0	1465000
6.1	7.6	9	7.7	6.7	9	8.9	8.9	8247300
4.4	0	4.4	4.4	7.2	4.4	4.4	4.4	625410
8.5	0	8.5	8.5	8.5	0	8.5	15.8	1112100
0	0	0	0	1.9	3.6	1.7	1.9	557620
17.6	13.7	29	31.6	24.7	37.9	37.9	29	10919000
0	4.9	5.5	10.4	5.5	10.4	10.4	4.9	725840
10.4	10.4	10.4	10.4	10.4	10.4	10.4	0	2328200
1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	8168200
0	0	0	0	0	0	7.8	7.8	210490
19.7	19.7	19.7	19.7	19.7	7	0	19.7	2325300
5.5	11.6	11.6	11.6	5.5	11.6	5.5	6.1	1138400
16.3	16.3	8.5	16.3	16.3	16.3	16.3	16.3	2450600
0	5.1	5.1	4.3	0	5.1	0	5.1	366260
11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	2264900
51	58.7	55.4	48.7	48.3	55	51	44	41350000
50.8	58.6	55.2	48.5	42.4	54.9	50.8	43.8	1887200
1.8	1.8	2.8	1.8	1.9	4.1	4.2	4	5061300
5.1	5.1	5.1	5.1	2.2	5.1	2.9	2.9	2112700
14.3	17.1	12.3	7.2	14.3	17.1	17.1	15.2	7920000
1.5	3.9	18.8	13.1	18.8	21.4	18.8	15.6	20429000
11.2	11.2	11.2	11.2	9.8	11.2	11.2	8.7	7644500
13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	2725700
0	0	5.2	2.2	2.2	2.2	2.2	3	541790
3.6	0	0	0	0	0	3.6	3.6	179360
27.9	24.3	31.1	27.5	33.1	33.3	40.1	40.1	22465000
22.6	17.9	14.2	18.3	9.2	22.6	36.1	32.3	19911000
24.2	27.7	18.9	19.1	18.1	29.3	34.2	35.6	25884000
20.8	23.3	16.7	10.1	10.5	30.7	30.7	33.5	13292000
14.8	12.6	14.2	16.6	16	15.6	19.4	20.2	21430000
25.9	23.1	15.8	21.8	21.7	31.6	36.1	36.1	21240000
26.1	17.9	25.7	27.6	27.6	33.8	36.5	34.5	29540000
5.3	10.7	12.4	8.5	7.5	17.3	18.6	20.5	16836000
0.5	0	1.8	1.8	1.8	0.5	1.2	1.8	1715200

0.8	2.1	2.1	0.8	0.8	0.8	2.1	1.2	668590
0	2.2	2.2	2.2	2.9	5.1	5.1	5.1	652980
9.6	14	5.1	9.6	14	9.6	14	4.5	12337000
27.6	27.6	12.4	12.4	12.4	12.4	12.4	12.4	13714000
35.8	35.8	35.8	35.8	26.1	35.8	21.8	35.8	13403000
0	0	0	6.3	6.3	0	0	15.7	1736700
5.4	5.4	5.4	5.4	0	5.4	5.4	5.4	1614700
10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	2205900
1.6	0	0	0	0	0	1.6	1.5	375510
17.1	21	29.5	21	27.6	31.4	51.4	51.4	1.03E+08
5.2	14	14	14	14	14	8.7	8.7	1349200
11.4	11.4	18.7	18.7	18.7	18.7	26.8	26.8	4772900
25.7	21.1	23.6	18.5	23.6	21.1	21.1	18.5	23924000
3.1	3.1	5	1.9	0	11.4	19.3	19.3	4035000
39.1	39.1	34	34	30.7	29.8	34.9	29.8	21287000
19.4	30.4	32.9	32.9	30.4	30.4	30.4	29.8	6999400
7.9	13.9	13.9	11.1	10.7	13.9	7.5	10.4	8634400
25.2	34.1	29.8	25.2	16.7	24.4	24.4	26.4	7633500
8.1	8.1	8.1	4	0	8.1	4	4	1960700
0.9	0.9	0.9	0.9	0	0.9	0	0.9	526630
0	0	12.1	12.1	16.3	30.4	29.2	30.4	6781900
0	0	0	0	0	0	5.4	0	113830
12.2	12.2	13.4	13.6	11.1	24.3	24.3	26.8	19495000
10.5	11.7	11.8	12.7	10.2	11.8	10.3	12.7	15696000
0	0	0	0	0	0	10.3	10.3	207590
6.7	6.7	0	0	0	0	0	0	226370
0	0	31.8	31.8	31.8	31.8	31.8	25	2677200
4.5	6.8	10.3	8.1	12.4	5.9	7.2	8.2	9129900
35.1	37.8	20.8	17.4	20.8	37.8	46	40.5	16145000
6	7.3	8.4	7.5	7	9	9	9.5	6271700
0	0	0	6.2	6.2	6.2	6.2	0	271200
20.3	18.1	18.1	7.7	12.4	14.9	15.3	18.1	11056000
11.2	11.2	11.2	11.2	11.2	10.2	10.2	11.2	11930000
0	0	0	0	0	0	0	0	866690
7.5	5.3	7.5	10.2	10.2	7.9	2.4	7.7	2956600
17.5	0	17.5	17.5	17.5	17.5	0	0	495240
11.5	11.5	11.5	11.5	14	11.5	14	10.9	8752000
0	0	3.2	3.2	3.2	3.2	0	0	411200
6.8	3.3	10.7	13.1	7.1	19.9	23.4	20.8	9925100
0.7	0.7	0.7	0.7	0.7	0.7	0	0.7	814540
0	0	3.3	11	3.3	20.9	20.9	16.9	1983600
38.2	38.2	38.2	38.2	38.2	48.3	38.2	48.3	4268700
17.7	17.7	17.7	17.7	11.5	28.3	28.3	22.1	3913500
0	0	0	0	0	1.2	2.2	1.2	222780
14.6	14.6	14.6	14.6	8.5	14.6	14.6	10.6	6274600
0	0	0	0	0	17.3	17.3	17.3	1230200
11	4.4	8.9	8.6	8.4	15.9	22.4	20.4	9190400
3.3	3.3	4	7.3	7.3	7.3	0	3.3	1470500
4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	709060
5.4	5.4	3.2	8.3	2.2	5.4	5.4	5.4	1056500

12.6	15.5	12.1	12.1	8.4	12.6	12.6	10.6	6015700
31.1	32.4	30.4	30.4	22.6	31.7	34.2	34.2	1.03E+08
12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	2042800
10.8	16.3	16.3	16.3	16.3	12.8	12.5	9	6859900
4.2	4.2	4.2	2	2	2	2	2	1148500
23.8	23.8	23.8	16.6	16.6	23.8	23.8	23.8	4115900
42.7	46.7	46.7	50.8	39.7	50.8	61.8	59.3	60181000
11.7	11.7	11.7	11.7	11.7	11.7	11.7	0	1674800
25.6	24.7	28.7	27.5	25.2	28.5	31.4	30.9	44124000
19.9	27	19.3	26.6	20.5	34.2	35.5	36.8	72236000
2.4	3.4	1.9	2	1.8	2.4	3.3	3.6	32002000
12.8	12.8	12.8	12.8	12.8	6.7	12.8	12.8	3033100
11.2	23.4	24.5	18.1	14.4	29.8	33.5	33.5	18887000
8.7	11.1	8.7	3.8	0	7.3	11.1	6.2	1040500
10.6	21.2	10.6	21.2	10.6	21.2	21.2	10.6	2942000
7	7	7	7	3.6	7	7	7	3661700
7.5	7.5	15	7.5	7.5	7.5	7.5	15	2700200
7.2	7.2	4.2	4.2	0	0	5.7	4.2	2659100
24.3	24.3	24.3	13.3	24.3	24.3	24.3	24.3	7996400
8	8	12.6	8	12.6	8	8	8	8595300
5.8	3.9	5.8	5.8	3.7	5.8	5.8	3.9	3462700
15.2	15.2	12.4	8.6	12.4	11.5	13.3	13.3	16210000
6.6	6.6	6.6	6.6	3.7	6.6	3.7	6.6	5741600
11.4	11.4	8.3	8.3	8.3	11.4	11.4	4.5	4613500
7.1	7.1	7.1	7.1	3.8	7.1	3.3	3.3	2210400
0	5.7	5.7	5.7	5.7	5.7	5.7	5.7	1438500
15	15	15	15	15	15	7.2	15	4023700
7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.8	4926500
21.3	17.1	13.3	9	17.5	17.1	8.1	8.1	4808800
9.6	9.6	9.6	9.6	4.4	9.6	5.2	5.2	2255600
21.3	21.3	14	14	21.3	21.3	21.3	11.9	7213800
5.9	5.9	5.9	5.9	5.9	5.9	5.9	4.3	2667400
9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	13975000
13.3	21.3	13.3	15.7	7.7	15.7	15.7	13.6	4039100
0	0	9.7	4.1	9.7	0	0	5.6	602110
11.2	11.2	11.2	11.2	11.2	0	0	11.2	1406000
0	0	10.8	10.8	0	0	0	0	663550
5.6	5.6	7.8	7.8	6.2	4.2	1.4	2.2	1740300
68.3	68.3	68.3	0	0	0	0	0	688160
9.9	9.9	9.9	9.9	0	9.9	9.9	9.9	3334400
14	14	14	14	11.5	14	7	12	6518900
13.6	13.6	17.6	14.9	17.6	17.6	8.7	10.5	8197700
6.1	8.5	6.7	8.5	4.3	8.5	6.7	6.7	4386600
10.2	10.2	10.2	10.2	0	14	3.8	0	1280400
6	6	6	6	2.1	3.8	4.8	4.8	4319200
8.3	10	8.5	9.8	11.2	10.5	11.4	8.3	18188000
10	10	10	10	2.6	10	10	10	7038700
27.8	27.8	32.4	26.2	22	26.7	28.4	26.2	61511000
31.6	29.2	31.6	29.4	29.4	28.5	25.7	29.6	33107000
3.6	2.5	3.6	3.6	1.6	5.6	5.6	5.6	2437300

33.3	30.9	36.9	30.1	41.4	71.1	78.7	78.7	1.15E+08
2.6	2.6	2.6	2.6	2.6	4.7	4.7	2.6	1046400
12.5	12.5	12.5	12.5	12.5	8.8	8.8	3.8	1042500
28.4	25.7	21.6	20.2	17.3	22.8	25.8	23.6	13908000
8	7.8	4.8	4.8	8	11	7.8	7.8	1482700
8.5	14.5	8.7	10.9	6.5	16.2	10.5	13.1	4684000
12.2	12.2	0	5.4	12.2	9.4	7.1	15.3	3973500
26.4	29.6	20.8	21.8	23.6	23.6	29.9	29.9	3485600
46.4	43.1	44.8	49.6	46.4	41.5	48	49.2	61627000
46.8	40.3	41.9	44	44	39.9	47.2	40.7	7580600
40.1	37.7	39.1	37.7	37.7	37.3	43.7	41.9	28285000
4	0	6.5	4	4	15.8	18.1	17.4	2985800
47.8	50	52.9	41.1	43.8	50	59.9	55	10335000
44.1	46.1	48.8	40.8	40.4	46.1	55.2	50.8	5.55E+08
38.3	40.1	42.4	28.3	30.4	40.1	43.4	44.1	2666100
46	46	50.8	46	42	46	57.5	50.8	22343000
48.4	42	41.8	38.3	29.6	41.8	45.5	48.4	1.04E+08
42.7	46.5	42.5	31.9	22.2	31.9	40.4	43.1	2247300
15.7	15.7	14.1	13.7	12.2	15.6	15.7	15.7	1174500
44	47.9	43.8	43.8	32.1	43.8	47.9	47.9	4.25E+08
18.4	18.4	14.3	14.3	15.7	14.3	14.6	14.6	1569700
21.4	21.4	21.2	20.9	20.9	21.2	21.4	21.4	1.6E+08
21.5	21.5	21.5	0	0	21.5	21.5	21.5	1163000
0	0	9.5	9.5	20.2	41.7	41.7	20.2	1630900
7.3	7.3	1.9	1.9	1.9	7.3	8.9	5.4	1846900
0	0	0	0	0	0	1.4	1.4	140750
3.6	3.6	3.6	3.6	3.6	3.6	3.6	0	702320
6.2	6.2	3.2	3.2	0	3	6.2	6.2	917640
0	0	8.2	25.5	0	31	33.2	33.2	2648800
0	4.5	23.4	23.4	8.6	30.6	30.6	30.6	4837200
18.8	18.8	18.8	18.8	14	22.8	22.8	22.8	3260400
1.1	0	1.1	1.1	1.1	1.1	1.1	1.1	558040
27.2	27.2	27.2	27.2	27.2	27.2	27.2	27.2	85846000
3.7	0	3.7	7.4	7.4	7.4	7.4	7.4	1195000
0	0	7.5	7.5	7.5	7.5	7.5	7.5	1004700
14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	4078400
8	6	9.3	7.6	10.6	9.2	3.4	5.4	6911200
13.4	10.6	13.4	13.4	10.4	10.8	7.7	10.8	3185400
14.3	12	12	16.3	14	21.1	18.2	21.1	7302800
6.1	6.1	4	4.2	4.2	6.1	6.1	6.1	1927500
12.7	12.7	12.7	6.5	3.4	12.7	12.7	12.7	2688100
8.5	6.2	10.3	12.6	10.3	14.6	13.5	17.6	4762400
0	5.6	0	0	0	0	14.8	14.8	244760
0	0	6.7	16.7	10	16.7	16.7	16.7	4610700
0	9.8	16.5	9.8	0	16.5	9.8	21.2	2379200
0	3.6	0	0	4.9	4.9	8.4	8.4	1456500
3.1	3.1	1.9	3.1	1.9	1.9	3.9	4.1	1871900
15.2	15.2	8.2	15.2	15.2	8.2	15.2	0	2190600
0	4.7	4.7	4.7	4.7	0	0	0	857370
0	3.5	5.8	8.5	10	3.6	5.8	8.5	1899200

5.2	5.2	2	2	2	5.2	5.2	0	1961000
4.4	4.4	4.4	4.4	2.5	4.4	4.4	4.4	1271900
5.7	8	8	5.9	5.9	5.9	5.9	2.3	2129600
3.1	3.1	3.1	3.1	0	3.1	3.1	3.1	544140
0	0	3.1	5.5	2.5	5.5	0	5.5	808780
6.6	7	5.4	6	3.9	7.5	8.6	8.1	13276000
11.8	3.4	11.8	11.8	3.4	11.8	14.6	14.6	2737500
0	0	0	20	20	20	20	20	734910
0	0	0	0	0	0	23.9	23.9	209730
8.6	8.6	2.9	5.9	5.9	14.1	14.1	11.2	6611400
20.6	0	20.6	20.6	0	20.6	0	20.6	832740
10.9	10.9	0	0	0	10.9	0	10.9	405270
0	0	1.6	0	0	3	1.6	3	492230
12.6	12.6	22.6	31.3	31.3	35.7	35.7	35.7	5448500
0	2.9	4.2	2.5	0	18.1	25	21.4	4590500
11	0	5	5	0	16.1	16.1	16.1	944440
0	0	8.1	3.9	3.9	8.1	8.1	3.9	540820
14.9	14.9	22.4	14.9	18.7	22.4	22.4	22.4	3700100
50.6	50.6	50.6	50.6	50.6	50.6	50.6	50.6	2.98E+08
1.4	0	1.4	3.7	5.1	3.7	6.5	3.7	1572100
15.7	15.7	15.7	0	0	0	27.9	27.9	1831900
0	0	7.5	7.5	0	12.5	21.5	21.5	1213500
0	11.7	11.7	11.7	0	11.7	11.7	11.7	1519100
13.8	13.8	6.6	19.7	19.7	19.7	26.3	32.9	5564200
2.7	2.7	7.8	7.8	7.8	10.5	7.8	7.8	4076000
6.9	6.9	13.8	13.8	13.8	20.7	20.7	20.7	2808400
18.5	18.5	18.5	18.5	0	18.5	18.5	18.5	1278400
12.6	16.4	18.4	17.6	14.3	24.3	28.7	25.1	33297000
0	12.3	24.7	0	12.3	24.7	24.7	12.3	773020
5	5	5	5	0	5	0	5	1008900
13.6	13.6	13.6	13.6	13.6	13.6	13.6	10.8	8671200
22.5	24.9	14.2	16.8	16.8	21.9	21.9	29.4	11713000
8.5	8.5	9.3	8.5	7.9	7.5	6.3	5.1	12382000
7	9	6.8	4.7	4.7	4.5	6.8	4.3	1737200
0	4.1	0	4.1	4.1	10.2	27	26	2436900
0	3.3	3.3	3.3	0	3.3	3.3	3.3	957720
3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8	544210
17.2	17.2	17.2	17.2	10.9	17.2	17.2	17.2	3593300
17.6	16.4	14.4	15.4	9.2	13.7	16.4	16.4	16734000
13.9	13.9	13	11.8	10.3	13.1	14	14	15580000
2.1	2.1	0	0	0	3.4	3.4	3.4	1055400
2.4	2.4	2.4	2.4	2.4	1.2	1.2	1.2	1657200
0	7	0	7	0	0	7	0	108890
0	12.4	0	12.4	0	0	12.4	12.4	828440
6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	1344600
43.1	43.1	43.1	43.1	25.9	43.1	25.9	43.1	11364000
11.9	2.6	0	0	0	2.6	11.9	14.2	1905700
7.6	15.3	0	7.6	0	16.7	24.3	16.7	906390
6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	12812000
0	0	0	0	0	8.3	8.3	8.3	359490

5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	12997000
0	0	0	2.4	2.4	4.7	8.3	5.9	1166800
13.2	11.2	13.7	17.6	13.7	19.8	23	23	14305000
11.9	11.9	11.9	11.9	11.9	11.9	0	0	1234100
5.2	14.4	14.4	14.4	14.4	14.4	8.9	8.9	2680900
0	71.4	71.4	71.4	71.4	71.4	71.4	71.4	1258600
10.1	7.2	10.1	11.8	4	11.8	8.9	8.9	6378100
5.6	5.6	5.6	5.6	2.9	5.6	2.7	0	916380
0	3.6	3.6	0	0	3.6	6.8	3.6	328290
5.2	3.7	3.6	3.6	2.6	6	6	6	3582300
3.1	3.1	3.1	3.1	3.1	3.1	0	3.1	402090
35.9	39.5	34.4	31.5	22.3	32.8	36.5	29	48113000
0	3.9	0	0	3.9	0	0	0	558160
19.3	19.3	15.2	13.5	10.8	15.2	15.2	11.3	12700000
4.3	6.9	6.9	4.3	2.5	6.9	12.3	6.9	8218500
7.1	7.1	7.1	7.1	0	7.1	7.1	10.4	3189900
9.3	9.3	9.3	9.3	9.3	9.3	9.3	0	2150200
52	52	52	52	52	45	36	40	12280000
23	33	33	33	33	33	10	10	6049100
12.4	12.4	12.4	12.4	12.4	12.4	7.6	12.4	4024900
25.5	22.6	22.6	22.6	25.5	22.6	17.7	25.5	7874000
1.6	1.6	1.6	0	1.6	0	1.6	0	400220
32.4	32.4	32.4	32.4	32.4	32.4	0	32.4	515920
20	20	20	20	20	20	20	20	5746300
15.7	7	9.6	9.6	6.5	9.6	3.1	3.1	5183300
5.3	7.4	4.5	3.3	5.6	6.8	8.2	8.2	6833100
5.3	4.5	6.6	10.5	11	17.7	18.2	20	24304000
9.3	9.3	4.6	4.6	4.6	4.6	0	0	3035200
5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	1269400
68.6	68.6	68.6	55.1	51.6	71	71	71	1.55E+08
70.4	70.4	66	70.4	60.9	65.6	55.8	63.3	1.65E+08
28.3	30	23	25.8	17.3	31.1	30	23.3	30677000
3.3	3.3	3.3	3.3	2.2	3.3	2.2	2.2	1193900
11.6	11.6	11.6	11.6	0	11.6	0	11.6	4476800
7.7	11.8	13.9	13.9	11.3	11.8	11.8	13	5944700
16.2	16.2	16.2	16.2	16.2	16.2	0	16.2	926680
8.8	8.8	10.8	12.5	11.9	18.2	15.9	18.2	9391900
0	36.4	36.4	36.4	0	36.4	36.4	0	564550
2.8	6.1	6.1	6.1	6.1	11.7	11.7	2.8	3611900
4	14.6	5.8	14.6	5.8	14.6	15.9	20.8	5277000
9.3	22	33.9	33.9	33.9	22	22	22	4608200
14.7	14.7	17.2	17.2	14.7	17.2	14.7	17.2	6014600
12.7	15	5	16.2	13.5	22.4	20.8	20.8	6904700
12.4	8.9	8.6	8.6	8.6	5.1	14.5	14.5	2932200
1	2.6	3.9	3.9	2.9	1	1	2.3	2065900
6.6	6.6	6.6	6.6	6.6	6.6	4	2.4	4438300
8.2	8.2	8.2	8	11.6	4.6	5.2	8.2	2151500
0	4.5	4.5	4.5	4.5	4.5	4.5	4.5	815080
0	0	0	0	0	0	33.3	33.3	199250
7.6	7.6	4.3	4.3	4.3	4.3	4.3	4.3	635030



1.1	1.1	1.1	1.1	1.1	2.2	0	0	412680
0	3.6	3.6	0	0	0	3.6	0	272920
23.4	24.5	16.8	11.2	11.1	25.4	29.8	28	23172000
11.8	13.5	15.4	19	16.7	21.2	25.8	25.1	23887000
37.6	20.5	43.9	41.3	43.9	43.9	43.9	41.3	8266800
0	0	0	0	0	0	4.3	4.3	354660
2.3	2.3	6	6	2.3	6	6	6	720470
0	0	0	0	13	13	13	13	519510
5.4	6	5.4	5.4	5.4	7.2	5.4	4.2	2971000
8.7	2.9	8.7	8.7	8.7	8.7	2.9	2.9	1246100
0	0	0	0	0	1.5	3.1	3.1	452250
4.3	2.4	4.3	1.9	1	4.3	3.3	2.9	915800
28.7	28.7	28.7	28.7	28.7	28.7	28.7	17.2	1977900
5.8	5.8	5.8	5.8	0	5.8	5.8	5.8	2286700
12.9	12.9	12.9	12.9	12.9	12.9	12.9	12.9	2337800
0	4	4	8	8	4	0	0	498690
0	0	3.5	9.8	9.8	9.8	9.8	9.8	1312000

Intensity 1_2	Intensity 2	Intensity 3	Intensity 4	Intensity 5	Intensity 6	Intensity D1	Intensity D2
11453000	15987000	16064000	14708000	18461000	9468700	6618700	8236300
1037900	2007600	972010	516540	816860	996550	1119100	1959600
71960	61352	115180	119180	105780	250870	275430	429240
1964000	3060000	3334600	3551500	3692400	6411200	6689600	6361700
2121400	2504200	5742300	6516700	4444400	17366000	15051000	19650000
1011000	1474800	1626300	1695300	1944800	3429100	3212100	3686400
1198600	819200	2621500	3374900	3967100	5592800	5719500	5687900
9021700	13029000	14640000	14338000	19521000	42662000	54546000	75320000
1582000	1778400	2881100	3302200	3144100	6731700	6609900	8330100
3488900	5301300	7167100	7997900	9486200	24082000	20737000	27581000
35520	0	41730	39974	36716	104350	108500	190070
240790	295520	399380	379220	379900	205070	98885	0
184270	137510	0	0	288920	0	0	0
1264600	3214100	2988600	2580500	2151100	1810800	1025400	1483600
231740	108640	0	0	62457	150910	197990	300870
1115100	1037600	516330	386050	241510	1162200	1271000	3288900
558380	718000	206110	552630	211020	1072400	1228800	1650400
829270	643080	512420	440690	435540	761490	997540	1024100
554330	511460	87554	92823	315430	435210	168600	597130
1068900	982250	536380	948680	658460	1828700	1906200	3193900
536820	788350	229930	588940	204710	548440	1187700	1262700
212160	335250	71445	137840	194340	464130	468690	1247000
92075	81590	0	73839	0	263360	249000	275210
541750	426780	302250	294400	352660	1300000	2017700	2049500
140190	307810	97277	123300	82380	640750	1143300	1178800
214490	157250	234470	228460	307920	787300	1216900	1405500
88417	97999	73410	49820	0	150710	163240	211990
905180	1821700	684260	672290	477950	1364400	2017600	2769500
498980	529920	454110	399970	219870	834550	687340	935610
0	0	0	52321	0	148940	0	243460
0	0	0	0	26280	22255	263810	347110
29951	202190	84092	114100	153140	518300	345520	380670
67134	48662	54226	63477	118110	154460	97227	499140
0	0	63193	39069	269710	808050	1176200	1224700
251420	233500	141980	61416	135700	97706	94870	122790
405870	325000	345360	304170	249770	251100	163000	192250
635220	555320	754630	725070	448300	366070	204720	465980
510770	1441100	1048900	935010	1165500	683950	459690	447730
394350	514550	387770	274540	156580	239660	204030	232230
71777	121510	31911	0	40196	407750	32679	0
440570	432540	370610	301990	220500	191950	156330	91535
112190	0	236070	151970	36003	129940	71060	101260
533900	807100	248310	93160	477370	377440	175520	175280
339510	303710	279940	292570	133370	119800	0	61192
125910	0	139770	231860	212780	32263	16462	0
159660	127070	202860	223720	277420	176420	49725	0
135040	151490	135110	163920	118890	81133	60809	68655
114080	156080	129120	196740	0	141210	179150	74845

599000	683740	644530	641580	265370	528000	189890	94034
44035	277170	135200	120170	0	166600	83053	146550
2691200	4884200	3498300	2901600	3008400	2224500	1580700	1616500
97132	148040	143600	161280	231870	83551	58615	46647
217760	309730	402500	510220	248360	249920	83995	334130
476600	485530	536820	468540	565320	330690	447570	585190
255460	216030	110670	60645	181500	91040	0	0
128280	157360	315850	324490	258070	198730	0	97007
258080	0	668330	203020	554850	181360	80143	346280
223680	190130	181280	174510	75577	120880	57769	45131
209310	186620	167000	119100	417580	0	0	0
133660	173970	88412	103200	157660	85592	83774	102140
359150	82589	339500	273490	119700	146250	98205	142480
0	197730	0	245900	0	0	0	0
113820	97851	117320	119950	233660	73723	57624	0
292820	275510	464410	441770	439040	255770	76422	59692
107150	94951	90956	83661	144200	74491	0	0
154920	189800	110420	95729	119040	81271	73469	89115
175330	262340	304290	79256	0	189990	73188	0
94318	111910	136470	125350	419170	95551	52469	58018
81529	127270	116130	85387	0	112120	70671	112300
2389300	6688900	2935700	1335000	796670	1587000	1547700	2022600
2999300	3958700	4893200	6503200	7352600	2984500	1882100	1945800
268240	317720	372510	357810	476520	79756	103840	174050
291300	350010	283800	255840	107860	200950	0	156880
142760	0	235890	284670	206860	498600	506140	799540
1325000	75778	46652	402350	0	855540	249840	2895400
4907400	6031400	3695500	3167500	2765300	3356900	4304300	8512800
3068700	4088600	2266600	1702000	1246900	3891100	5941000	6767300
1245000	2888100	1572200	1455100	522000	2272100	4097700	3999200
5613400	7126700	6061000	5270400	4440100	5873000	5118100	6563400
3256800	3185800	1840100	1060900	420920	1770600	2317900	2350500
2548100	4029700	2035000	1455500	836420	2159600	3284200	4001800
4524000	3994400	2170000	1502200	1601800	3369800	4550900	1842000
4915600	6834400	3139600	2768800	1472700	4645600	6322100	6292300
2744600	1686100	1462900	2582500	458200	4338500	5278400	3694700
7285200	7566800	4923300	3672400	2143600	5690300	4619900	6430600
864670	1296200	822330	508320	790680	1108500	1207500	1602500
390390	605520	812690	479100	295300	1933000	1875500	1905300
1601900	2479900	890570	630050	283290	1128400	1693100	3757000
1369100	1523900	1029900	592830	879780	1129300	1687500	919190
1046700	1658200	910880	583030	457370	1979400	1737400	2339200
2485000	3039000	1463400	1306300	346020	1958000	2262000	1139000
3186200	4004700	2646700	1954100	2147100	2258200	2534200	3477900
394700	2942000	3018900	2518600	1198900	4408600	5050700	5214700
135630	196430	184180	145170	101260	405070	892960	0
12501000	15017000	9003900	6161400	4446600	9027300	8428900	10763000
146810	354120	472070	542970	242560	1268600	1393900	1400000
5137100	11865000	5382300	2874400	2179200	4172500	8197000	10670000
7238100	11813000	4029600	3945700	2151600	5109000	6635500	9515400

2964000	4560300	1946000	1543800	958440	2234500	2336200	4079100
4436000	10064000	5010900	6909700	4501600	5140700	4641300	9195000
915760	4036900	1226000	1101700	488020	1447400	6795900	1962400
11761000	14846000	11042000	9450100	7748300	8169300	9510400	10233000
5930100	11339000	6437400	4620300	1877500	6601000	7339500	8619200
4573700	5762600	4223800	3181100	3358600	7760000	8370200	19618000
33902000	48372000	46388000	38776000	30505000	28740000	27505000	53493000
165920	261010	133310	113100	121890	242570	326070	0
162640	50036	188690	46191	60089	57639	47822	105450
66668000	90429000	85830000	75586000	83420000	49494000	31164000	50262000
3190900	8136900	7152100	6253600	2534400	10172000	9953500	12299000
50330	5348900	2054500	1137900	0	3796900	4908000	2816000
4039400	7382800	7325300	7507000	3004000	7009600	6818400	24522000
9383500	9733100	6754500	3029000	5214100	4335200	5446700	4735900
2661000	4631000	3935800	2729700	2102100	3331200	4110500	5262800
4772200	6451700	4978700	5419400	2500300	3194400	3727100	3718100
92545	91331	68958	67444	71849	37349	64580	0
4437900	5350600	7312700	6617800	8865300	8359000	8035500	11765000
3533200	10331000	4978100	3509300	3933400	4554700	5004800	6773300
2817200	4934500	3065500	2529100	2099700	2892000	3587800	3342600
3895300	4625200	3624700	2651800	3748500	2480700	2870700	3400300
5590800	7318200	4763000	3251700	2781800	3957500	4512800	6681500
2687500	4324500	844350	603410	566820	564420	3068500	5207900
5237900	6795700	6477100	6233800	4851700	4073000	3981100	4892100
5006700	4941400	4711600	3774600	3914200	3483700	3374600	4098600
1613000	1551300	716870	130420	217990	409440	2197900	1904400
2471300	3218400	4047300	3748800	3313700	4151800	3389500	3917300
5246200	4158900	3571000	3880800	2149400	3289000	2762100	9120900
1293400	2301100	2193600	2107500	2242600	2928600	3324300	4475300
3695000	4831800	3577200	2794900	1890200	1671300	3724800	2170100
1549500	6339200	4987600	2117800	1965100	3407500	4658400	5919500
2875900	3453900	2078900	2107600	1209700	1922600	3321700	3322000
3294100	3484200	2562800	2624200	302850	3153300	4027100	5962600
3647300	5362300	2623700	2065800	2316900	2424500	3163400	3672000
0	897910	740180	629860	584910	1046600	1261200	2081100
11120000	13340000	9021600	6417700	7128600	6150700	9157600	10366000
3320800	6412200	3486400	3026400	3199400	3102000	5148300	5584300
2126300	2458600	2253200	1571200	2581200	1582300	1960000	2683600
2362800	3500200	2616000	2108900	1402700	2337800	3035600	3398000
3754600	5262500	4048500	3847800	1021300	2869400	2942000	4698800
843150	1131100	1018000	902970	102540	1235700	1548900	3506100
2563800	3747400	1846000	1672200	2078700	2672800	2301100	2708900
2918600	3126800	2901300	2427300	1040600	3208600	2846500	3496400
1544700	2094300	1511500	1394900	1689600	1861100	2352400	3043800
543940	1417500	1419200	824290	774630	781590	1596200	3153600
199590	184160	280160	252370	367200	157150	248140	581290
10642000	14587000	14231000	10265000	6949800	9962400	9680900	15263000
3515800	5955500	4561100	3230700	1773800	5228000	7526400	8446000
6032200	7728500	6377900	3759700	3043100	6238000	6902700	7505700
5237300	7654000	5167800	3989200	3379800	4407500	5950100	6932400

8008300	12235000	8384200	6843700	5376800	7213500	8714500	10790000
164740	209590	183710	125800	151420	119780	96171	96959
2408900	5424900	5567500	3585000	5499000	4364200	3492000	6851000
2807400	2261900	1410200	1894800	1500600	1448100	1985200	2154500
0	29287	0	0	0	66931	96972	1441000
265560	553550	908020	646280	653490	4450900	5859600	8406600
0	0	0	91771	115420	247170	108440	115390
0	37376	44499	66643	33810	86726	62244	282310
43904000	56724000	59068000	55383000	64737000	43860000	31516000	36756000
2496900	4039800	3670300	4164100	2387900	2489200	1646800	1288300
570900	0	0	0	0	398210	225330	336040
98457	61530	154010	116040	162420	112620	140000	153020
0	224610	249670	0	248060	0	52638	0
44718	166850	125620	0	44810	519620	1791500	349760
1751500	1816800	2131900	2140900	2266700	1272600	723310	1037800
203680	191300	124850	0	163610	207460	158220	165360
64953	0	144270	85135	0	1727800	2086300	4395500
0	0	0	0	0	240120	1089400	1608200
1495400	1790800	1915400	1375800	2254800	1143200	666280	1430200
1262500	1037200	1686500	1993200	6187500	3263900	3290400	1504900
97604000	171190000	167840000	194380000	173230000	267030000	315300000	432430000
23912000	32973000	19961000	10805000	2870900	31860000	49814000	51247000
425600	386730	806690	693270	1198300	674060	930910	1624300
0	180430	196580	212650	375880	687420	969200	967680
220710	195510	226550	284750	273010	265360	803050	703110
43083	129700	140700	83448	121400	662980	830550	742360
0	0	0	0	0	0	357350	0
159130	222870	315980	347130	592150	602420	791320	1456300
190310	112280	232240	150170	207220	567720	213210	385500
0	26181	20802	29208	0	77622	81225	535780
499020	311880	952320	855850	681930	2069500	2477100	2612100
508810	763010	673980	735760	791610	2241700	992040	1267100
39202	120160	97473	393810	343770	1276400	1805800	2060900
0	0	0	0	234580	0	0	0
168670	353090	201020	105660	123050	312780	159540	55766
1750800	5602500	3379100	1503300	213870	2351400	2945500	1559900
1627600	1690300	1601500	1249300	711720	917200	569130	945020
1655600	1694600	1394100	1674600	1485100	778270	883880	958500
240550	312450	642540	777880	447940	3668200	4308100	4065300
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LFQ intensi	LFQ intensi	LFQ intensi	LFQ intensi	LFQ intensi	LFQ intensi	LFQ intensi	LFQ intensi	MS/MS col
11281000	13085000	13435000	12840000	15353000	7149100	4838900	4604400	7
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2166300	2478000	5422100	5614400	3587400	12977000	11754000	9969800	2
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8095800	8965200	13493000	14946000	16414000	30296000	35782000	39972000	8
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189110	214630	148240	200330	67346	269850	952600	640760	0
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886990	867790	792580	739870	979090	435860	322710	400520	1
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251260	213150	158880	169810	140910	255990	0	98112	1
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488470	551060	416480	491150	253910	315900	242640	248170	1
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192350	196560	347110	305260	492250	187350	106300	0	0
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0	52127	0	0	0	47487	52655	355350	0
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55112	73132	65654	75710	43463	0	0	47589	0
156170	265210	149160	136680	144250	108350	163270	103240	1
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232630	144920	141600	162870	465090	201730	303730	0	1
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373540	192350	168810	157850	245120	440960	384130	509470	1
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111740	147180	248330	350830	553550	866130	1164400	1370400	0
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404140	444040	982010	1175300	1202500	486560	314730	511530	1
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264960	299290	459310	563630	611870	319920	283270	277350	0
71785	51924	118230	69696	111990	52834	0	42942	0
27603	0	0	59564	0	0	0	0	0
7138200	6170100	4706000	3824600	2221800	6162700	8799800	8039800	5
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533400	594500	831950	1191300	1879900	664820	461750	395930	1
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674290	474010	585620	662370	1179600	406280	0	264680	0
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531360	482660	1119700	1549300	2457600	3575800	3710800	3345000	1
5761800	6506900	10190000	9861000	13518000	11614000	11240000	9770500	0
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17326000	22958000	23027000	21700000	23939000	21293000	19544000	23639000	10
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6502200	5477800	3217800	2657200	3529400	4826200	5582100	4946200	6
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7001800	6398600	3355400	2809800	4348200	5107000	5052700	5410300	13
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260310	267540	277640	247030	233800	203260	207930	166000	1
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92261	163550	262300	325360	122130	91257	105050	81030	0
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642100	0	466440	0	860950	330870	0	0	0
58446000	1.56E+08	1.39E+08	1.05E+08	1.14E+08	75988000	56308000	59166000	7
17167000	22235000	18695000	22149000	13199000	25964000	12770000	15067000	5
80597000	1.5E+08	1.51E+08	1.35E+08	16749000	1.21E+08	96632000	73758000	16
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9169900	6946300	8812600	7440800	6313800	4775200	4681200	4043400	8
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946340	1107900	1188400	1347800	1674800	616630	524880	398020	1
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242380	162710	256210	292550	334760	115310	144050	133960	1
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231560	84325	147590	235350	293450	60358	42152	52504	1
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227690	0	0	0	265560	102340	171580	0	0
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947820	797890	640100	664960	1036600	293710	239770	281060	3
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2267200	2062800	2899100	3033000	2871900	1574400	962380	712740	3
93141	0	109110	81408	144120	82821	0	81914	0
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55186	206630	129280	170680	0	0	0	61595	0
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3665300	3981400	1927000	2005500	2485600	2934400	2809000	2798400	7
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473890	447690	518360	513130	631950	402830	256180	230510	2
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94346	68409	93256	66036	70648	48213	0	39666	0
4693500	4073000	5145100	4718800	4345300	3126000	2205000	1793200	6
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471720	689780	594040	321920	376980	331590	253060	173220	1
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Reverse	Potential cr id	Peptide IDs	Peptide is r	Mod. pepti	Evidence	IC MS/MS	IDs	Best MS/M
1408	1545;3188;	True;True;	f	1558;3212;	9499;9500;	5117;5118;	5117;10416	
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1523	1117;1118;	True;True;	f	1124;1125;	6840;6841;	3670;3671;	3673;3675;	
1414	1035;1165;	True;True;	f	1042;1174;	6333;6334;	3395;3396;	3396;3828;	
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1972	1711;1877;	True;True;	f	1724;1892;	10517;10518;	5624;6177;	5624;6177;	
2036	2778;1071;	True;True		2798;1079	17297;17298;	9131;9132;	9132;35408	
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1259	824;4143;5	True;True;	f	831;4170;5	5015;5016;	2690;1359	2690;13594	
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676	1040;4142;	True;True;	f	1047;4169;	6368;6369;	3414;1359	3414;13592	
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732	1842;3052;	True;True;	f	1856;3076;	11374;11375;	6060;6061;	6061;10010	
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607	1720;7218;	True;True;	f	1733;7277;	10559;10560;	5638;2363;	5638;23632	
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675 5509;6800 True;True 5549;6848 34180;420 18241;223 18241;2236;  
1327 442;2032;3 True;True; 443;2048;3 2688;1260 1490;6700;1490;6700;  
719 2559;6775 True;True 2578;6823 15909;159 8397;2226 8397;2226;  
1219 3265;1086 True;True 3290;1095 20251;202 10684;359 10684;3590;  
1000 546;1404;1 True;True; 548;1414;1 3272;3273;1774;1775;1774;4665;  
2075 3187;6518; True;True; 3211;6564;19797;197 10410;104 10411;2141;  
1752 1660 TRUE 1673 10183;101 5464;5465 5464  
135 5110;9750; True;True; 5147;9826;31619;316 16944;319 16944;3195;  
173 2731 TRUE 2751 17002;170 8975;8976 8976  
1959 1027;1077 True;True 1034;1086 6293;6294;3377;3562 3377;3562;  
1119 2164;3085; True;True; 2180;3109;13423;134 7145;7146;7147;10115;  
748 5168 TRUE 5205 31965;319 17125;171 17126  
599 1315;1765; True;True; 1325;1778;8065;8066;4359;5765;4359;5765;  
1853 4638;8827 True;False 4668;8894 28533;285 15216;287 15216;2871;  
174 1718;3229; True;True; 1731;3254;10549;105 5634;1053 5634;10534;  
1381 391;1073;1 False;False 392;1080;1 2359;2360;1308;1309;1315;3539;  
1466 391;1073;1 True;True; 392;1080;1 2359;2360;1308;1309;1315;3539;  
1438 391;1073;1 False;False 392;1080;1 2359;2360;1308;1309;1315;3539;  
890 471;6018;7 True;True; 472;6061;8 2844;2845;1578;1983 1578;1984;  
1397 1255;1741; True;True; 1264;1754;7710;1068 4153;5700;4153;5701;  
770 1156;2961; True;True; 1164;2985;7060;7061;3792;9705;3792;9705;  
771 1450;4741; True;True; 1461;4771;8882;8883;4814;4815;4814;15556;  
310 6038 TRUE 6081 37406 19907 19907  
100 293;2545;9 True;True; 294;2564;9 1776;1777;982;983;83 982;8360;3  
213 5469 TRUE 5509 33886;338 18111;181 18112  
1933 573 TRUE 575 3458;3459; 1899 1899  
1396 302;2029;3 True;True; 303;2045;3 1836;1837;1016;1017;1016;6695;  
1345 1463;2697; True;True; 1474;2717;8969;8970;4848;4849;4850;8853;  
874 1429;1490; True;True; 1440;1502;8757;8758;4745;4746;4745;4957;  
1774 9242 TRUE 9312 56962 30095 30095  
752 6252;6839 True;True 6295;6887 38777;387 20578;225 20578;2251;  
295 9845;1047 True;True 9922;1055 60868;608 32312;346 32312;3461;  
2000 3054;3726; True;True; 3078;3752;19010;190 10012;100 10012;1225;  
749 4057;7710 True;True 4083;7772 25141;251 13296;132 13298;2524;  
96 7849;9693; True;True; 7911;9768;48483;484 25707;257 25709;3174;  
2021 9700 TRUE 9775 59936;599 31781;317 31782  
637 4451;7871 True;True 4480;7933 27385;273 14586;257 14586;2578;  
2125 1900;4464; True;True; 1915;4493;11731;117 6231;6232;6233;14630;  
57 626;908;97 True;True; 630;915;98 3789;3790;2060;2950;2060;2950;  
871 3059;1013 True;True 3083;1021 19042;190 10028;100 10028;3330;  
1735 8413 TRUE 8477 51823;518 27372 27372  
613 216;1654;8 True;True; 216;1667;8 1314;1315;724;725;54 724;5446;2  
1814 3379;9327 True;True 3404;9397 20946;575 11059;303 11059;3038;  
1359 36 TRUE 36 189;190;1988;89;90 89  
1112 413;582;98 True;True; 414;584;99 2511;2512;1397;1919;1397;1921;  
511 718;792;10 True;True; 725;799;11 4374;4375;2357;2358;2359;2584;

1134 1083;6264 True;True 1090;6308 6638;6639;3575;3576;3575;20617  
 903 996;2885;4 True;True; 1003;2908;6105;6106;3273;3274;3275;9480;  
 66 941;10720 True;True 948;10805 5722;5723;3065;3543;3065;3543;  
 1175 2570;5676; True;True; 2589;5718;15977;1598444;8445;8444;18760  
 1505 639;2618;2 True;True; 643;2638;2 3867;3868;2089;8621;2089;8623;  
 2018 3797;5238; True;True; 3823;5275;23552;23512477;12412479;1739  
 1669 9387 TRUE 9458 57896;57830578;30530580  
 929 125;1514;2 True;True; 125;1526;2 746;747;74410;411;41411;5023;8  
 1017 126;1513;2 True;True; 126;1525;2 754;755;75418;419;42421;5014;8  
 1940 783;8914;1 True;True; 790;8981;1 4774;4775;2558;2559;2559;29029  
 1399 1436;4863; True;True; 1447;4896;8797;8798;4766;1604.4766;16049  
 301 4863;4994; False;True; 4896;5031;29989;29916042;16016045;1653  
 276 1436;4863; False;False 1447;4896;8797;8798;4766;1604.4766;16049  
 1434 3239;4862; True;True; 3264;4895;20110;20110565;10510567;1604  
 2043 1748;2412 True;True 1761;2429 10725;1075727;5728;5728;7927  
 177 2725;8243; True;True; 2745;8306;16962;1698949;8950;8952;26920  
 2145 4259;1050. True;True 4286;1058026387;26313982;34713982;3470  
 60 2060;3004; True;True; 2076;3028;12779;1276802;6803;6803;9859;  
 730 10653 TRUE 10738 66128;66135211;352135211  
 590 6265 TRUE 6309;6310 38858;38820619;20620619  
 508 4809;6217 True;True 4842;6260 29670;29615832;15815833;2048  
 1295 905;1798;5 True;True; 912;1812;5 5494;5495;2942;2943;2946;5880;  
 1036 100;3794;7 True;True; 100;3820;7 591;592;59311;312;12311;12462;  
 1013 336;382;45 True;True; 337;383;45 2022;2023;1117;1277;1117;1279;  
 1277 740;1063;2 True;True; 747;1070;2 4505;4506;2403;2404;2408;3495;  
 1179 2252;1049. True;True; 2268;1057013993;1397425;34687425;34689  
 1521 496;2269;4 True;True; 497;2285;4 2999;3000;1657;1658;1658;7478;  
 229 496;2269;4 False;False 497;2285;4 2999;3000;1657;1658;1658;7478;  
 88 4172;4301; False;False 4199;4328;25873;25813709;14013709;1409  
 1045 4297;9033; True;True; 4324;9101;26555;26514085;14014085;2942  
 726 940;2766;2 True;True; 947;2786;2 5714;5715;3061;3062;3061;9094;  
 1994 3311 TRUE 3336 20538;2051083610836  
 445 10742 TRUE 10827 66712;66735515;35535515  
 1176 4223;1093. True;True 4250;1101026173;26113860;13813861;3610  
 1021 145;456;45 True;True; 145;457;45 886;887;88498;499;50498;1532;1  
 796 146;147;45 True;True; 146;147;45 894;895;89503;504;50505;507;15  
 149 3571;4018; True;True; 3596;4044;22212;22211752;11711754;1314  
 1398 157 TRUE 157 939;940;94528;529;53530  
 168 7441 TRUE 7501 45946;4592434824348  
 942 119;120;10 True;True; 119;120;10 702;703;70383;384;38387;391;35  
 1680 6104;1068. True;True 6147;1076037840;37820107;20120110;3530  
 116 10067 TRUE 10145 62285;6223304133041  
 720 2083;4579; True;True; 2099;4609;12905;12906871;6872;6873;15029  
 1235 10867 TRUE 10952 67473;67435899;35935900  
 1096 3359;4636; True;True; 3384;4666;20845;20810996;10910997;1521  
 1558 3426;4665; True;True; 3451;4695;21244;21211227;11211227;1530  
 1569 3297;8432; True;True; 3322;8496;20448;20410789;10710789;2744  
 186 266;339;49 True;True; 266;340;50 1606;1607;901;1123;1901;1123;1  
 1767 5858;9590 True;True 5901;9663 36289;36219363;19319368;3136  
 433 1184;1292; True;True; 1193;1301;7261;7262;3896;3897;3897;4266;

1529 208;1050;2 True;True; 208;1057;2 1259;1260;694;695;69 695;3452;9  
2161 8041 TRUE 8104 49618;496 26259;262 26261  
163 5726 TRUE 5768 35506;355 18937 18937  
916 128;129;69 True;True; 128;129;69 768;769;77 423;424;42 423;425;22  
2093 4133 TRUE 4160 25629;256 13565;135 13566  
1316 1423;1497; True;True; 1434;1509; 8724;8725;4734;4973; 4734;4974;  
952 252;1170;1 True;True; 252;1179;1 1508;1509;840;841;84 841;3839;3  
1019 636;931;14 True;True; 640;938;15 3846;3847;2084;3024; 2084;3025;  
981 102;277;14 True;True; 102;278;14 598;599;60 318;319;32 318;941;49  
974 3144;3436; True;True; 3168;3461; 19549;195 10292;112 10292;112  
1087 712;1488;2 True;True; 719;1500;2 4352;4353;2345;4952; 2345;4953;  
1032 1352;1474; True;True; 1362;1485; 8279;8280;4484;4485; 4484;4902;  
1264 242;349;81 True;True; 242;350;82 1463;2099;816;1168;2 816;1168;2  
148 8187;8612 True;True 8250;8678 50571;505 26743;267 26748;280  
1549 1440;1446; True;True; 1451;1457; 8827;8828;4787;4788; 4788;4808;  
631 505;2554 True;True 506;2573 3055;3056;1683;8389 1683;8389  
881 150;1517;6 True;True; 150;1529;6 906;907;93 511;5028;2 511;5028;2  
19 1440;5136; False;False 1451;5173; 8827;8828;4787;4788; 4788;1702  
39 4974;8782; True;True; 5011;8849; 30719;307 16421;285 16421;285  
753 1726 TRUE 1739 10591;105 5651 5651  
2120 3864 TRUE 3890 23978;239 12689 12689  
1847 3403;8511 True;True 3428;8575 21091;210 11138;276 11138;276  
917 2633;3589; True;False; 2653;3615; 16402;164 8678;8679; 8679;1180  
205 1416 TRUE 1427 8689;8690;4707;4708; 4708  
661 562;5035 True;True 564;5072 3393;3394;1861;1665 1861;1666  
531 9081;1027; True;True 9149;1035 55950;559 29572;338 29572;338  
1970 2566;2858; True;True; 2585;2881; 15953;159 8436;8437; 8438;9406;  
1534 4667;6982; True;True; 4697;7035; 28705;287 15311;153 15314;229  
884 76;1280;15 True;True; 76;1289;15 442;443;44 240;241;42 240;4235;5  
2189 286;3155;4 True;True; 287;3179;4 1736;1737; 962;963;96 963;10325;  
55 9451 TRUE 9522 58310;583 30860 30860  
1346 1162;1681; True;True; 1171;1694; 7109;7110;3816;3817; 3816;5535;  
966 715;2093;4 True;True; 722;2109;4 4362;4363;2349;2350; 2352;6909;  
798 2340;2665; True;True; 2356;2685; 14511;145 7701;7702; 7702;8762;  
1067 5175;7607; True;True; 5212;7669; 32010;320 17152;249 17152;249  
900 886;1400;2 True;True; 893;1410;2 5382;5383;2889;2890; 2889;4639;  
1042 169;1032;2 True;True; 169;1039;2 1011;1012; 564;3392;8 564;3392;8  
1736 4737;8629 True;True 4767;8695 29148;291 15533;155 15533;281  
1555 819;2341;5 True;True; 826;2357;5 4987;4988;2679;2680; 2680;7703;  
211 5048 TRUE 5085 31204;312 16705;167 16707  
1837 5071;9767 True;True 5108;9844 31363;313 16800;320 16800;320  
247 7438;8928; True;True; 7498;8995; 45933;459 24337;243 24338;290  
494 1671;2760 True;True 1684;2780 10251;102 5501;5502; 5501;9072  
1117 4430;4431; True;True; 4459;4460; 27290;272 14524;145 14525;145  
904 6072 TRUE 6115 37611;376 20006;200 20007  
1124 765;1060;2 True;True; 772;1067;2 4664;4665;2505;2506; 2506;3486;  
940 194;476;49 True;True; 194;477;49 1160;1161; 640;641;64 640;1588;1  
853 425;5191;5 True;True; 426;5228;5 2591;3210 1448;1720 1448;1720  
1163 811;4568 True;True 818;4598 4943;4944;2647;2648; 2649;1497  
1369 2473;1084; True;True 2491;1093 15363;153 8122;8123; 8124;3583



1366 963;1526 True;True 970;1538 5852;5853;3121;5052;3121;5052  
 456 5202;9819; True;True; 5239;9896; 32177;321 17246;172 17248;322  
 1215 191;2879;3 True;True; 191;2902;3 1144;1145; 630;9463;9 630;9466;1  
 1281 3573;6570; True;True; 3598;6616; 22228;222 11761;117 11765;215  
 1080 3015;8082; True;True; 3039;8145; 18782;187 9898;2639 9898;2639  
 2042 1414;4919; True;True; 1425;4956; 8677;8678; 4702;4703; 4702;1623  
 31 365 TRUE 366 2189;2190;1212;1213 1212  
 1147 4478;9210 True;True 4508;9280 27569;275 14690;146 14692;300  
 1400 4023;7615; True;True; 4049;7677; 24913;249 13159;249 13159;249  
 586 4674;6445 True;True 4704;6491 28759;287 15344;211 15344;211  
 2081 6233 TRUE 6276 38667;386 20532;205 20532  
 2038 4603 TRUE 4633 28323;283 15102 15102  
 1338 334;531;11 True;True; 335;533;11 2015;2016; 1113;1114; 1113;1742;  
 1071 511;9553;9 False;False 512;9626;9 3099;3100; 1698;1699; 1701;3120  
 964 4624;4695; True;True; 4654;4725; 28448;284 15167;151 15171;154  
 1508 511;1758;2 True;True; 512;1771;2 3099;3100; 1698;1699; 1701;5754;  
 858 1241;1986; True;True; 1250;2002; 7640;7641; 4125;4126; 4126;6536;  
 724 3980;8142; True;True; 4006;8205; 24671;246 13026;265 13026;265  
 1266 84;8927;10 True;True; 84;8994;10 492;493;54 271;29051; 271;29051;  
 1537 37;82;296; True;True; 37;82;297; 193;194;1991;92;93;9 96;264;988  
 62 1816;3069; True;True; 1830;3093; 11207;112 5965;5966; 5966;1006  
 2044 2480;2670; True;True; 2498;2690; 15405;154 8143;8144; 8144;8769;  
 496 2339;8968 True;True 2355;9036 14509;145 7700;2919 7700;2920  
 546 816;7145;7 True;True; 823;7204;7 4972;4973; 2671;2339 2671;2339  
 727 540;2476;3 False;False 542;2494;3 3243;3244; 1762;1763; 1763;8136;  
 123 1673;1729; True;True; 1686;1742; 10265;106 5504;5663; 5504;5663;  
 86 7288 TRUE 7347 45016;450 23873 23873  
 1821 424;5962;7 True;True; 425;6005;7 2584;2585; 1447;1970 1447;1970  
 1786 2508;8952 True;True 2527;9020 15587;155 8235;8236; 8236;2914  
 663 10750 TRUE 10835 66747;667 35525 35525  
 882 6157 TRUE 6200 38189;381 20279;202 20280  
 883 2538;4549; True;True; 2557;4579; 15787;157 8340;8341; 8342;1492  
 122 2047;5033 True;True 2063;5070 12698;126 6758;1665 6758;1665  
 842 1532 TRUE 1544;1545 9417;9418; 5077;5078; 5084  
 1494 10901 TRUE 10986 67677 35986 35986  
 1751 322;1641;2 True;True; 323;1654;2 1946;1947; 1077;1078; 1078;5404;  
 413 1420;1948; True;True; 1431;1964; 8713;8714; 4728;6406; 4728;6406;  
 1209 3058;4020; True;True; 3082;4046; 19034;190 10021;100 10027;131  
 1322 298;5706;6 True;True; 299;5748;6 1808;1809; 998;999;10 999;18866;  
 1676 4377 TRUE 4406 26968;269 14337 14337  
 164 6886;9064; True;True; 6934;9132; 42583;425 22616;226 22616;295  
 12 2272;2573; True;True; 2288;2592; 14092;140 7483;7484; 7484;8449;  
 1409 8961;1036; True;True; 9029;1044 55220;552 29179;291 29180;342  
 1584 9044 TRUE 9112 55707;557 29451;294 29451  
 1247 10745 TRUE 10830 66723;667 35520 35520  
 1697 1611;4853; True;True; 1624;4886; 9877;9878; 5333;1602 5333;1602  
 1365 2491;4313; True;True; 2509;4340; 15477;154 8185;1412 8185;1412  
 1566 4400;6199; True;True; 4429;6242; 27084;270 14400;204 14400;204  
 956 528;1173;1 True;True; 530;1182;1 3189;3190; 1737;3858; 1737;3858;  
 1033 2308;6311 True;True 2324;6357 14300;143 7603;7604; 7604;2076

1186 356;613;20 True;True; 357;616;20 2147;2148; 1198;1199; 1198;2013;  
 1808 5498 TRUE 5538 34106;3410 18194 18194  
 48 1698;9774 True;True 1711;9851 10422;104 5582;5583; 5583;32068  
 477 11530 TRUE 11616 71590;715 38007;380 38011  
 2088 6140;7649; True;True; 6183;7711; 38085;380 20214;202 20214;2504  
 1349 11493 TRUE 11579 71392;713 37901 37901  
 2066 800;3183 True;True 807;3207 4865;4866; 2598;1040 2598;1040  
 1842 9162;1008 True;True 9231;1016 56462;564 29833;298 29833;3310  
 2028 5943;6599 True;True 5986;6645 36849;368 19668;216 19668;216  
 1879 2090;3226; True;True; 2106;3251; 12956;129 6897;6898; 6898;10528  
 617 294 TRUE 295 1781;1782; 984 984  
 680 2805;6043; True;True; 2826;6086; 17489;174 9213;9214; 9216;19920  
 486 88;1468;34 True;True; 88;1479;34 517;518;51 276;4869;1 276;4869;1  
 849 1649;7241; True;True; 1662;7300; 10108;101 5436;5437; 5438;23695  
 440 7537 TRUE 7598 46554;465 24664 24664  
 499 50;80;629; True;True; 50;80;633; 288;289;29 141;253;25 141;256;20  
 35 7228;7717 True;True 7287;7779 44659;446 23665;252 23665;252  
 1101 1824;3338; True;True; 1838;3363; 11258;112 5996;1093 5996;1093  
 1921 4763;4957; True;True; 4794;4994; 29322;306 15628;163 15628;163  
 1778 5434 TRUE 5473 33637;336 18004 18004  
 2094 445;913;17 True;True; 446;920;17 2705;2706; 1503;1504; 1505;2958;  
 1729 4396;4482; True;True; 4425;4512; 27070;270 14393;143 14395;1470  
 242 34;1773;40 True;True; 34;1786;40 181;182;18 83;84;85;8 84;5799;13  
 2010 287;2464;5 True;True; 288;2482;5 1742;1743; 967;968;81 968;8105;1  
 1141 258;547;80 True;True; 258;549;81 1559;1560; 872;873;87 873;1776;2  
 9 4843;8944; True;True; 4876;9012; 29886;298 15988;159 15988;2912  
 953 3620;3688; True;True; 3646;3714; 22474;224 11899;119 11902;1213  
 1069 4912;5770; True;True; 4949;5812; 30317;303 16212;162 16212;1908  
 113 1962;5408; True;True; 1978;5446; 12173;334 6448;1794 6448;1794  
 223 443;1187;1 True;True; 444;1196;1 2689;2690; 1491;1492; 1494;3906;  
 1140 2688;3371; True;True; 2708;3396; 16733;167 8827;8828; 8832;11029  
 802 1670;3689; True;True; 1683;3715; 10250;228 5500;1213 5500;1213  
 998 6706;8572; True;True; 6754;8636; 41508;415 22025;220 22030;2789  
 632 168 TRUE 168 1003;1004; 561;562;56 563  
 526 6313;7924; True;True; 6359;7987; 39131;391 20764;259 20764;259  
 905 2667;8366; True;True; 2687;8429; 16610;166 8765;8766; 8766;27220  
 1057 1970;2392; True;True; 1986;2409; 12221;122 6476;7883; 6476;7883;  
 855 1759;2058; True;True; 1772;2074; 10786;107 5755;6800; 5755;6800;  
 1311 2611;3499; True;True; 2631;3524; 16247;162 8601;1150 8601;1150  
 1114 592;2072;6 True;True; 594;2088;6 3554;3555; 1949;1950; 1949;6839;  
 372 3018;9959; True;True; 3042;1003 18802;188 9903;3267 9903;3267  
 414 3364;3669 True;True 3389;3695 20870;227 11004;120 11004;120  
 130 3227;1155 True;True 3252;1164 20035;200 10529;105 10529;3810  
 475 2539;3129 True;True 2558;3153 15795;157 8343;1023 8343;1023  
 1962 7036;7778 True;True 7091;7840 43467;434 23068;254 23068;254  
 913 218;227;22 True;True; 218;227;22 1328;1329; 729;730;73 731;752;75  
 1099 4049;4103; True;True; 4075;4130; 25080;250 13246;132 13248;1343  
 1201 11;488;521 True;True; 11;489;523 69;70;71;7 26;27;28;2 28;1628;17  
 226 381;4366;6 True;True; 382;4393;6 2303;2304; 1271;1272; 1272;14273  
 313 663;3115;4 True;True; 667;3139;4 4018;4019; 2161;2162; 2164;10205

151 1826;2312;True;True;1840;2328;11274;1126005;6006;6009;7626;  
 1091 1129;4407;True;True;1136;4436;6910;6911;3714;3715;3714;1443;  
 1012 1199;1538;True;True;1208;1551;7350;7351;3954;5101;3954;5103;  
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 1518 638;4070 True;True 642;4096 3860;3861;2088;1333 2088;1333;  
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772	1237;4858	True;True	1246;4891 7614;7615;	4110;1603	4110;1603	
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 1132 20;56;623; True;True; 20;56;627; 112;113;1149;50;51;550;162;204  
 1027 412;882;11True;True; 413;889;112503;2504;1396;2872;1396;2874;  
 267 3754;5750;True;True; 3780;5792;23296;23212350;12312350;1901  
 1260 3610;5969;True;True; 3636;6012;22417;22411863;11811865;1971

1293 238;1709;2 True;True; 238;1722;2 1439;1440;796;797;79 797;5617;7  
 1958 1210 TRUE 1219 7416;7417;3990;3991; 3992  
 97 6936 TRUE 6987 42914;429 22790;227 22790  
 488 10525 TRUE 10609 65290;652 34786 34786  
 1310 761;4209;4 True;True; 768;4236;4 4636;4637;2485;2486;2487;13808  
 864 4836;6200; True;True; 4869;6243;29838;298 15937;159 15940;2042  
 714 8088 TRUE 8151 49913;499 26408;264 26408  
 2057 1788;4807; True;True; 1802;4840;11011;110 5856;5857;5857;15815  
 406 378;829;34 True;True; 379;836;34 2283;2284;1260;1261;1262;2706;  
 1157 1543;2793; True;True; 1556;2814;9489;9490;5114;5115;5114;9183;  
 1943 1686;2221; True;True; 1699;2237;10352;103 5548;5549;5550;7325;  
 567 7246;9807; True;True; 7305;9884;44763;447 23711;237 23712;3217  
 1039 818;1658;2 True;True; 825;1671;2 4983;4984;2675;2676;2676;5456;  
 821 525;7832 True;True 527;7894 3177;3178;1733;2564 1733;2564  
 1492 222;8731;1 True;True; 222;8798;1 1348;1349;740;28418;740;28424;  
 1248 1388;1946; True;True; 1398;1962;8497;8498;4587;4588;4587;6398;  
 112 5999;7751; True;True; 6042;7813;37166;371 19795;253 19795;2537  
 1165 327;831;23 True;True; 328;838;23 1972;1973;1091;1092;1094;2715;  
 1495 3678 TRUE 3704 22827;228 12102;121 12104  
 901 136;137;10 True;True; 136;137;10 814;815;81 445;446;44 450;460;33  
 394 1126;1445; True;True; 1133;1456;6895;6896;3707;3708;3708;4805;  
 245 551;3567;5 True;True; 553;3592;5 3306;3307;1793;1794;1793;11732  
 578 4467;6938 True;True 4496;6989 27495;274 14641;146 14641;2275  
 947 1980;2639; True;True; 1996;2659;12301;123 6516;6517;6517;8695;  
 1926 5763 TRUE 5805 35748;357 19057;190 19060  
 723 1036;8425 True;True 1043;8489 6336;6337;3397;3398;3398;27424  
 1798 3235;7988; True;True; 3260;8051;20091;200 10554;260 10554;2605  
 1633 4873;1128 True;True; 4906;1137 30039;300 16065;160 16068;3720  
 2063 6689 TRUE 6736 41395;413 21971;219 21972  
 791 5039;6705 True;True 5076;6753 31157;311 16680;220 16680;2202  
 838 160;2120;5 True;True; 160;2136;5 950;951;95 536;537;70 536;7026;1  
 387 1647;5049; True;True; 1660;5086;10093;100 5426;5427;5429;16712  
 1892 1232;1438; True;True; 1241;1449;7571;7572;4090;4091;4090;4780;  
 65 5129;7428 True;True 5166;7488 31733;317 16999;170 17000;2430  
 1993 1592 TRUE 1605 9777;9778;5273;5274; 5274  
 1844 5542 TRUE 5582 34375;343 18335;183 18336  
 1382 1017;1531; True;True; 1024;1543;6240;6241;3343;3344;3343;5076;  
 1230 1486;1988; True;True; 1498;2004;9136;9137;4948;6539;4948;6543;  
 1047 2644;4352; True;True; 2664;4379;16472;164 8707;8708;8708;14231  
 255 3601;6609; True;True; 3627;6655;22374;223 11836;216 11836;2168  
 275 3;541 True;True 3;543 20;21;22;2 13;1764 13;1764  
 696 2932;3491 True;True 2956;3516 18278;182 9625;9626;9625;11483  
 1276 1148;2195; True;True; 1155;2211;7012;7013;3766;3767;3767;7246;  
 930 2627;4926; True;True; 2647;4963;16361;163 8657;1625 8657;16253  
 1086 1427;2053; True;True; 1438;2069;8746;8747;4740;4741;4740;6787;  
 1242 397;4306;4 True;True; 398;4333;4 2400;2401;1334;1335;1341;14105  
 269 790;6863 True;True 797;6911 4820;4821;2580;2257 2580;22575  
 1608 728;2183;2 True;True; 735;2199;2 4438;4439;2378;7209;2378;7214;  
 1364 815;3296;3 True;True; 822;3321;3 4968;4969;2669;2670;2670;10788  
 1917 1504;2544; True;True; 1516;2563;9251;9252;4994;8354;4994;8355;



780 3461;4642;True;True;13486;4672;21504;21511;11377;15211377;1521  
1377 5931;6086;True;True;15974;6129;36761;367119615;19619618;2004  
735 3180;1056;True;True;13204;106519769;19710396;10310397;3490  
693 2203;2463;True;True;12219;2481;13678;15317259;8100;7259;8100;  
47 2302;2381;True;True;12318;2398;14265;14217586;7587;7586;7860;  
1581 1849;2318;True;True;11863;2334;11406;11416079;7645;6079;7647;  
585 1453;5156 True;True 1464;5193 8898;8899;4818;4819;4818;17098  
707 2629 TRUE 2649 16373;16318664;8665 8665  
200 3505;5545;True;True;13530;5585;21785;217111519;18311519;1834  
469 6250 TRUE 6293 38766;387120572;205120572  
1519 77;530;166 True;True;177;532;167449;450;45242;1741;5242;1741;5  
360 1723;8882 True;True 1736;8949 10580;10515648;289415648;28946  
416 2186;9095;True;True;12202;9163;13585;13517219;7220;7221;29610  
1640 1168;2125;True;True;11177;2141;7154;7155;3836;7036;3836;7036;  
1354 2248;6422 True;True 2264;6468 13975;13917417;211017417;21102  
647 2204;2205;True;True;12220;2221;13679;13617260;7261;7262;7267;  
26 4406;4870;True;True;14435;4903;27133;27114426;16014426;1605  
1370 906;4283;6 True;True;1913;4310;65502;5503;2947;2948;2948;14041  
216 5647 TRUE 5688 35030;35018676;18618679  
1708 2477;3650;True;True;12495;3676;15389;15318137;120018137;12012  
1600 5968 TRUE 6011 36983;36919716 19716  
1636 6607;1064;True;True 6653;1073140907;409121680;351121680;3519  
471 5514;9102 True;True 5554;9170 34204;34218254;29618254;2963  
766 1503;1938;True;True;11515;1954;9243;9244;4991;4992;4991;6376;  
1356 30;31;673;True;True;130;31;677;163;164;1675;76;218275;76;2184  
2007 1124;8431 True;True 1131;8495 6883;6884;3699;274313699;27438  
1945 671;1133;1 True;True;1675;1140;14065;4066;2180;3722;2180;3722;  
404 656;752;82 True;False; 660;759;833976;4578;2146;2446;2146;2450;  
2148 103;762;11 True;True;1103;769;11606;607;60325;326;32325;2493;3  
1541 226;317;95 True;True;1226;318;951371;1372;748;749;75750;1063;3  
1335 2005;2143;True;True;12021;2159;12440;1246605;6606;6605;7093;  
1274 200;2149;2 True;True;1200;2165;21194;1195;658;7103;7658;7104;7  
1275 2042;5386;True;True;12058;5424;12663;12616736;6737;6737;17889  
1874 4485;4677;True;True;14515;4707;27621;27614727;14714727;1534  
13 524;3647;3 True;True;1526;3673;43171;3172;1732;11991732;12001  
1894 4556;4995;True;True;14586;5032;28031;28014938;14914939;1653  
1035 1016;7869;True;True;11023;7931;6236;6237;3341;3342;3342;25774  
1878 482;3267;5 True;True;1483;3292;52902;2903;1605;1606;1607;10693  
1677 2883;3553;True;True;12906;3578;17985;17919474;116819474;11689  
140 143;165;42 True;True;1143;165;42874;875;87491;492;54491;550;14  
1504 1033;6814;True;True;11040;6862;6323;6324;3393;224213393;22425  
462 565;4728;7 True;True;1567;4758;73414;3415;1872;1873;1873;15509  
677 2456;2989;True;True;12474;3013;15263;15218078;9796;8078;9796;  
534 3471;4523;True;True;13496;4553;21563;215111405;14811405;1483  
911 2520;4646;True;True;12539;4676;15668;15618265;8266;8266;15235  
1693 6885 TRUE 6933 42582 22615 22615  
1095 241;267;27 True;True;1241;267;271456;1457;810;811;81815;903;91  
831 188;279;28 True;True;1188;280;281126;1127;625;626;94625;947;95  
1830 619;1578 True;True 622;1591 3735;3736;2033;5222;2033;5222  
1233 2110;6015;True;True;12126;6058;13091;13016977;6978;6982;19835

+

1159 1290;6385;True;True; 1299;6431;7894;7895;4263;4264;4263;2098;  
854 866;5076;5 True;True; 873;5113;5 5274;5275;2828;2829;2830;1681;  
393 2840;6103;True;True; 2861;6146;17688;176 9320;2010 9320;2010  
85 1180;2172 True;True 1189;2188 7238;7239;3877;3878;3877;7186  
239 726;2202;2 True;True; 733;2218;2 4425;4426;2376;7258;2376;7258;  
287 5917;8002 True;True 5960;8065 36674;366 19575;195 19575;261;  
809 6500 TRUE 6546 40277;402 21359 21359  
914 92;93;569; True;True; 92;93;571; 543;544;54 282;283;28 283;284;18  
989 1328;1537;False;False 1338;1550;8146;8147;4409;4410;4411;5100;  
960 8;32;502;4 True;True; 8;32;503;4 52;53;54;5 22;77;78;7 22;77;1678  
1626 8682 TRUE 8749 53526;535 28275;282 28275  
457 373;4559;6 True;True; 374;4589;6 2241;2242;1238;1495 1238;1495;  
976 140;1555;1 True;True; 140;1568;1 850;851;85 476;477;47 486;5159;6  
1072 5024;8155 True;True 5061;8218 31066;310 16635;166 16636;266;  
1539 1062;2585;True;True; 1069;2604;6512;6513;3492;8503;3492;8503;  
1379 10088;108 True;True 10166;109 62414;624 33109;358 33109;358  
826 503;7509;1 True;True; 504;7570;1 3042;3043;1680;2457 1680;2457;  
1678 2847;3540;True;True; 2868;3565;17750;177 9354;9355;9358;1165  
1991 1587;1059;True;True 1600;1067 9750;9751;5253;5254;5253;3501;  
352 370;859;18 True;True; 371;866;18 2226;2227;1235;2804;1235;2805;  
1553 6504 TRUE 6550 40303;403 21366 21366  
1478 729;793;29 True;True; 736;800;29 4442;4443;2379;2586;2379;2589;  
818 2682;9167 True;True 2702;9236 16689;166 8806;8807;8806;2985  
544 6817 TRUE 6865 42179;421 22432 22432  
2060 8453;9947 True;True 8517;1002 52095;615 27498;326 27498;326;  
545 10342 TRUE 10425 64156;641 34168;341 34170  
365 3039;4774;True;True; 3063;4806;18929;189 9976;1568 9976;1568;  
1010 1563;1800;True;True; 1576;1814;9594;9595;5173;5896;5173;5896;  
99 1994;4265;True;True; 2010;4292;12380;123 6570;1399 6570;1399;  
694 863;1231;1 True;True; 870;1240;1 5251;5252;2814;2815;2814;4089;  
893 552;572;11 True;True; 554;574;12 3314;3315;1800;1801;1803;1897;  
379 11077;111 True;True 11162;112 68763;695 36570;369 36570;369;  
1286 5851 TRUE 5894 36249;362 19341;193 19342  
1935 871;4006;1 True;True; 878;4032;1 5300;2483 2847;1310 2847;1310;  
865 1369;1570;True;True; 1379;1583;8374;8375;4529;4530;4529;5198;  
1527 1322;2422;True;True; 1332;2439;8104;8105;4383;4384;4383;7959;  
1278 1001;2074;True;True; 1008;2090;6137;6138;3284;6841;3284;6841;  
856 2496;5722 True;True 2514;5764 15512;155 8205;1892 8205;1892;  
1768 2027 TRUE 2043 12564;125 6676;6677; 6676  
895 637;3685;5 True;True; 641;3711;5 3854;3855;2085;2086;2085;1213;  
431 430;2828;7 True;True; 431;2849;7 2613;1762 1460;9290;1460;9290;  
1480 4014;4255;True;True; 4040;4282;24873;248 13142;131 13143;139  
975 648;895;18 True;True; 652;902;18 3918;3919;2117;2118;2122;2915;  
921 3447;4780;True;True; 3472;4812;21398;213 11307;113 11316;157  
1696 2244 TRUE 2260 13946;139 7399;7400; 7399  
1256 1366;1452;True;True; 1376;1463;8357;8358;4519;4520;4522;4817;  
167 7104;8450 True;True 7162;8514 43892;438 23267;232 23268;274  
1244 3539;9022;True;True; 3564;9090;22024;220 11650;116 11651;293  
1304 11032 TRUE 11117 68510;685 36426;364 36426  
303 6816 TRUE 6864 42175;421 22429;224 22430

497 2560;4883;True;True; 2579;4916;15912;159 8398;1610 8398;1610;  
 2076 4447 TRUE 4476 27361;273 14573 14573  
 1200 3475;3621;True;True; 3500;3647;21593;215 11430;114 11430;1190  
 1306 154;2526;4True;True; 154;2545;4924;925;15522;523;82522;8291;1  
 1861 189;642;29True;True; 189;646;29 1134;1135;627;2097;2 627;2097;9  
 515 5628;5728;True;True; 5669;5770;34914;349 18627;186 18628;1893  
 1992 2394;8458 True;True 2411;8522 14896;148 7886;2750 7886;2750;  
 2002 795;2824;5True;True; 802;2845;5 4843;4844;2591;9280;2591;9280;  
 1988 5012 TRUE 5049 30981;309 16591 16591  
 233 57 TRUE 57 333;334;33 167;168;16 171  
 1538 2505;5721;True;True; 2524;5763;15568;155 8230;1892 8230;1892;  
 1762 5232 TRUE 5269 32379;323 17374;173 17375  
 363 7402 TRUE 7461 45707 24218 24218  
 2157 6370;8329 True;True 6416;8392 39455;394 20914;271 20914;271;  
 492 5153;9569 True;True 5190;9642 31886;318 17086;170 17086;3128  
 1986 325;8769 True;True 326;8836 1964;5401 1089;2853 1089;28538  
 2008 1730;2666;True;True; 1743;2686;10615;106 5664;5665;5666;8763;  
 2091 10058 TRUE 10136 62223;622 33004;330 33005  
 908 6822;9328 True;True 6870;9398 42207;422 22450;224 22450;3038  
 248 94;3238;43True;True; 94;3263;43 555;556;55 286;287;28 287;10562;  
 285 564 TRUE 566 3408;3409;1867;1868; 1868  
 566 2423 TRUE 2440 15052;150 7960;7961; 7960  
 1333 3341;3737 True;True 3366;3763 20737;207 10938;122 10938;122;  
 1460 1907;2455;True;False; 1922;2473;11779;117 6246;8077;6246;8077;  
 925 706;2455;2True;False; 712;2473;2 4296;4297;2321;8077;2321;8077;  
 2074 885;5730;8True;True; 892;5772;8 5375;5376;2883;2884;2883;18944  
 1446 131;5257;5True;True; 131;5294;5 783;784;78 430;17469;430;17471;  
 1447 138;2563;5True;True; 138;2582;5 830;831;83 461;462;46 463;8408;1  
 973 2455;2920;True;True; 2473;2944;15256;152 8077;9578;8077;9578;  
 1307 6185;1016 True;True 6228;1024 38363;383 20374;203 20374;3340  
 1459 688;6184;7True;False; 692;6227;7 4165;4166;2238;2036 2238;2036;  
 1155 6185;9784 False;True 6228;9861 38363;383 20374;203 20374;3210  
 1614 777 TRUE 784 4739;4740 2547 2547  
 1465 305;1498;1True;True; 306;1510;1 1850;1851;1028;1029;1028;4980;  
 1956 8667;8994 True;True 8734;9062 53448;534 28227;282 28227;2930  
 557 2880 TRUE 2903 17972;179 9468 9468  
 2051 1353;1027 True;True 1363;1035 8285;8286;4486;4487;4490;33843  
 2048 211;4791;9True;True; 211;4824;9 1278;1279;706;707;15 706;15755;  
 820 786;1895;4True;True; 793;1910;4 4795;4796;2570;2571;2570;6221;  
 1715 243;1499;2True;True; 243;1511;2 1464;1465;817;4983;7 817;4983;7  
 1547 2952 TRUE 2976 18407;184 9682;9683 9682  
 127 14;249;363True;True; 14;249;364 89;90;91;1 37;38;830;38;830;121  
 1199 314;353;40True;True; 315;354;40 1906;1907;1052;1053;1053;1184;  
 1065 880;975;18False;False 887;982;18 5353;5354;2866;2867;2866;3171;  
 1003 881;1028;1True;True; 888;1035;1 5356;5357;2869;2870;2869;3379;  
 841 7308 TRUE 7367 45130;451 23915;239 23916  
 1850 403;1659;1True;True; 404;1672;1 2437;2438;1355;1356;1358;5463;  
 1561 346;850;23True;True; 347;857;23 2075;2076;1147;1148;1149;2766;  
 922 848;849;15True;True; 855;856;16 5164;5165;2760;2761;2762;2764;  
 957 202;760;12False;True; 202;767;12 1202;1203;663;664;66 669;2483;4

965 181;202;63 True;True; 181;202;63 1089;1090;610;663;66 610;669;20  
 1348 881;1405;3 False;True; 888;1416;3 5356;5357;2869;2870;2869;4670;  
 666 2201;6891; True;True; 2217;6939; 13673;136 7257;2263 7257;2263  
 179 6890;9935 True;True 6938;1001 42618;426 22634;326 22634;326  
 1174 1313;3445; True;True; 1323;3470; 8054;8055;4355;1130 4355;1130  
 1719 755 TRUE 762 4594;4595;2460;2461 2460  
 + 323 1066;6949; True;True; 1073;7000; 6530;6531;3501;3502;3502;2282  
 1476 3043;6011; True;False; 3067;6054; 18949;372 9985;1982 9985;1983  
 + 316 1320;8452; True;True; 1330;8516; 8092;8093;4377;2749 4377;2749  
 643 10248 TRUE 10328 63496;634 33739;337 33744  
 1325 1244;3951; True;True; 1253;3977; 7662;7663;4131;1292 4131;1292  
 204 3453;5741; True;True; 3478;5783; 21444;214 11338;113 11338;189  
 364 2900;4654; True;True; 2924;4684; 18072;180 9519;9520;9522;1526  
 1568 2199;3690; True;True; 2215;3716; 13657;136 7251;7252;7253;1213  
 513 2216;2219; True;False; 2232;2235; 13762;137 7308;7309;7309;7320;  
 1326 2217;2220; True;True; 2233;2236; 13768;137 7310;7311;7311;7324;  
 576 2737;2910; True;True; 2757;2934; 17040;170 8994;9549;8994;9550;  
 22 3583;1044 True;True; 3609;1053 22282;222 11791;345 11791;345  
 1331 994;1766;4 True;True; 1001;1779; 6085;6086;3256;3257;3258;5770;  
 423 994;1744;3 False;True; 1001;1757; 6085;6086;3256;3257;3258;5719;  
 1362 1744;2377; False;True; 1757;2394; 10698;106 5712;5713;5719;7853;  
 1187 993;1000;1 True;True; 1000;1007; 6077;6078;3252;3253;3254;3283;  
 1413 2656;3636; True;True; 2676;3662; 16542;165 8740;8741;8742;1195  
 1041 535;5104;5 True;True; 537;5141;5 3218;3219;1750;1692 1750;1692  
 1328 58;152;192 True;True; 58;152;192 340;341;34 174;175;17 175;513;63  
 813 439;1705;1 True;True; 440;1718;1 2669;2670;1484;5609;1484;5609;  
 789 439;1778;2 False;True; 440;1792;2 2669;2670;1484;5834;1484;5835;  
 1502 782;1131;1 True;True; 789;1138;1 4772;4773;2557;3719;2557;3719;  
 74 7192;7689; True;True; 7251;7751; 44425;444 23550;251 23550;251  
 1685 42;732;121 True;True; 42;739;122 230;231;23 117;118;11 119;2383;4  
 1105 2031;2219; True;True; 2047;2235; 12595;125 6698;6699;6699;7320;  
 218 111;3577;5 True;True; 111;3603;5 652;653;65 354;355;35 354;11778;  
 419 518;911;12 True;True; 519;918;12 3132;3133;1715;2954;1715;2954;  
 1083 519;925;98 True;True; 520;932;99 3136;3137;1716;3000;1716;3001;  
 1178 3153;9828 True;True 3177;9905 19598;195 10313;103 10317;322  
 977 4354;4796; True;True; 4381;4829; 26808;268 14234;142 14235;157  
 362 5353;7091 True;False 5391;7148 33146;331 17792;232 17792;232  
 405 9226 TRUE 9296 56877;568 30069 30069  
 1066 2675;5440; True;True; 2695;5479; 16646;166 8779;1802 8779;1803  
 485 3541 TRUE 3566 22038;220 11657 11657  
 1301 1176;1269; True;True; 1185;1278; 7211;7212;3866;3867;3868;4204;  
 220 1864;1129 True;True 1878;1138 11502;115 6126;6127;6126;3724  
 764 6247 TRUE 6290 38752;387 20566;205 20566  
 1855 6005;8780; True;True; 6048;8847; 37202;372 19807;198 19809;285  
 951 4128;7099; True;True; 4155;7157; 25600;256 13547;135 13550;232  
 1060 555;921;40 True;True; 557;928;41 3342;3343;1823;1824;1823;2990;  
 993 555;921;40 False;False 557;928;41 3342;3343;1823;1824;1823;2990;  
 1059 556;1002;4 True;True; 558;1009;4 3350;3351;1830;1831;1832;3295;  
 1846 687;11588 True;True 691;11674 4157;4158;2235;2236;2237;3821  
 144 421;4331;7 True;True; 422;4358;7 2562;2563;1424;1425;1439;1416

990 421;1005;3 False;True; 422;1012;3 2562;2563;1424;1425;1439;3311;  
1709 463;1897 False;True 464;1912 2801;2802;1544;1545;1545;6227  
1055 421;4331;7 False;False 422;4358;7 2562;2563;1424;1425;1439;14165  
1929 705;2441;2 False;False 709;710;71 4273;4274;2294;2295;2317;8013;  
946 705;2441;2 False;False 709;710;71 4273;4274;2294;2295;2317;8013;  
1791 705;2794;2 False;False 709;710;71 4273;4274;2294;2295;2317;9184;  
819 705;2441;2 True;True; 709;710;71 4273;4274;2294;2295;2317;8013;  
1718 2411;7750; True;True; 2428;7812;14979;1497 7925;2536;7925;25371  
1440 1437;1802; True;True; 1448;1816;8799;8800;4767;4768;4772;5900;  
1544 193;2066;3 True;True; 193;2082;3 1152;1153;632;633;63 636;6818;1  
1675 4353;6334; True;False; 4380;6380;26805;2680 14232;142 14233;2081  
1058 806;1160;1 True;False; 813;1169;1 4908;4909;2624;2625;2625;3804;  
1171 805;1160;1 True;True; 812;1169;1 4900;4901;2616;2617;2616;3804;  
131 2039;1116; True;False 2055;1124; 12648;126 6724;6725;6724;36839  
1172 805;1160;1 False;False 812;1169;1 4900;4901;2616;2617;2616;3804;  
1173 807;1160;1 True;False; 814;1169;1 4914;4915;2630;2631;2636;3804;  
1867 807;1159;1 False;True; 814;1168;1 4914;4915;2630;2631;2636;3802;  
1313 497;501;29 True;True; 498;502;29 3006;3007;1660;1661;1663;1676;  
1673 2010;2324; True;True; 2026;2340;12471;124 6625;6626;6626;7663;  
615 8960 TRUE 9028 55212;552 29174;291 29178  
125 374;1954;3 True;True; 375;1970;3 2249;2250;1239;1240;1239;6425;  
1212 4216;7343 True;True 4243;7402 26137;261 13836;240 13836;2403  
1506 951;6546;7 True;True; 958;6592;7 5786;5787;3096;3097;3097;21499  
1744 1540;5541; True;True; 1553;5581;9472;9473;5106;5107;5108;18330  
899 8768;9278; True;True; 8835;9348;54007;540 28536;302 28536;3020  
50 240;2103;3 True;True; 240;2119;3 1448;1449;805;806;80 805;6962;9  
158 7329 TRUE 7388 45273;452 23990;239 23991  
1329 2156;3734; True;True; 2172;3760;13385;133 7123;7124;7124;12286  
746 1079;2075; True;True; 1086;2091;6623;6624;3566;3567;3566;6843;  
740 297;2075 True;False 298;2091 1800;1801;992;993;99 997;6843  
1330 2077;9008 True;True 2093;9076 12861;128 6845;6846;6845;29347  
1630 2748;2785; True;True; 2768;2806;17104;171 9029;9030;9031;9153;  
572 3168;5643; True;True; 3192;5684;19694;350 10365;186 10365;1866  
872 2004;7513; True;True; 2020;7574;12439;463 6604;2458 6604;24583  
1905 4329;9938 True;True 4356;1001 26688;266 14160;326 14160;3260  
1580 1494;1108; True;True 1506;1116 9184;9185;4966;3657 4966;36574  
1746 5813;7326 False;True 5856;7385 36044;360 19220;239 19220;2398  
1747 5813;9717 True;True 5856;9792 36044;360 19220;318 19220;3182  
2024 1915;1062; True;True 1930;1070 11833;118 6280;3512 6280;35126  
2121 1541;9769 True;True 1554;9846 9479;9480;5112;3204 5112;32040  
1646 86;1839;37 True;True; 86;1853;37 501;502;50 273;274;60 273;6052;1  
1963 4543;6093 True;True 4573;6136 27958;279 14902;200 14902;2007  
564 710;1683;2 True;True; 716;1696;2 4335;4336;2335;2336;2335;5542;  
1616 714;4673;5 True;True; 721;4703;5 4357;4358;2347;2348;2348;15343  
737 1878;5145; True;True; 1893;5182;11609;116 6178;1704 6178;17048  
2115 1827;6627; True;True; 1841;6673;11282;112 6010;6011;6011;21742  
41 6807 TRUE 6855 42104;421 22380;223 22382  
1068 375;494;13 True;True; 376;495;13 2256;2257;1241;1242;1244;1655;  
1127 53;8599;10 True;True; 53;8665;10 305;306;30 149;150;27 149;28000;  
1107 244;343;13 True;True; 244;344;13 1467;1468;818;819;11 818;1139;4

	945	458;912;30	True;True;	459;919;31	2771;2772;1537;1538;1538;2955;
	37	1359;5912	True;True	1369;5955	8324;8325;4504;1956;4504;1956;
	936	1198;1678;	True;True;	1207;1691;7344;7345;	3953;5520;3953;5527;
	1056	598;1308;2	True;True;	601;1317;23596;3597;	1976;4326;1976;4327;
	932	966;10368	True;True	973;10451	5868;5869;3129;3130;3129;3424;
	1048	2782;8405;	True;True;	2803;8469;17334;173	9141;2735;9141;2735;
	209	2912;3768;	True;True;	2936;3794;18144;181	9555;1238;9555;1238;
	466	7113	TRUE	7172	43940;439;23295;232
	1084	2420;4086;	True;True;	2437;4113;15038;150	7954;7955;7955;1338;
	240	4857;4871;	True;True;	4890;4904;29964;299	16033;160;16033;160;
	1559	304;1114;1	True;True;	305;1121;11848;1849;	1026;1027;1026;3667;
	1686	9295	TRUE	9365	57286;572;30256;302
	375	11349	TRUE	11434	70486;704;37404
	595	770;1333;2	True;True;	777;1343;24702;8170;	2531;4418;2531;4421;
	1320	1085;2654;	True;True;	1092;2674;6647;6648;	3579;8733;3579;8736;
	850	985;1190;1	True;True;	992;1199;16027;6028;	3225;3226;3226;3916;
	1245	774;3110;5	True;True;	781;3134;54724;4725;	2540;1019;2540;1019;
	2034	1088;1904;	True;True;	1095;1919;6666;6667;	3590;6242;3590;6242;
	291	5140	TRUE	5177	31797;317;17037;170
	1043	83;376;641	True;True;	83;377;645484;485;48	266;267;26;267;1251;2
	2155	1100;1558;	True;True;	1107;1571;6748;6749;	3627;3628;3629;5163;
	686	3816	TRUE	3842	23660;236;12555;125
+	334	1389;4043;	True;True;	1399;4069;8504;8505;	4589;1323;4589;1323;
+	335	418;594;13	True;True;	419;597;142548;2549;	1414;1415;1415;1960;
+	339	417;594;12	True;False;	418;597;122542;2543;	1410;1411;1411;1960;
	937	838;874;93	True;True;	845;881;945107;5108;	2736;2737;2738;2853;
+	330	68;590;789	True;True;	68;592;796389;390;39	197;198;19;200;1944;2
+	1205	1629;3315;	True;True;	1642;3340;9976;9977;	5370;1084;5370;1084;
+	327	3165;4031;	True;True;	3189;4057;19677;196	10359;131;10359;131;
+	341	877;2953;3	False;False;	884;2977;35336;5337;	2859;2860;2860;9685;
+	336	876;1971;2	True;True;	883;1987;25328;5329;	2856;2857;2858;6479;
+	324	220;236;50	True;True;	220;236;511334;1335;	733;734;73736;794;16
	920	220;236;87	False;False;	220;236;881334;1335;	733;734;73736;794;28
+	350	234;548;54	True;True;	234;550;551414;1415;	776;777;77777;1788;1
+	328	235;875;93	True;True;	235;882;941423;1424;	788;789;79792;2854;3
	1533	4847;5282;	True;True;	4880;5319;29911;299	16003;160;16004;175;
	1771	7156;8085;	True;True;	7215;8148;44200;442	23417;264;23417;264;
	1195	3643;6065;	True;True;	3669;6108;22608;226	11983;119;11987;199;
	1641	474	TRUE	475	2857;2858;1584;1585;
	625	257;2104;2	True;True;	257;2120;21552;1553;	870;871;69870;6964;9
	1592	4872	TRUE	4905	30035;300;16063;160
	697	7142;7548;	True;True;	7201;7609;44115;441	23388;233;23389;246;
	1681	6459	TRUE	6505	39973;399;21199;212
	1520	1516;3603	True;True	1528;3629	9320;9321;5025;5026;5026;1184;
	426	3830;3977;	True;True;	3856;4003;23750;237	12591;125;12593;130;
	1249	1144;3264;	True;True;	1151;3289;6990;6991;	3751;3752;3752;1068;
	1250	2612;3412;	True;True;	2632;3437;16253;162	8602;8603;8606;1117;
	1624	2934;7222;	True;True;	2958;7281;18289;182	9632;2364;9632;2364;
	1092	408;694;13	True;True;	409;698;132468;2469;	1376;1377;1379;2254;
	1517	285;406;60	True;True;	286;407;601729;1730;	960;961;13961;1373;1

84	10855	TRUE	10940 67396;673	35865;358	35867
775	3401;4253;	True;True;	3426;4280;21083;210	11136;139	11136;139
1595	43;2333;34	True;True;	43;2349;34 234;235;23	120;121;12	126;7683;1
1001	1583;2141;	True;True;	1596;2157;9726;9727;	5236;5237;	5236;7088;
1596	622;834;11	True;True;	626;841;12 3761;3762;	2042;2043;	2042;2728;
439	8810	TRUE	8877 54245;542	28668;286	28668
107	1260;2909;	True;True;	1269;2933;7740;7741;	4180;9547;	4180;9547;
1285	2727;2812;	True;True;	2747;2833;16975;169	8957;9234;	8957;9234;
1507	557;558;55	True;True;	559;560;56 3358;3359;	1838;1839;	1838;1848;
7	2759;6167;	True;True;	2779;6210;17173;171	9071;2032	9071;2032
1621	1178;6153	True;True	1187;6196 7225;7226;	3874;3875;	3874;2026
1805	1064;3530	True;True	1071;3555 6522;6523;	3496;1162	3496;1162
867	164;6147;9	True;True;	164;6190;9982;983;98	547;548;20	548;20243;
1253	328;377;47	True;True;	329;378;47 1980;1981;	1098;1099;	1099;1257;
1688	398;720;44	True;True;	399;727;44 2408;2409;	1342;1343;	1342;2362;
837	9030	TRUE	9098 55622;556	29415;294	29419
1790	2547;7169;	True;True;	2566;7229;15850;158	8365;2347	8365;2347
1875	1008;1106;	True;True;	1015;1113;6190;6191;	3321;3322;	3322;3646;
2068	2980;4081;	True;True;	3004;4108;18566;185	9768;9769;	9769;1337
2092	3805;8378;	True;True;	3831;8441;23598;235	12509;272	12509;272
1177	2962;5357;	True;True;	2986;5395;18465;184	9706;1780	9706;1780
1540	2331;4618;	True;True;	2347;4648;14454;144	7679;7680;	7681;1513
988	517;1552;2	True;True;	518;1565;2 3130;3131;	1713;1714;	1714;5156;
1627	3623;5226;	True;True;	3649;5263;22489;224	11907;119	11909;173
500	2590;3911;	True;True;	2609;3937;16117;161	8527;1282	8527;1282
1775	1939;7947;	True;True;	1955;8010;12009;120	6377;2599	6377;2599
892	1684;1868;	True;True;	1697;1882;10341;103	5543;5544;	5544;6145;
948	3132;3557;	True;True;	3156;3582;19456;194	10250;102	10252;116
688	3319;4811;	True;True;	3344;4844;20584;205	10859;108	10860;158
1733	428;3924;8	True;True;	429;3950;8 2604;2605;	1453;1454;	1455;1285
876	2878;3556;	True;True;	2901;3581;17957;179	9462;1169	9462;1169
811	4714;6412;	True;False;	4744;6458;29007;290	15472;210	15472;210
1118	4602;6810;	True;True;	4632;6858;28320;283	15099;151	15099;224
650	4713;7245;	True;True;	4743;7304;29000;290	15470;154	15471;237
1761	9100	TRUE	9168 56071;560	29626;296	29628
657	5571;9239;	True;True;	5611;9309;34542;345	18419;184	18420;300
935	2897;3291;	True;True;	2921;3316;18060;204	9512;1077	9512;1077
305	7641	TRUE	7703 47200;472	25025	25025
1638	2413;4481;	True;True;	2430;4511;14993;149	7931;7932;	7933;1470
1738	9994;1057	True;True;	10071;106 61802;618	32783;349	32783;349
132	6340;9710	True;True	6386;9785 39289;392	20831;208	20832;318
1754	1111;2887;	True;True;	1118;2910;6808;1800	3656;9482;	3656;9482;
1732	6056	TRUE	6099 37509;375	19949;199	19950
1904	104;105;40	True;True;	104;105;40 613;614;61	328;329;33	328;331;13
159	10354	TRUE	10437 64219;642	34199;342	34199
1007	653;1299;8	True;True;	657;1308;8 3956;3957;	2132;2133;	2135;4291;
1025	1307;4966	True;True	1316;5003 8004;8005;	4323;4324;	4324;1639
577	3216;5967	True;True	3241;6010 19967;199	10487;197	10487;197
1034	6110;7764	True;True	6153;7826 37878;378	20120;254	20120;254
1234	723;2363;7	True;True;	730;2380;7 4401;4402;	2366;7803;	2366;7803;

+

18 3617;7813;True;True;1 3643;7875;22450;2241 11885;1181 11889;2558  
949 4289;4773;True;True;1 4316;4805;26525;294 14059;1561 14059;1568  
367 788 TRUE 795 4810;4811;2576;2577 2576  
1866 2711 TRUE 2731 16875;1681 8893;8894; 8893  
175 2779;11061 True;True 2799;11141 17304;1731 9134;36521 9134;36521  
1625 813;845;98 True;True;1 820;852;99 4958;4959;2662;2663;2663;2754;  
264 2593;2637;True;True;1 2612;2657;16127;1611 8532;8691;8532;8691;  
1238 368;741;23 True;True;1 369;748;24 2202;2203;1216;1217;1219;2411;  
1609 2940;5303;True;True;1 2964;5341;18328;1831 9641;17641 9641;17641  
2099 3370 TRUE 3395 20901;2091 11027;1101 11027  
2152 11399 TRUE 11484 70776 37561 37561  
641 35;6244 True;True 35;6287 188;38732;87;20554;287;20556  
1594 2875;3335;True;True;1 2898;3360;17940;1791 9456;9457;9456;10918  
1807 8462 TRUE 8526 52139;5211 27523;2751 27523  
1289 24;3517 True;True 24;3542 133;134;1360;61;62;162;11567  
138 1697;1903;True;True;1 1710;1918;10416;1041 5581;6239;5581;6241;  
1308 3829;7511;True;True;1 3855;7572;23742;2371 12590;2451 12590;2458  
1618 47;475;752 True;True;1 47;476;758 266;267;26138;1587;2138;1587;2  
395 387 TRUE 388 2346 1298 1298  
257 2253;5248 True;True 2269;5285 13995;1391 7426;7427;7427;17421  
970 219;1291;8 True;True;1 219;1300;8 1331;1332;732;4265;2732;4265;2  
1796 10661 TRUE 10746 66184;6611 35243;3521 35248  
733 1528;2326;True;True;1 1540;2342;9385;9386;5062;7666;5062;7666;  
773 1524;3777;True;True;1 1536;3803;9356;9357;5045;5046;5046;12411  
183 3523 TRUE 3548 21919;2191 11592 11592  
193 1884;1920;True;True;1 1899;1935;11647;1161 6191;6298;6191;6298;  
263 8214;10481 True;True 8277;10561 50723;5071 26827;3461 26827;3465  
912 1186;8427 True;True 1195;8491 7276;51931 3904;27421 3904;27421  
860 1656;2285;True;True;1 1669;2301;10159;1011 5449;5450;5450;7530;  
1590 2175;5095;True;True;1 2191;5132;13520;1351 7189;7190;7189;16881  
288 722;9708 True;True 729;9783 4394;4395;2365;31801 2365;31801  
630 1089 TRUE 1096 6673;6674;3591;3592 3592  
1339 5934;6226;True;True;1 5977;6269;36795;3671 19641;2051 19641;2051  
536 584;3956 True;True 586;3982 3511;3512;1927;12941 1927;12950  
1368 3353;3792;True;True;1 3378;3818;20799;2081 10975;1241 10975;1245  
2072 11470 TRUE 11556 71247;7121 37814 37814  
2014 107;5114;1 True;True;1 107;5151;1 632;633;63344;16955;344;16955;  
432 8581 TRUE 8645 52879;5281 27921;2791 27924  
1936 8469 TRUE 8533 52180;5211 27547 27547  
453 9479 TRUE 9550 58480;5841 30956 30956  
156 6651;8990 True;True 6698;9058 41161;4111 21843;2921 21843;2925  
17 1268;8583 True;True 1277;8647 7776;7777;4202;4203;4202;27934  
306 18;1331;65 True;True;1 18;1341;65 104;8164;847;4416;2147;4416;21  
683 7003 TRUE 7057 43299;4331 22995;2291 22995  
1684 81;1054;24 True;True;1 81;1061;25 474;475;47259;260;26259;3465;8  
1923 11020 TRUE 11105 68447;6841 36391;3631 36397  
761 8686;10401 True;True 8753;10491 53552;5351 28292;2821 28293;3438  
1002 716 TRUE 723 4369;4370 2354 2354  
1662 1103;3038;True;True;1 1110;3062;6765;6766;3640;9974;3640;9975;  
249 5615;10011 True;True;1 5655;10091 34810;3481 18569;1851 18569;3286



450 5332;1151(True;True 5370;1159(33010;330:17727;379:17727;379:  
 1947 11563 TRUE 11649 71799;718( 38118 38118  
 1819 3050;3574;True;True; 3074;3599;18991;189:10004;117(10004;117:  
 1793 7364 TRUE 7423 45498;454:24115;241: 24115  
 644 106;1132;2 True;True; 106;1139;2 624;625;62 332;333;33 341;3721;7  
 1760 6393;1085(True;True; 6439;1094: 39583;395:21006;358(21006;358:  
 571 1298;2826;True;True; 1307;2847;7944;7945;4288;4289;4288;9285;  
 2163 3802;5650;True;True; 3828;5691;23575;235:12499;186(12499;186:  
 2078 3448;5866;False;False 3473;5909;21406;214(11318;113:11321;193:  
 2136 3823;9234 True;True 3849;9304 23705;237(12577;300(12577;300:  
 443 4146;5508 True;True 4173;5548 25698;256:13604;136(13610;182:  
 2150 5692;1087 True;True 5734;1096: 35297;352:18812;188:18813;359:  
 794 2414;3575;True;True; 2431;3601;15000;150(7934;7935;7935;1177:  
 717 4949 TRUE 4986 30550;305:16325;163: 16325  
 805 232;3125 True;True 232;3149 1401;1402;767;768;76 768;10223  
 166 6641 TRUE 6688 41100;411(21800;218( 21803  
 2032 25;3486;64 True;True; 25;3511;65 137;138;13 63;64;65;6(67;11471;2  
 1666 640;3245;9 True;True; 644;3270;9 3874;3875;2090;1059(2090;1059:  
 889 2517;3374;True;True; 2536;3399;15654;156:8258;8259;8258;1104:  
 861 9;948;1257 True;True; 9;955;1266 60;61;62;6:23;24;3090 24;3090;41  
 290 1281 TRUE 1290 7841;7842; 4236 4236  
 1924 10163 TRUE 10243 62933;629:33397;333: 33397  
 309 2576;7444;True;True; 2595;7504;16016;160:8458;2435:8458;2435:  
 1550 1964;2657;True;True; 1980;2677;12178;121:6451;8743;6451;8744;  
 836 3330;8989;False;True; 3355;9057;20666;206(10903;109(10903;292:  
 1148 794;10167 True;True 801;10247 4840;4841;2590;3340(2590;3340:  
 682 6316;6842;True;True; 6362;6890;39146;391:20767;225:20767;225:  
 1780 960;4091 True;True 967;4118 5836;5837;3118;1339(3118;1339:  
 1965 5179;1003(True;True; 5216;1011(32031;320:17157;171:17158;329:  
 1128 602;678;75 True;True; 605;682;75 3624;3625;1988;1989;1989;2203;  
 1344 48;1935 True;True 48;1951 272;273;27 139;6360;6 139;6360  
 28 366;1511;6 True;True; 367;1523;6 2195;2196;1214;5004;1214;5004;  
 252 2971;1039(True;True 2995;1048: 18516;645:9733;3436(9733;3436:  
 463 779;865;13 True;True; 786;872;13 4749;4750;2550;2551;2552;2824;  
 2095 2321;4171;True;True; 2337;4198;14387;143:7657;7658;7658;1370:  
 520 8852 TRUE 8919 54490;544:28808;288( 28810  
 474 3969 TRUE 3995 24600;246(12988;129: 12988  
 420 141;972;18 True;True; 141;979;18 861;862;86 487;488;31 488;3164;6  
 70 8324;1054 True;True 8387;1062:51326;513:27112;348:27112;348:  
 1937 451;1010;1 True;True; 452;1017;1 2735;2736;1516;1517;1519;3324;  
 2035 567;11571 True;True 569;11657 3424;3425;1880;1881;1881;3814:  
 869 2052;5453;True;True; 2068;5492;12739;127:6783;6784;6785;1806:  
 810 7501 TRUE 7562 46333;463:24553;245: 24554  
 281 674;10000 True;True 678;10078 4078;4079;2185;3281(2185;3281:  
 2059 162;253;74 True;True; 162;253;75 966;967;96 542;543;85 542;859;24  
 938 2361 TRUE 2378 14697;146:7799;7800 7799  
 512 620;1202;1 True;True; 623;1211;1 3737;3738;2034;2035;2035;3966;  
 559 2142;2649 True;True 2158;2669 13305;133(7089;7090;7089;8720  
 679 1020;1553;True;True; 1027;1566;6260;6261;3354;3355;3358;5157;  
 1207 170;172;46 False;False 170;172;46 1016;1017;565;566;56 565;576;15

1211 1303;2212;False;False 1312;2228;7980;7981;4304;4305;4305;7297;  
 1758 1303;2212;False;False 1312;2228;7980;7981;4304;4305;4305;7297;  
 1206 170;172;17 True;True; 170;172;17 1016;1017;565;566;56 565;576;58  
 299 1206;3922 True;True 1215;3948 7391;7392;3982;1285 3982;1285  
 1154 41;250;251 True;True; 41;250;251 229;1494;1 116;831;83 116;837;83  
 756 6248;9263 True;True 6291;9333 38756;387 20568;301 20568;301  
 1766 2664;4916 True;True 2684;4953 16594;165 8760;8761;8761;1622  
 1975 440;904;27 True;True; 441;911;27 2677;2678;1485;1486;1485;2941;  
 129 2497;2643;True;True; 2515;2663;15518;164 8206;8706;8206;8706;  
 1583 16;2134;10 True;True; 16;2150;10 97;13253;142;7068;70 42;7069;33  
 231 2338;5004;True;True; 2354;5041;14500;145 7697;7698;7699;1656  
 161 1277;1832;True;True; 1286;1846;7819;7820;4230;6027;4230;6028;  
 1949 6573 TRUE 6619 40731;407 21575;215 21575  
 56 11608 TRUE 11694 72094;720 38300 38300  
 482 6367 TRUE 6413 39442;394 20907;209 20908  
 612 2373;1154 True;True 2390;1163 14771;147 7841;7842;7842;3807  
 401 26;1953 True;True 26;1969 151;152;15 69;70;6422 69;6422  
 827 4731;5669 True;True 4761;5711 29118;291 15515;187 15515;187  
 839 11048 TRUE 11133 68597;685 36465;364 36465  
 629 3960 TRUE 3986 24541;245 12955;129 12955  
 894 754;1640;3 True;True; 761;1653;3 4586;4587;2452;2453;2452;5403;  
 1283 9408 TRUE 9479 58029;580 30648 30648  
 92 5766;5993;True;True; 5808;6036;35766;357 19071;190 19071;197  
 1061 1539;2960;True;True; 1552;2984;9468;9469;5104;5105;5105;9704;  
 402 5634;6319 True;True 5675;6365 34954;349 18643;207 18643;207  
 418 1628;4574 True;True 1641;4604 9968;9969;5367;5368;5369;1501  
 2117 6815 TRUE 6863 42172;421 22428 22428  
 1946 246 TRUE 246 1479;1480 823;824 824  
 121 17;4987 True;True 17;5024 98;99;100; 43;44;45;4 44;16498  
 1392 2065;5839;True;True; 2081;5882;12807;128 6816;6817;6817;1930  
 2105 2495;1137 True;True 2513;1145 15506;155 8203;8204;8204;3748  
 1546 184;185;18 True;True; 184;185;18 1109;1110;621;622;62 621;622;62  
 421 10966 TRUE 11051 68108;681 36208;362 36209  
 2156 5219;5446;True;True; 5256;5485;32296;322 17331;173 17332;180  
 1622 283;338;14 True;True; 284;339;14 1720;1721;951;952;95 955;1121;4  
 1623 283;338;14 False;False 284;339;14 1720;1721;951;952;95 955;1121;4  
 1254 2829;8533 True;True 2850;8597 17629;176 9291;9292;9291;2776  
 1665 1361;2872;True;True; 1371;2895;8335;1792 4508;9447;4508;9450;  
 98 5210;8400;True;True; 5247;8463;32239;322 17289;172 17290;273  
 1483 8853;9336;True;True; 8920;9406;54495;544 28811;288 28814;304  
 253 3428 TRUE 3453 21259;212 11234;112 11234  
 208 6121;7794;True;True; 6164;7856;37959;379 20167;201 20168;254  
 1911 2893;3010;True;True; 2917;3034;18045;180 9500;9881;9500;9882;  
 1871 7076;7190;True;True; 7133;7249;43734;437 23190;231 23190;235  
 1258 1104;1737;True;True; 1111;1750;6768;6769;3641;3642;3641;5692;  
 1741 8993 TRUE 9061 55431;554 29299;293 29299  
 704 6441 TRUE 6487 39857;398 21146;211 21148  
 51 2721;3998;True;True; 2741;4024;16934;169 8930;8931;8930;1307  
 931 2362;7719;True;True; 2379;7781;14703;147 7801;7802;7802;2526  
 1647 388;627;11 True;True; 389;631;11 2347;2348;1299;1300;1300;2061;

1102 4680;5142;True;True;1 4710;5179;28790;2879 15354;1535 15356;1704  
 681 6187;1123;True;True;1 6230;1132;38376;383 20377;370 20377;370  
 2107 954;1725;2 True;True;1 961;1738;2 5801;5802;3102;5650;3102;5650;  
 1952 9620 TRUE 9694 59350;593 31446;314 31446  
 581 5427;6894;True;True;1 5466;6943;33595;335 17988;226 17988;226  
 1545 1012;5705;True;True;1 1019;5747;6213;6214;3328;3329;3329;1886  
 522 8500 TRUE 8564 52397;523 27650;276 27651  
 378 4211 TRUE 4238 26107;261 13812;138 13813  
 1759 2218;3470;True;True;1 2234;3495;13772;137 7314;1140 7314;1140  
 2113 3209;3995;True;True;1 3234;4021;19926;199 10465;130 10465;130  
 1631 29;71;262;True;True;1 29;71;262;162;410;41 74;210;211 74;214;886  
 1374 4969;8076;True;True;1 5006;8139;30682;306 16400;263 16400;263  
 1828 2890;2908;True;True;1 2913;2932;18019;180 9493;9545;9493;9545;  
 1302 4972;7610;True;True;1 5009;7672;30705;307 16418;164 16418;249  
 428 1265;2584;True;True;1 1274;2603;7768;7769;4196;4197;4196;8500;  
 529 1377;3611;True;True;1 1387;3637;8422;8423;4546;1186 4546;1186  
 1852 958;1749;1 True;True;1 965;1762;1 5822;5823;3108;3109;3110;5729;  
 90 956;7662;7 True;True;1 963;7724;7 5810;5811;3105;2508 3105;2508  
 2096 10142 TRUE 10222 62811;628 33328;333 33332  
 671 1381;2078 True;True 1391;2094 8441;8442;4553;4554;4553;6851  
 649 901;3171;3 True;True;1 908;3195;3 5476;5477;2934;2935;2937;1037  
 622 4851;5808;True;True;1 4884;5851;29933;299 16018;160 16018;192  
 1336 223;666;36 True;True;1 223;670;36 1354;1355;741;742;74 744;2169;1  
 1223 1634;2499;True;True;1 1647;2518;10002;100 5381;5382;5383;8216;  
 1823 1059;1042 True;True;1 1066;1051 6490;6491;3481;3482;3481;3446  
 1813 3347 TRUE 3372 20774;207 10956 10956  
 1597 148;1688;4 True;True;1 148;1701;4 900;901;90 508;509;55 508;5558;1  
 1412 166;4999;5 True;True;1 166;5036;5 994;30911;553;16548;553;16549;  
 1982 1034;5487;True;True;1 1041;5527;6329;6330;3394;1815 3394;1815  
 781 5984 TRUE 6027 37081;370 19759;197 19760  
 1468 2192;2193;True;True;1 2208;2209;13621;136 7237;7238;7242;7243;  
 1513 6359;6585;True;True;1 6405;6631;39398;393 20883;208 20884;216  
 77 1812;8995;True;True;1 1826;9063;11177;111 5945;5946;5946;2930  
 2139 5738;6572;True;True;1 5780;6618;35580;355 18973;215 18973;215  
 1824 11592 TRUE 11678 71986 38227 38227  
 1967 224;1509;4 True;True;1 224;1521;4 1361;1362;745;746;50 746;5002;1  
 808 917 TRUE 924 5553;5554 2967 2967  
 2001 4880;1161 True;True 4913;1169 30081;300 16087;383 16087;383  
 430 2224 TRUE 2240 13821;138 7336;7337 7336  
 63 8092 TRUE 8155 49936;499 26422 26422  
 744 2128;3849;True;True;1 2144;3875;13212;132 7046;7047;7048;1265  
 2123 2107;4220;True;True;1 2123;4247;13078;130 6973;6974;6973;1385  
 1996 4002;7850 True;True 4028;7912 24802;248 13083;130 13084;257  
 2026 116;785;18 True;True;1 116;792;19 678;679;68 371;372;37 372;2565;6  
 447 3167;8065;True;True;1 3191;8128;19686;196 10361;103 10362;263  
 1082 604;2124;2 True;True;1 607;2140;2 3635;3636;1992;1993;1992;7035;  
 308 8163 TRUE 8226 50417 26677 26677  
 943 1485;3962;True;True;1 1496;1497;9116;9117;4936;4937;4946;1296  
 501 10279 TRUE 10361 63715;637 33878;338 33881  
 1809 4600;8112;True;True;1 4630;8175;28306;283 15095;264 15095;264

1810 961;8783;8 True;True; 968;8850;8 5843;5844; 3119;2857; 3119;2857;  
 1757 8717;9092; True;True; 8784;9160; 53729;537; 28382;296 28382;296  
 1884 318;5235;6 True;True; 319;5272;6 1924;1925; 1067;1068; 1070;1737;  
 1018 957;2388;2 True;True; 964;2405;2 5816;5817; 3106;3107; 3106;7877;  
 133 6502 TRUE 6548 40290;402 21361;213 21362  
 1051 1886;3496; False;False 1901;3521; 11658;116 6193;1149 6193;1149  
 1104 1886;1887; True;True; 1901;1902; 11658;116 6193;6194; 6193;6194;  
 256 5678;7623; True;True; 5720;7685; 35215;352 18765;187 18772;249  
 312 23;183;663 True;True; 23;183;668 129;130;13 58;59;620; 58;620;217  
 1910 1890;6389 True;True 1905;6435 11672;116 6203;2099 6203;2099  
 382 825 TRUE 832 5020;5021; 2691 2691  
 307 4691 TRUE 4721 28864;288 15397 15397  
 1698 2177;4232; True;True; 2193;4259; 13536;135 7197;7198; 7198;1387;  
 21 10833 TRUE 10918 67249;672 35786;357 35793  
 2023 1057;2178; True;True; 1064;2194; 6479;6480; 3470;3471; 3472;7199;  
 1920 9733 TRUE 9808 60125;601 31883 31883  
 157 7056 TRUE 7111 43588;435 23121;231 23123  
 678 7055 TRUE 7110 43584;435 23117;231 23120  
 919 362;2764;2 True;True; 363;2784;2 2173;2174; 1207;1208; 1208;9088;  
 1859 9588 TRUE 9661 59160;591 31356;313 31356  
 1217 2086;3079; True;True; 2102;3103; 12924;129 6877;1010 6877;1010  
 2047 5572 TRUE 5612 34549;345 18422;184 18422  
 1660 4560;7656; True;True; 4590;7718; 28052;280 14953;250 14953;250  
 171 2807 TRUE 2828 17502;175 9218;9219; 9220  
 236 9141 TRUE 9210 56328;563 29762 29762  
 1840 2951;5879; True;True; 2975;5922; 18404;184 9680;9681; 9680;1943  
 728 66;1253;34 True;True; 66;1262;35 380;7705;7 194;4150;4 194;4151;1  
 763 780;7748 True;True 787;7810 4757;4758; 2554;2555; 2555;2536;  
 1888 1615;8564 True;True 1628;8628 9896;9897; 5340;5341; 5340;2786;  
 1454 2356;3013; False;False 2372;2373; 14653;146 7767;7768; 7768;9889;  
 1453 2356;3013; True;True; 2372;2373; 14653;146 7767;7768; 7768;9889;  
 1109 1518;1680; True;True; 1530;1693; 9333;9334; 5029;5030; 5029;5534;  
 1261 10043 TRUE 10121 62122;621 32951;329 32951  
 1170 576;3243;4 False;True; 578;3268;4 3474;2013 1906;1058 1906;1058  
 1455 4156;4178; True;True; 4183;4205; 25762;257 13644;136 13645;137  
 1133 4177;6759 True;True 4204;6807 25890;258 13716;137 13716;222  
 1499 4175;5771; True;True; 4202;5813; 25881;258 13712;190 13712;190  
 1511 600;997;11 True;True; 603;1004;1 3612;3613; 1985;1986; 1986;3278;  
 725 9412 TRUE 9483 58059;580 30716;307 30719  
 2135 1519;1049 True;True 1531;1057 9338;9339; 5035;3468 5035;3468  
 1826 1510 TRUE 1522 9282 5003 5003  
 660 9637;9891 True;True 9711;9968 59481;594 31523;315 31523;324  
 383 4924;7027 True;True 4961;7082 30401;304 16245;230 16245;230  
 816 1616;1965; True;True; 1629;1981; 9903;9904; 5342;6452; 5342;6454;  
 1648 205;3898;1 True;True; 205;3924;1 1233;1234; 680;681;68 682;12791;  
 1530 167;978;97 True;True; 167;985;98 995;996;99 554;555;55 554;3193;3  
 1192 980;3799;5 True;True; 987;3825;5 5982;5983; 3200;3201; 3204;1249  
 1570 2036;3798; True;False; 2052;3824; 12633;126 6713;6714; 6714;1249  
 1160 3302;4139; True;True; 3327;4166; 20473;204 10800;108 10805;135  
 1158 1529;1642; True;True; 1541;1655; 9393;9394; 5063;5064; 5068;5408;

640	1894	TRUE	1909	11698;116	6215	6215
1863	3378	TRUE	3403	20944;209	11058	11058
832	3634;4973	True;True	3660;5010	22566;225	11954;164	11954;164
1323	1023;1042;	True;True;	1030;1049;	6281;6282;	3368;3369;	3372;3422;
712	8875	TRUE	8942	54670;546	28923	28923
246	385;4015;5	True;True;	386;4041;5	2335;2336;	1295;1314	1295;1314
268	9610	TRUE	9683	59292;592	31411;314	31413
1755	1364;4508	True;True	1374;4538	8347;8348;	4517;1479	4517;1479
705	4012;1078	True;True;	4038;1087	24861;248	13135;356	13135;356
2033	54;899;173	True;True;	54;906;174	311;312;31	151;2927;2	151;2931;5
1838	5661;8589	True;True	5703;8653	35135;351	18738;279	18738;279
1497	3071;4048;	True;True;	3095;4074;	19118;191	10075;132	10075;132
878	313	TRUE	314	1899;1900;	1049;1050;	1050
1167	796;1201;3	True;True;	803;1210;3	4845;4846;	2592;2593;	2593;3965;
278	6571	TRUE	6617	40721;407	21569;215	21570
91	1138;2482;	True;True;	1145;2500;	6960;1541	3738;8147;	3738;8148;
1588	7231;7601;	True;True;	7290;7663;	44667;446	23668;248	23668;248
1287	8247	TRUE	8310	50922;509	26929;269	26931
1683	1279;2871;	True;True;	1288;2894;	7828;7829;	4232;4233;	4232;9446;
1220	209;3046;7	True;True;	209;3070;7	1267;1268;	700;701;70	702;9994;2
1891	332	TRUE	333	2001;2002;	1107	1107
902	133;400;48	True;True;	133;401;48	799;800;80	434;435;43	437;1347;1
1077	647;701;32	True;True;	651;705;33	3910;3911;	2113;2114;	2114;2283;
1779	2024;5884	True;True	2040;5927	12552;125	6669;6670;	6669;1945
283	8821;1114	True;True	8888;1122	54304;543	28693;367	28693;367
292	2440	TRUE	2457	15145;151	8010	8010
2154	603;943;11	True;True;	606;950;11	3631;3632;	1990;1991;	1991;3070;
289	4516	TRUE	4546	27798;277	14817;148	14819
1984	1727;6642;	True;True;	1740;6689;	10594;105	5652;5653;	5652;2180
745	9867	TRUE	9944	61016	32386	32386
1598	3828;6239	True;True	3854;6282	23738;237	12589;205	12589;205
1930	481;4993	True;True	482;5030	2895;2896;	1604;1653;	1604;1653
2141	405;1687;4	True;True;	406;1700;4	2451;2452;	1368;1369;	1370;5556;
1085	7130;8226;	True;True;	7189;8289;	44034;440	23343;233	23344;268
1804	2102;2274;	True;True;	2118;2290;	13048;130	6956;6957;	6959;7487;
928	4062;4968;	True;True;	4088;5005;	25180;251	13320;133	13323;163
1031	28;247;605	True;True;	28;247;608	160;161;14	72;825;72	828;199
87	315;605;10	True;False;	316;608;10	1909;1910;	1055;1056;	1058;1995;
1255	3133;3697;	True;True;	3157;3723;	19463;194	10255;121	10255;121
1475	2518	TRUE	2537	15662;156	8263	8263
1832	8471	TRUE	8535	52194;521	27549;275	27549
1645	65;326;426	True;True;	65;327;427	379;1965;1	193;1090;1	193;1090;1
795	9054;1052	True;True	9122;1060	55761;557	29483;347	29483;347
823	7371	TRUE	7430	45537;455	24136;241	24136
767	2145;3060;	True;True;	2161;3084;	13319;133	7098;1003	7098;1003
987	306;316;93	True;True;	307;317;94	1858;1914;	1030;1060;	1030;1060;
2045	9034	TRUE	9102	55651;556	29427	29427
1650	1332;2784;	True;True;	1342;2805;	8168;8169;	4417;9145;	4417;9146;
1651	536;2784;4	True;False;	538;2805;4	3223;3224;	1751;1752;	1752;9146;
134	568;1621;5	True;True;	570;1634;5	3429;3430;	1884;5352;	1884;5352;

1015 586;2301;3 True;True; 588;2317;3 3519;3520;1931;1932;1934;7585;  
1769 0;9957 True;True 0;10034 0;1;2;3;4;6 0;1;2;3;4;3 1;32663  
217 586;2300;3 False;True; 588;2316;3 3519;3520;1931;1932;1934;7581;  
371 4606;6654 True;True 4636;6701 28338;283 15106;151 15106;2184  
224 5786 TRUE 5828 35866;358 19115;191 19119  
498 9130;1048 True;True 9199;1056 56264;562 29724;346 29724;346  
1731 991;992;23 True;True; 998;999;23 6061;6062;3243;3244;3246;3248;  
1548 49;2429;33 True;True; 49;2446;34 280;281;28 140;7982;7 140;7982;1  
415 1870;6897; True;True; 1884;6946;11542;115 6148;6149;6149;22651  
146 2034;2372; True;True; 2050;2389;12610;126 6702;6703;6703;7838;  
880 1525;2372; True;False; 1537;2389;9364;9365;5050;5051;5050;7838;  
1818 1045;7669; True;True; 1052;7731;6400;6401;3435;3436;3436;25106  
190 577 TRUE 579 3475;3476;1907;1908; 1907  
384 5518 TRUE 5558 34231;342 18268;182 18269  
2089 3463 TRUE 3488 21514 11379 11379  
467 7411 TRUE 7471 45783;457 24260;242 24260  
909 123;124;44 True;True; 123;124;44 725;726;72 402;403;40 406;409;15  
2103 1031;3120; True;True; 1038;3144;6315;6316;3387;3388;3391;10216  
834 5538;9238 True;True 5578;9308 34344;343 18319;183 18321;3008  
863 90;113;450 True;True; 90;113;451 527;528;52 279;365;36 279;366;15  
1734 643;902;91 True;True; 647;909;92 3893;3894;2101;2102;2101;2939;  
1800 11634 TRUE 11720 72273;722 38397;383 38397  
786 2849;6461; True;True; 2870;6507;17764;177 9365;9366;9366;21208  
2100 11273 TRUE 11358 70010;700 37169 37169  
2087 2459;3185 True;True 2477;3209 15276;152 8086;8087;8087;10407  
1784 900;4820;6 True;True; 907;4853;6 5469;5470;2932;2933;2932;15867  
1687 1942;5077; True;True; 1958;5114;12030;120 6384;6385;6385;16815  
1703 1843;2223; True;True; 1857;2239;11377;113 6062;6063;6065;7333;  
1897 9240 TRUE 9310 56948;569 30090;300 30093  
1267 1691;2546; True;True; 1704;2565;10386;103 5566;5567;5568;8362;  
194 4688 TRUE 4718 28840;288 15377;153 15377  
165 769;1356;1 True;True; 776;1366;1 4694;4695;2524;2525;2524;4500;  
254 85;142;654 True;True; 85;142;658 494;495;49 272;489;49 272;489;21  
518 1109;5519 True;True 1116;5559 6799;6800;3653;1827 3653;18271  
110 1401;4188; True;True; 1411;4215;8586;8587;4642;1374 4642;13746  
1978 5003;9109 True;True 5040;9178 30929;309 16564;165 16564;2965  
668 769;2026;2 False;True; 776;2042;2 4694;4695;2524;2525;2524;6674;  
521 10202 TRUE 10282 63168;631 33534;335 33535  
1129 3973;1074 True;True 3999;1083 24630;246 13012;130 13013;3552  
2006 2804;9181 True;True 2825;9250 17487;174 9212;2990 9212;29901  
78 2756;5700; True;False; 2776;5742;17155;171 9064;9065;9065;18846  
1899 9236 TRUE 9306 56929 30086 30086  
603 2598 TRUE 2617 16147;161 8537;8538; 8537  
2143 1166;4842 True;True 1175;4875 7146;7147;3833;3834;3834;15986  
633 1058;2572; True;True; 1065;2591;6487;6488;3478;3479;3478;8448;  
1801 651;6732;7 True;True; 655;6780;7 3942;3943;2126;2127;2126;22118  
1512 872;4649;8 True;True; 879;4679;8 5301;5302;2848;1524 2848;15246  
410 5195;8527 True;True 5232;8591 32128;321 17216;172 17220;2774  
814 1780;1983; True;True; 1794;1999;10963;109 5844;6526;5844;6529;  
955 1374;1913; True;True; 1384;1928;8399;8400;4536;4537;4542;6262;

1829 3141;4242;True;True; 3165;4269;19519;1951 10282;1021 10283;1390  
 1695 5245 TRUE 5282 32474 17413 17413  
 0 466;11430 True;True 467;11516 2818;2819;1560;3765 1560;3765;  
 1202 44;64;1755 True;True; 44;64;1768 242;243;24 127;128;12 133;187;57  
 1919 96;833;175 True;True; 96;840;176 567;568;56 296;297;29 297;2726;5  
 1016 256;1181;1 True;True; 256;1190;1 1545;1546;865;866;86 869;3883;5  
 2109 61;635;232 True;True; 61;639;234 358;359;36 181;2083;7 181;2083;7  
 1029 4112;4218;True;True; 4139;4245; 25492;2541 13468;1341 13469;1384  
 784 8019;9186;True;True; 8082;9255;49481;566 26192;299 26192;2991  
 1282 5172;1043 True;True; 5209;1051 31989;319 17139;171 17139;3447  
 298 1266;1556;True;True; 1275;1569; 7770;7771;4198;4199;4199;5160;  
 755 329;4279 True;True 330;4306 1986;1987;1100;1101;1100;14031  
 1999 3061;5478;True;True; 3085;5518;19056;190 10033;100 10033;1813  
 45 1999;2025;True;True; 2015;2041;12411;124 6590;6671;6590;6671;  
 2067 798;10835 True;True 805;10920 4857;4858;2596;3579 2596;35796  
 1628 2319;4085;True;True; 2335;4112;14375;143 7648;1338 7648;13386  
 1671 9094;9949 True;True 9162;1002 56029;560 29605;296 29609;3264  
 1528 772;773;50 True;True; 779;780;50 4712;4713;2537;2538;2537;2538;  
 59 1247;1475 True;True 1256;1486 7674;7675;4135;4903;4135;4904  
 702 5164;8976;True;True; 5201;9044;31948;319 17115;292 17115;2924  
 490 625 TRUE 629 3783;3784;2058;2059 2059  
 6 5596;6682 True;True 5636;6729 34686;346 18505;185 18508;2196  
 594 982;4440;6 True;True; 989;4469;6 6006;6007;3215;3216;3215;14558  
 538 523;1209;4 True;True; 525;1218;4 3163;3164;1730;1731;1731;3986;  
 1125 855;856;28 True;True; 862;863;28 5206;5207;2790;2791;2790;2794;  
 1126 1070;8959;True;True; 1077;9027;6557;6558;3519;3520;3521;29173  
 1143 510;2255;2 True;True; 511;2271;2 3091;3092;1693;1694;1696;7434;  
 759 538;633;48 True;True; 540;637;49 3235;3236;1755;1756;1756;2078;  
 1142 891;5338;6 True;True; 898;5376;6 5413;5414;2905;1774 2905;17742  
 128 10910 TRUE 10995 67729;677 36016;360 36018  
 1090 409;1982;3 True;True; 410;1998;3 2476;2477;1382;1383;1385;6525;  
 1298 10151;1161 True;True 10231;117 62859;628 33359;333 33361;3845  
 23 3077;7210 True;True 3101;7269 19157;191 10105;236 10105;2360  
 1144 8207;1079 True;True 8270;1087 50680;670 26812;356 26812;3565  
 1146 543;974;38 True;True; 545;981;39 3253;3254;1767;3168;1767;3168;  
 1145 5502;8209;True;True; 5542;8272;34138;341 18212;182 18212;2681  
 1912 989;4100 True;True 996;4127 6054;6055;3239;3240;3239;13434  
 651 5929;6266 True;True 5972;6311 36750;367 19613;206 19613;2062  
 2052 7774;9840;True;True; 7836;9917;47986;479 25431;254 25432;3229  
 1928 6;1011;398 True;True; 6;1018;401 38;39;40;4 16;17;3325 16;3325;13  
 589 1458;3946 True;True 1469;3972 8939;8940;4838;1292 4838;12920  
 1820 2437 TRUE 2454 15132;151 8007 8007  
 1243 1950;1039 True;True 1966;1047 12095;120 6409;6410;6411;34343  
 510 1638;4931;False;True; 1651;4968;10038;100 5400;1626 5400;16265  
 137 5743;6229 True;True 5785;6272 35614;356 18987;205 18987;2052  
 2097 97;5460;93 True;True; 97;5499;94 572;573;57 299;300;18 300;18089;  
 187 11425 TRUE 11511 70917;709 37640;376 37640  
 270 9910 TRUE 9987 61295;612 32532;325 32534  
 1914 2018;2019;True;True; 2034;2035;12514;125 6647;6648;6647;6648;  
 1210 6108;6672;True;True; 6151;6719;37864;378 20116;201 20117;2193

126 4248;5942;True;True;1 4275;5985;26313;2631 13935;1961 13935;1961  
 950 570;1981;2 True;True;1 572;1997;2 3440;3441;1889;1890;1889;6520;  
 1168 1549;1840;True;True;1 1562;1854;9530;9531;5140;5141;5142;6054;  
 1028 1721;2946;True;True;1 1734;2970;10566;1056 5639;5640;5641;9664;  
 1643 1990;3569;True;True;1 2006;3594;12351;1235 6552;1174 6552;1174  
 227 6905 TRUE 6955 42712;4271 22689;2268 22691  
 1843 516;6063;7 True;True;1 517;6106;7 3123;3124;1711;1712;1711;19970  
 1291 1626;3434;True;True;1 1639;3459;9959;9960;5360;5361;5362;11251  
 634 1716 TRUE 1729 10542;1054 5631 5631  
 1691 2817;6680 True;True 2838;6727 17563;4131 9255;21951 9255;21951  
 517 2189;3149;True;True;1 2205;3173;13597;1359 7225;7226;7227;10305  
 687 4109 TRUE 4136 25473;2547 13459;1345 13460  
 1845 527;1819;6 True;True;1 529;1833;6 3184;3185;1735;1736;1735;5972;  
 2039 1396;1874;True;True;1 1406;1888;8552;8553;4620;4621;4623;6161;  
 1745 390;436;74 True;True;1 391;437;75 2351;2352;1302;1303;1304;1478;  
 1806 4370 TRUE 4397 26905;2690 14290;1429 14291  
 1694 4915;6915;True;True;1 4952;6965;30338;3033 16220;1622 16221;2272  
 1564 7153;10821 True;True 7212;1091 44188;4418 23411;3571 23411;3571  
 549 4330 TRUE 4357 26691;2669 14161;1416 14162  
 550 4328 TRUE 4355 26684;2668 14159 14159  
 1481 1217;2617 True;True 1226;2637 7462;7463;4022;4023;4025;8620  
 142 689;1141 True;True 693;1148 4171;4172;2239;3743;2239;3745  
 442 5016;5603 True;True 5053;5643 31011;3101 16605;1660 16605;1853  
 1246 955 TRUE 962 5805;5806;3103;3104 3103  
 238 1112;1113 True;True 1119;1120 6809;6810;3657;3658;3660;3665  
 533 2713;9483 True;True 2733;9554 16895;1689 8906;8907;8907;30963  
 1973 6353;7425 True;True 6399;7485 39361;3936 20869;2421 20869;2421  
 1770 2226;6598;True;True;1 2242;6644;13833;1383 7341;2165 7341;2165  
 495 4706;4736 True;True 4736;4766 28950;2895 15446;1544 15446;1553  
 579 7260 TRUE 7319 44848;4484 23767 23767  
 1869 11010 TRUE 11095 68396;6839 36364;3636 36369  
 1849 1708;2265;True;True;1 1721;2281;10502;1050 5615;7458;5615;7459;  
 1969 2655;2881;True;True;1 2675;2904;16538;1653 8739;9469;8739;9469;  
 1931 1797;4176 True;True 1811;4203 11063;1106 5876;5877;5876;13715  
 2080 7046 TRUE 7101 43532;4353 23096;2309 23098  
 1877 11146;1114 True;True 11231;1123 69202;6920 36783;3678 36783;3678  
 243 4605 TRUE 4635 28336;2833 15104;1510 15104  
 779 1169;2268;True;True;1 1178;2284;7161;7162;3837;7474;3837;7475;  
 1152 749;949;12 True;True;1 756;956;12 4567;4568;2442;3092;2442;3093;  
 400 1426;2152 True;True 1437;2168 8744;8745;4739;7110 4739;7110  
 2065 392;1108;1 True;True;1 393;1115;1 2374;2375;1317;1318;1317;3651;  
 72 10309 TRUE 10391 63942;6394 34026;3402 34028  
 1619 460;522;13 True;True;1 461;524;13 2786;2787;1541;1729;1541;1729;  
 941 2594;6418 True;True 2613;6464 16132;1613 8533;2109 8533;2109  
 1385 2294;2295;True;True;1 2310;2311;14216;1421 7558;7559;7558;7564;  
 1191 1259;1598;True;True;1 1268;1611;7733;7734;4176;4177;4179;5294;  
 1916 8830 TRUE 8897 54365;5436 28731;2873 28731  
 2016 1774;4476;True;True;1 1787;4506;10887;1088 5801;5802;5803;14682  
 1890 6042;6058 True;True 6085;6101 37425;3742 19916;1991 19916;1991  
 1150 2567;2568;True;True;1 2586;2587;15956;1595 8439;8440;8439;8440;



801 7948;8375 True;True 8011;8438 49102;4911 26000;2721 26000;2726  
 1361 1969;2787; True;True; 1985;2808; 12208;1221 6468;6469; 6473;9164;  
 1503 2288;2558; True;True; 2304;2577; 14183;1411 7539;7540; 7544;8395;  
 1076 410;3000;6 True;True; 411;3024;6 2491;2492; 1387;1388; 1387;9840;  
 601 8538 TRUE 8602 52624;526 27770;277 27772  
 636 1533;3815 True;True 1546;3841 9435;9436;5087;5088; 5089;12554  
 1854 6124;6222; True;True; 6167;6265; 37978;379 20176;201 20177;2050  
 554 8506;9048 True;True 8570;9116 52440;524 27679;294 27679;2946  
 373 7484 TRUE 7545 46243;462 24513 24513  
 234 354;2823;4 True;True; 355;2844;4 2132;2133; 1187;1188; 1191;9279;  
 1378 3407;7745; True;True; 3432;7807; 21120;211 11157;111 11159;2535  
 1375 6918 TRUE 6968 42797;427 22727;227 22728  
 160 1245 TRUE 1254 7666;7667; 4132 4132  
 180 9356 TRUE 9427 57713;577 30494;304 30495  
 1870 8238 TRUE 8301 50873;508 26905;269 26907  
 75 588;2600;5 True;True; 590;2619;5 3533;3534; 1936;1937; 1939;8549;  
 434 6406;1122 True;True; 6452;1130 39657;396 21048;210 21048;3701  
 261 38;39;2898 True;True; 38;39;2922 200;201;20 97;98;99;1 99;103;951  
 1536 1787;4379; True;True; 1801;4408; 11004;110 5853;5854; 5853;14346  
 806 1602;1022 True;True; 1615;1030 9830;9831; 5300;3363 5300;3363  
 898 3036;3065; True;True; 3060;3089; 18916;189 9972;1004 9972;1004  
 237 2243;4090; True;True; 2259;4117; 13943;139 7398;1339 7398;1339  
 448 1984;2033; True;True; 2000;2049; 12327;126 6533;6701; 6533;6701;  
 804 3758;7547 True;True 3784;7608 23314;233 12357;246 12357;246  
 1692 7006 TRUE 7060 43310;433 22999 22999  
 624 1905 TRUE 1920 11766;117 6243;6244 6243  
 1471 1567;1568; True;True; 1580;1581; 9620;9621; 5187;5188; 5187;5190;  
 1700 202;2468;4 False;False 202;2486;4 1202;1203; 663;664;66 669;8112;1  
 1699 2213;2350; False;False 2229;2366; 13744;137 7298;7299; 7299;7738;  
 1702 2328;5143; True;True; 2344;5180; 14433;144 7670;1704 7670;1704  
 1714 4022;8302 True;True 4048;8365 24905;249 13157;131 13157;2705  
 700 585 TRUE 587 3515;3516; 1928;1929; 1930  
 33 2851;1045 True;True 2872;1053 17779;648 9371;3454 9371;3454  
 102 5535;7566; True;True; 5575;7627; 34327;343 18310;247 18310;247  
 1716 6235 TRUE 6278 38681;386 20535;205 20535  
 184 6914 TRUE 6964 42777;427 22723 22723  
 14 4732;8874 True;True 4762;8941 29122;291 15516;155 15519;2892  
 1011 171;233;57 True;True; 171;233;57 1023;1024; 569;570;57 570;774;19  
 967 2431;5746; True;True; 2448;5788; 15092;150 7985;7986; 7986;19000  
 1006 1515;2383; True;True; 1527;2400; 9312;9313; 5024;7863; 5024;7866;  
 736 9250 TRUE 9320 57011;570 30118;301 30119  
 1037 273;274;41 True;True; 273;274;27 1656;1657; 919;920;92 929;934;14  
 1038 273;274;41 False;False 273;274;27 1656;1657; 919;920;92 929;934;14  
 1309 1722;2444; True;True; 1735;2461; 10572;105 5643;5644; 5643;8025;  
 1977 9617;9862; True;True; 9691;9939; 59333;593 31440;323 31440;323  
 1727 5394;6378; True;True; 5432;6424; 33403;334 17913;179 17913;2094  
 120 4087 TRUE 4114 25334;253 13388 13388  
 1265 350;2417;2 True;True; 351;2434;2 2101;2102; 1169;7950; 1169;7950;  
 1257 1944;3181; True;True; 1960;3205; 12049;120 6393;6394; 6394;10398  
 1579 1507;2101; True;True; 1519;2117; 9266;1304 5000;6953; 5000;6955;

1272 610;661;99 True;True; 613;665;10 3677;3678; 2006;2007; 2007;2158;  
 1654 4326;6711 True;True 4353;6759 26677;415 14153;220 14153;220  
 1458 1086;1371; True;True; 1093;1381; 6651;6652; 3580;3581; 3581;4532;  
 1046 1087;1371; True;False; 1094;1381; 6659;6660; 3585;3586; 3586;4532;  
 2011 7088;1028 True;True 7145;1036 43792;437 23219;338 23219;338  
 1391 3044;5461; True;True; 3068;5500; 18950;189 9986;9987; 9988;1809  
 1670 537;843;34 True;True; 539;850;34 3229;3230; 1754;2746; 1754;2748;  
 1395 199;2016;3 True;True; 199;2032;3 1187;1188; 657;6642; 6 657;6643;1  
 2019 3325;4776; True;True; 3350;4808; 20633;206 10884;108 10884;156  
 1441 2281;2933; True;True; 2297;2957; 14140;141 7508;7509; 7513;9631;  
 1979 2281;2933; False;False 2297;2957; 14140;141 7508;7509; 7513;9631;  
 2098 13;4425;69 True;True; 13;4454;70 82;83;84;8 34;35;36;1 34;14508;2  
 1373 537;11085 False;True 539;11170 3229;3230; 1754;3658 1754;3659  
 604 3152 TRUE 3176 19590;195 10309;103 10309  
 1390 1142;2397; True;True; 1149;2414; 6980;6981; 3746;3747; 3746;7897;  
 1593 401;1007;1 True;True; 402;1014; 12422;2423; 1349;1350; 1349;3320;  
 483 2944;1120 True;True 2968;1128 18356;183 9659;3695 9659;3695  
 1777 1922 TRUE 1937 11884;118 6300 6300  
 1317 3026;4120; True;True; 3050;4147; 18859;188 9936;9937; 9936;1351  
 1089 6463;6742; True;True; 6509;6790; 40000;400 21215;212 21218;221  
 1318 817;1006;1 True;True; 824;1013; 14975;4976; 2672;2673; 2672;3316;  
 765 1207;6462; True;False; 1216;6508; 7396;7397; 3983;2121 3983;2121  
 1388 6183;7315; False;True; 6226;7374; 38339;383 20361;203 20361;239  
 1319 1432;8221; True;True; 1443;8284; 8771;8772; 4755;2684 4755;2684  
 635 312;8222;1 True;True; 313;8285; 1 1891;1892; 1043;1044; 1044;2685  
 1401 4940;6818; True;True; 4977;6866; 30498;421 16295;224 16295;224  
 1402 563;962;11 True;True; 565;969;11 3400;3401; 1862;1863; 1865;3120;  
 992 5681;6331; False;True; 5723;6377; 35233;352 18783;187 18783;208  
 1415 5681;6823; True;True; 5723;6871; 35233;352 18783;187 18783;224  
 1380 7793 TRUE 7855 48091;480 25489;254 25490  
 1500 4252;5276; True;True; 4279;5313; 26339;263 13954;139 13956;175  
 1352 4586;1114 True;True 4616;1123 28218;282 15047;367 15047;367  
 995 149;1608;3 True;True; 149;1621; 3903;904;90 510;5320;5 510;5324;1  
 1942 70;3555;89 True;True; 70;3580;89 405;406;40 205;206;20 207;11694;  
 1078 1963;5939; True;True; 1979;5982; 12174;121 6449;6450; 6450;1966  
 1880 311;2752;7 True;True; 312;2772; 7 1883;1884; 1040;1041; 1041;9047;  
 597 1105 TRUE 1112 6775;6776; 3643;3644 3644  
 1862 1572 TRUE 1585 9647;9648; 5206 5206  
 1827 4278;8035 True;True 4305;8098 26462;264 14022;140 14023;262  
 1203 2365;4757; True;True; 2382;4788; 14718;147 7805;7806; 7807;1561  
 1240 2798;7439; True;True; 2819;7499; 17450;174 9195;9196; 9195;2434  
 311 5044;8836 True;True 5081;8903 31181;311 16696;287 16696;287  
 1239 10982;115 True;True 11067;116 68206;682 36264;381 36264;381  
 244 2214;4752; True;True; 2230;4783; 13752;137 7306;1559 7306;1559  
 1054 151;4526 True;True 151;4556 908;909;91 512;14849 512;14849  
 1138 973;8681 True;True 980;8748 5927;5928; 3165;3166; 3165;2827  
 1649 4339;4433; True;True; 4366;4462; 26749;267 14196;145 14196;145  
 593 2122;1055 True;True; 2138;1063 13183;131 7031;7032; 7031;3485  
 2022 3943;4136; True;True; 3969;4163; 24437;244 12907;129 12911;135  
 939 1080 TRUE 1087 6627;6628; 3568;3569; 3572

1811 7498;9811 True;True 7559;9888 46322;4631 24550;3211 24550;3211  
 1787 2660;9256; True;True; 2680;9326; 16561;1651 8751;8752; 8752;3013  
 1816 2442;4036; True;True; 2459;4062; 15157;1511 8017;8018; 8023;1320  
 2012 330;10076 True;True 331;10154 1993;1994; 1105;3307 1105;3307  
 662 264;8773;8 True;True; 264;8840;8 1597;1598; 894;895;89 898;28552;  
 487 756;9739 True;True 763;9814 4600;4601; 2462;2463; 2463;3190  
 1535 3177;4372; True;True; 3201;4401; 19755;1971 10391;1431 10391;1431  
 1632 8455 TRUE 8519 52103 27501 27501  
 962 2864;4256; True;True; 2887;4283; 17880;1781 9429;9430; 9432;1397  
 1493 1371;2691; False;True; 1381;2711; 8387;8388; 4532;4533; 4532;8838;  
 1026 2489;2588; True;True; 2507;2607; 15463;1541 8176;8177; 8178;8523;  
 1115 2690;6322; True;True; 2710;6368; 16749;3911 8837;20771 8837;20771  
 170 21;1480;33 True;True; 21;1491;33 124;125; 1253;54;55; 4153;4918;10  
 1384 3305;7118; True;False; 3330;7177; 20494;2041 10815;1081 10816;2331  
 1014 3306;7118; True;True; 3331;7177; 20501;2051 10820;1081 10826;2331  
 2144 6128 TRUE 6171 38007;3801 20186 20186  
 857 45;1013;14 True;True; 45;1020;14 256;257; 25135;136; 33135;3330;4  
 669 5490;5605; True;True; 5530;5645; 34042;3401 18164;1851 18164;1851  
 1367 239;301;55 True;True; 239;302;55 1447;1829; 804;1014; 1804;1015;1  
 1865 87;7644;10 True;True; 87;7706;11 509;510; 51275;25031; 275;25034;  
 2130 6227 TRUE 6270 38624;3861 20516;2051 20518  
 1620 265;423;44 True;True; 265;424;44 1605;2577; 900;1445; 1900;1445;1  
 1606 1756;5569; True;True; 1769;5609; 10763;1071 5745;5746; 5748;18411  
 1822 3203;3369; True;True; 3228;3394; 19894;1981 10456;1101 10456;1101  
 71 7771;9857; True;True; 7833;9934; 47973;4791 25425;2541 25425;3234  
 1974 3686;5230; True;True; 3712;5267; 22878;2281 12134;1731 12134;1731  
 1639 1182;3271 True;True 1191;3296 7250;7251; 3886;3887; 3889;1070  
 49 6675;8747 True;True 6722;8814 41317;4131 21940;2191 21941;2848  
 1722 3662;4601; True;True; 3688;4631; 22750;2831 12054;1501 12054;1501  
 80 830;1415;1 True;True; 837;1426; 15046;5047; 2708;4705; 2708;4706;  
 1883 2761;4503; True;True; 2781;4533; 17179;1711 9073;9074; 9077;1478  
 369 7327 TRUE 7386 45264;4521 23986 23986  
 1227 591;1930;1 True;True; 593;1946; 13549;3550; 1945;1946; 1948;6332;  
 1906 857;858;96 True;True; 864;865;97 5217;5218; 2795;2796; 2799;2800;  
 1907 977;4656;9 True;False; 984;4686;9 5967;5968; 3189;3190; 3191;1526  
 1300 545;2922;5 True;True; 547;2946;5 3265;3266; 1772;1773; 1773;9586;  
 2069 7000 TRUE 7054 43280 22989 22989  
 2046 321;1282;2 True;True; 322;1291;2 1939;1940; 1075;1076; 1075;4239;  
 176 4814;5006 True;True 4847;5043 29697;2961 15844;1581 15844;1651  
 141 1703;3715; True;True; 1716;3741; 10474;1041 5602;5603; 5603;1221  
 2153 2941;3604; True;True; 2965;3630; 18333;1831 9642;9643; 9642;1184  
 202 114;115;38 True;True; 114;115;38 670;671; 67367;368; 36368;370;12  
 611 63;771;131 False;True; 63;778;132 363;364; 36184;185; 25184;2536;4  
 619 5624 TRUE 5664 34874;3481 18614 18614  
 2029 3332;7820 True;True 3357;7882 20676;2061 10909;2561 10909;2561  
 1707 5794;6415; True;True; 5836;6461; 35916;3591 19147;1911 19150;2108  
 602 1604;4189 True;True 1617;4216 9837;9838; 5302;5303; 5302;1375  
 1720 5566;8893 True;True 5606;8960 34509;3451 18403;1841 18405;289  
 713 724;725;70 True;True; 731;732;71 4405;4406; 2367;2368; 2369;2375;  
 1728 6181 TRUE 6224 38327;3831 20357 20357

181	9800	TRUE	9877 60591;605	32149;321	32153
535	4107	TRUE	4134 25461;254	13456;134	13457
1704	699;9729;1	True;True;	703;9804;1 4237;4238; 2276;3187	2276;3187	
2134	3874;4170;	True;True;	3900;4197; 24040;258	12714;137	12714;137
2112	612;869;10	True;True;	615;876;11 3689;3690; 2011;2012; 2012;2842;		
2111	60;609;109	True;True;	60;612;110 353;354;35 179;180;20 179;2005;3		
1181	3366;4510;	True;True;	3391;4540; 20879;208	11012;110	11016;148
509	3080;5165	True;True	3104;5202 19173;191	10108;101	10109;171
1062	707;721;13	True;True;	713;728;13 4303;4304; 2322;2323; 2323;2363;		
1655	217;500;13	True;True;	217;501;13 1321;1322; 726;727;72 728;1671;4		
1607	217;1084;1	False;True;	217;1091;1 1321;1322; 726;727;72 728;3578;4		
258	2763	TRUE	2783 17190;171	9082;9083;	9082
1542	5644	TRUE	5685 35010;350	18667	18667
1833	670;3093;6	True;True;	674;3117;6 4061;4062; 2179;1014	2179;1014	
1551	514;9159;1	True;True;	515;9228;1 3115;3116; 1706;1707; 1708;2982		
46	7661	TRUE	7723 47325;473	25078;250	25078
769	9562	TRUE	9635 58965;589	31246;312	31252
760	860;7688;8	True;True;	867;7750;8 5237;5238; 2806;2807; 2806;2516		
1868	870	TRUE	877	5299	2846
1204	10105	TRUE	10185 62569;625	33203	33203
215	9215	TRUE	9285 56805;568	30037	30037
1589	384;1341;1	True;True;	385;1351;1 2328;2329; 1288;1289; 1290;4450;		
1491	2899;4641	True;True	2923;4671 18064;180	9516;9517; 9517;1522	
1198	67;351;695	True;True;	67;352;699 381;382;38 195;196;11 196;1173;2		
2031	4166;4959;	True;True;	4193;4996; 25838;258	13685;136	13686;163
777	1606;2461;	True;True;	1619;2479; 9843;9844; 5305;5306; 5307;8094;		
778	2180;8618	True;True	2196;8684 13552;135	7201;7202; 7203;2807	
199	6870	TRUE	6918	42515	22592
2108	51;2652;77	True;True;	51;2672;78 291;292;29 142;8724;2 142;8724;2		
670	1394;1589;	True;True;	1404;1602; 8537;8538; 4610;5257; 4610;5258;		
840	1392;7973	True;True	1402;8036 8523;8524; 4601;2605	4601;2605	
1524	628	TRUE	632 3800;3801;	2063	2063
654	1393;9330;	True;True;	1403;9400; 8529;8530; 4602;4603; 4608;3039		
61	341;1896;7	True;True;	342;1911;7 2048;2049; 1132;1133; 1133;6226;		
1576	1385;6075;	True;False;	1395;6118; 8469;8470; 4574;4575; 4579;2002		
1577	1386;6075;	True;True;	1396;6118; 8485;8486; 4585;2002	4585;2002	
104	355;1373;7	True;True;	356;1383;7 2140;2141; 1195;1196; 1197;4535;		
1575	1391;1594;	True;True;	1401;1607; 8516;8517; 4597;4598; 4600;5280;		
235	5517;9057	True;True	5557;9125 34225;342	18266;182	18267;294
412	1876;1081	True;True	1891;1090	11600;116	6175;6176; 6176;3574
296	8713	TRUE	8780 53703;537	28371	28371
1571	4074;4778;	True;True;	4101;4810; 25258;252	13352;133	13353;156
588	2419	TRUE	2436 15031;150	7953	7953
1462	5836;7146	True;True	5879;7205 36180;361	19299;193	19299;233
1169	5546;6298;	True;True;	5586;6344; 34400;344	18345;183	18345;207
192	6724;9593;	True;True;	6772;9666; 41612;416	22089;220	22090;313
1467	1250;2493;	True;True;	1259;2511; 7689;7690; 4142;4143; 4144;8194;		
1893	396;506;76	True;True;	397;507;76 2393;2394; 1330;1331; 1331;1684;		
1417	483;3890;4	False;False	484;3916;4 2907;2908; 1609;1610; 1610;1277		
1418	483;3890;4	True;True;	484;3916;4 2907;2908; 1609;1610; 1610;1277		

409 3854;5841 True;True 3880;5884 23911;239 12663;193 12663;193  
 618 2433;4628; True;True; 2450;4658; 15115;284 7995;1518 7995;1518  
 507 197;483;38 True;False; 197;484;39 1174;1175; 648;1609;1 648;1610;1  
 2137 3309;7933; True;True; 3334;7996; 20525;205 10834;259 10834;259  
 1296 2602;6177; True;True; 2621;6220; 16184;161 8561;8562; 8564;2034  
 710 5124;6376 True;True 5161;6422 31702;317 16989;209 16989;209  
 69 3197;4938; True;True; 3222;4975; 19870;198 10449;104 10450;162  
 1221 144;1767;1 True;True; 144;1780;1 877;878;87 493;494;49 495;5773;6  
 2 3909;4459; True;True; 3935;4488; 24233;242 12817;128 12817;146  
 1312 1098;1099; True;True; 1105;1106; 6738;6739; 3621;3622; 3623;3626;  
 1960 2771;3385; True;True; 2791;3410; 17247;172 9113;1108 9113;1108  
 136 5885 TRUE 5928 36446;364 19451;194 19452  
 628 9300 TRUE 9370 57311;573 30263 30263  
 1713 9093;1115 True;True 9161;1124 56023;560 29602;296 29602;368  
 2027 7752;1050 True;True 7814;1059 47881;478 25373;253 25373;347  
 83 470;2579;6 True;True; 471;2598;7 2840;2841; 1575;1576; 1576;8478;  
 2004 5907;7340; True;True; 5950;7399; 36602;366 19546;240 19546;240  
 600 7030;1046 True;True 7085;1055 43441;434 23060;345 23060;345  
 2162 7015;1120 True;True; 7070;1129 43373;433 23028;230 23030;369  
 20 1851;5292; True;True; 1865;5330; 11417;114 6087;6088; 6087;1761  
 1389 7459;7627; True;True; 7520;7689; 46086;460 24423;244 24425;249  
 596 5113;5347; True;True; 5150;5385; 31645;316 16954;177 16954;177  
 42 7889;9577 True;True 7951;9650 48743;487 25828;258 25828;313  
 1294 4385;6851; True;True; 4414;6899; 27004;270 14359;225 14359;225  
 2151 1957;2286; True;True; 1973;2302; 12140;121 6429;6430; 6435;7534;  
 2084 1745;3033; True;True; 1758;3057; 10713;107 5720;5721; 5721;9964;  
 859 630;9481;1 True;True; 634;9552;1 3812;3813; 2065;2066; 2066;3096  
 656 2135;2580; True;True; 2151;2599; 13256;132 7070;8479; 7070;8479;  
 1856 1501 TRUE 1513 9230;9231; 4989 4989  
 851 7755 TRUE 7817 47896;478 25382;253 25382  
 1522 4565;7848; True;True; 4595;7910; 28079;280 14966;257 14966;257  
 532 5233 TRUE 5270 32390;323 17376;173 17376  
 698 5959;9854 True;True 6002;9931 36937;369 19702;197 19702;323  
 1429 1306;4122 True;True 1315;4149 8001;8002; 4321;4322; 4321;1352  
 1430 6543;7540 True;True 6589;7601 40555;405 21489;246 21489;246  
 1431 4233;7480; True;True; 4260;7541; 26222;262 13882;138 13886;244  
 1432 3174;6027; True;True; 3198;6070; 19732;197 10384;103 10385;198  
 672 1262;3559; True;True; 1271;3584; 7746;7747; 4184;4185; 4185;1170  
 848 3158;5505; True;True; 3182;5545; 19635;196 10333;182 10333;182  
 260 7959;8491; True;True; 8022;8555; 49167;491 26032;276 26032;276  
 1410 9511;1018 True;True 9582;1026 58646;586 31037;310 31037;334  
 541 6136 TRUE 6179 38057 20209 20209  
 926 118;155;19 True;True; 118;155;19 694;695;69 380;381;38 381;525;62  
 927 1149;1462; True;True; 1156;1473; 7016;7017; 3768;3769; 3768;4847;  
 1350 4537;7804; True;True; 4567;7866; 27915;279 14879;255 14879;255  
 505 2802;5906 True;True 2823;5949 17473;174 9206;9207; 9206;1954  
 1908 8734;9185; True;True; 8801;9254; 53822;538 28436;284 28438;299  
 1831 658;3915;5 True;True; 662;3941;5 3985;3986; 2149;2150; 2149;1283  
 627 5899 TRUE 5942 36532;365 19497;194 19497  
 547 3939;7787 True;True 3965;7849 24414;244 12897;254 12897;254

1004 4065;7937;True;True;1 4091;8000;25195;25113327;133:13327;2597  
2025 8147 TRUE 8210 50295;5021 26602 26602  
1501 4;704;4344True;True;1 4;708;437127;28;29;314;2291;2214;2291;14  
274 1289;1791;True;True;1 1298;1805;7893;11024262;5861;4262;5862;  
2146 5779;1099True;True 5821;1108:35831;358:19104;363:19104;3632  
2106 3495;8815 True;True 3520;8882 21714;217:11488;114:11488;2868  
812 3490;6069 True;True 3515;6112 21685;216:11480;114:11481;1999  
2037 290;842;19True;True;1 291;849;191756;1757;977;978;97977;2745;6  
1957 248;837 True;True 248;844 1487;1488;829;2734;2829;2735  
124 230;1347;1True;True;1 230;1357;11391;1392;759;760;44760;4469;4  
27 1695;2159;True;True;1 1708;2175;10403;1045577;5578;5578;7129;  
391 5314;7217;True;True;1 5352;7276;32913;329:17677;176:17679;2362  
623 929;2985 True;True 936;3009 5643;5644;3017;9782 3017;9782  
563 649;923 True;True 653;930 3926;3927;2123;2994 2123;2994  
1599 540;2476;3True;True;1 542;2494;33243;3244;1762;1763;1763;8136;  
1659 7942;7943;True;True;1 8005;8006;49072;49025991;259:25991;2599  
1656 932;6625;9True;True;1 939;6671;95659;5660;3029;3030;3029;21740  
1556 2647;8839;True;True;1 2667;8906;16494;1648717;8718;8718;28764  
843 1955;3639;True;True;1 1971;3665;12128;121:6427;1196:6427;11961  
1585 117;990;50True;True;1 117;997;51686;687;68379;3241;3379;3242;1  
1653 2037;3086;True;True;1 2053;3110;12642;126:6719;1012:6719;10123  
2132 5121;7148 True;True 5158;7207 31684;316:16976;169:16979;2340  
991 7506;8241;True;True;1 7567;8304;46360;46324565;245:24565;2691  
701 713;2551;5True;True;1 720;2570;54356;1586:2346;8379;2346;8380;  
1108 284;1127;1True;True;1 285;1134;11728;6900;958;959;37958;3711;4  
1834 797;4710;1True;True;1 804;4740;14850;4851;2594;2595;2595;15458  
459 737;1278;2True;True;1 744;1287;24491;4492;2399;4231;2399;4231;  
503 8348 TRUE 8411 51440 27169 27169  
24 3813;7174;True;True;1 3839;7234;23652;236:12550;234:12550;2349  
1612 731;888;88True;True;1 738;895;894455;4456;2382;2895;2382;2902;  
1749 163;1952;2True;True;1 163;1968;2974;975;97544;545;54546;6419;6  
1063 922;2768;2True;True;1 929;2788;25598;5599;2992;2993;2992;9103;  
385 596 TRUE 599 3585;3586;1971;1972; 1971  
1706 3287;9521 True;True 3312;9593 20378;203:10746;107:10746;3107  
58 3707 TRUE 3733 22999;23012193;121: 12193  
1664 708;1092;1True;True;1 714;1099;14311;4312;2324;2325;2326;3603;  
40 309;802;96True;True;1 310;809;971869;1870;1034;1035;1036;2603;  
1839 5946 TRUE 5989 36864;36819673;196: 19675  
1229 544;711;83True;True;1 546;717;713259;3260;1768;1769;1771;2342;  
1190 15;583;669True;True;1 15;585;67392;93;94;9:39;40;41;1:40;1926;21  
2015 702;9558 True;True 706;9631 4253;4254;2284;2285;2285;31234  
458 11258 TRUE 11343 69915;699:37121;371: 37121  
870 595;2645;3True;True;1 598;2665;33577;3578;1969;1970;1970;8711;  
2110 1751;2266;True;True;1 1764;2282;10743;107:5731;7460;5731;7460;  
556 361;6289;6True;True;1 362;6335;62171;2172;1206;2069:1206;20699  
424 1817;1947;True;True;1 1831;1963;11210;112:5967;6402;5967;6402;  
1180 52;132;354True;True;1 52;132;356297;298;29143;144;14143;431;11  
1340 4735;6039;True;True;1 4765;6082;29140;37415527;19915527;1990  
2070 4519;4800;True;True;1 4549;4833;27810;278:14822;148:14827;1579  
1895 3056;4868;True;True;1 3080;4901;19022;190:10019;160:10019;1609

1363 394;435;38 True;True; 395;436;39 2384;2385;1324;1325;1326;1477;  
 198 3179;6390; True;True; 3203;6436;19763;19710393;10310394;2099  
 2166 303;2358;4 True;True; 304;2375;4 1840;1841;1018;1019;1020;7785;  
 219 3852 TRUE 3878 23901;2390 12655 12655  
 203 4094;7488; True;True; 4121;7549;25375;25313407;13413409;2452  
 438 9563 TRUE 9636 58981;58931253;3121 31255  
 1251 1975;8775 True;True 1991;8842 12263;1226504;6505;6504;28554  
 897 3498;4418; True;True; 3523;4447;21734;21711503;11511505;1448  
 918 542;1508;3 True;True; 544;1520;33250;3251;1765;1766;1766;5001;  
 2124 607;5778;7 True;True; 610;5820;7 3659;3660;1999;2000;2000;19103  
 1941 5315 TRUE 5353 32919 17680 17680  
 101 6364;6420; True;True; 6410;6466;39428;39420898;208120898;2110  
 1657 10616 TRUE 10701 65891;65835089;3501 35092  
 776 3993;8929 True;True 4019;8996 24750;24713062;13013062;2905  
 847 5261;9890; True;True; 5298;9967;32562;32517485;17417485;3247  
 852 1752;1051 True;True 1765;1060 10747;6525732;34765732;34769  
 506 210;1631;1 True;True; 210;1644;1 1273;1274;704;705;53704;5372;3  
 807 1624;2755; True;True; 1637;2775;9943;9944;5356;5357;5357;9061;  
 265 269;4783 True;True 269;4815 1629;1630;911;912;15912;15719  
 225 4449;6059 True;True 4478;6102 27376;37514582;19914582;1996  
 392 6428;9120 True;True 6474;9189 39790;39721119;29621119;2969  
 1915 139;1293;2 True;True; 139;1302;2 842;843;84469;470;47474;4268;9  
 785 10175;1081 True;True 10255;10963007;63033439;35833439;3588  
 1674 2822 TRUE 2843 17587;1759266;9267; 9268  
 2003 109 TRUE 109 642;643;64348;349;35 348  
 879 9334 TRUE 9404 57568;57530411 30411  
 610 1779;4582 True;True 1793;4612 10952;1095841;5842;5843;15036  
 1079 2323;7533 True;True 2339;7594 14396;1437660;7661;7661;24645  
 1182 447;5100 True;True 448;5137 2717;2718;1510;1511;1510;16904  
 797 1102;1124 True;True 1109;1132 6764;69833639;37073639;37072  
 782 2287;9747 True;True 2303;9823 14175;1417535;7536;7535;31948  
 741 744;1926;3 True;True; 751;1941;3 4530;4531;2421;2422;2422;6309;  
 742 743;1926;3 True;False; 750;1941;3 4523;4524;2416;2417;2417;6309;  
 2142 135;159;58 True;True; 135;159;58 812;813;94444;535;19444;535;19  
 89 10942;1111 True;True 11027;11267954;67936139;36836139;3684  
 1567 3074;3328; True;True; 3098;3353;19137;19110088;10010094;1089  
 1857 63;3525;75 True;True; 63;3550;76 363;364;36184;185;11184;11596;  
 259 2581;3850; True;True; 2600;3876;16056;1608480;8481;8481;12653  
 762 10922 TRUE 11007 67808;67836055;3601 36062  
 1815 4562;7227; True;True; 4592;7286;28061;28014955;23614955;2366  
 1966 6429 TRUE 6475 39792;39721120 21120  
 1073 342;1460;2 True;True; 343;1471;2 2056;2057;1135;4841;1135;4843;  
 1479 62;942;142 True;True; 62;949;143 361;362;57182;183;30183;3067;4  
 1315 624;1157;1 True;True; 628;1165;1 3775;3776;2049;2050;2057;3793;  
 397 2619;2801; True;True; 2639;2822;16301;1638625;9204;8625;9204;  
 1927 1009;1183; True;True; 1016;1192;6196;6197;3323;3893;3323;3894;  
 1292 578;717;10 True;True; 580;724;10 3481;3482;1911;1912;1913;2355;  
 1314 490;763;10 True;True; 491;770;10 2952;2953;1632;1633;1634;2496;  
 1236 655;1569;2 True;True; 659;1582;2 3971;3972;2144;2145;2144;5192;  
 1721 3787;5166; True;True; 3813;5203;23492;23412441;12412441;1711

+

1723 898;6349 True;True 905;6395 5457;5458;2926;2086! 2926;2086!  
2082 7650;9919 True;True 7712;9996 47259;472! 25045;325! 25045;325!  
455 1601;1010! True;True; 1614;1018! 9824;9825; 5298;5299; 5298;3319!  
504 7545;8118; True;True; 7606;8181; 46613;466! 24687;246! 24688;265!  
188 7471;7927; True;True; 7532;7990; 46167;461! 24473;244! 24476;259!  
189 513;5295 True;True 514;5333 3114;3279! 1705;1762! 1705;1762!  
815 10357 TRUE 10440 64236;642! 34205;342! 34205  
886 8474 TRUE 8538 52215;522! 27560;275! 27560  
1334 11173;116! True;True 11258;117! 69391;693! 36870;384! 36870;384!  
996 1296;2462; True;True; 1305;2480; 7928;7929; 4278;4279; 4279;8099;  
887 4838;1053! True;True 4871;1061! 29851;298! 15946;159! 15946;348!  
1939 9308;9658; True;True; 9378;9733; 57361;573! 30281;302! 30284;315!  
1803 571;2928;4 True;True; 573;2952;4 3444;3445; 1891;1892; 1894;9611;  
10 3586;6260; True;True; 3612;6303; 22294;222! 11796;205! 11796;205!  
1162 352;1763;2 True;True; 353;1776;2 2117;2118; 1177;1178; 1179;5763;  
790 372;4555;4 True;True; 373;4585;4 2233;2234; 1237;1493! 1237;1493!  
1987 1512;6220; True;True; 1524;6263; 9290;9291; 5007;2049! 5007;2049!  
2126 379;2194;2 True;True; 380;2210;2 2290;2291; 1265;1266; 1265;7244;  
1682 10124;106! True;True 10204;107! 62693;626! 33270;332! 33271;351!  
111 5691 TRUE 5733 35291;352! 18811 18811  
1772 195;6916;7 True;True; 195;6966;7 1166;1167; 645;646;22 646;22725;  
1726 6956 TRUE 7008 43033 22846 22846  
1131 276;289;51 True;True; 277;290;51 1685;1686; 938;939;94 940;976;17  
961 1796;3331; True;True; 1810;3356; 11055;110! 5875;1090! 5875;1090!  
608 3275 TRUE 3300 20312;203! 10714;107! 10715  
708 7604 TRUE 7666 46977;469! 24901 24901  
1433 8477;8478 True;True 8541;8542 52238;522! 27578;275! 27579;275!  
2122 894;903;22 True;True; 901;910;22 5438;5485; 2911;2940; 2911;2940;  
1661 1143;1155; True;True; 1150;1163; 6987;6988; 3749;3750; 3750;3791;  
150 310;337;72 True;True; 311;338;73 1876;1877; 1037;1038; 1038;1118;  
846 10155 TRUE 10235 62884;628! 33373 33373  
1776 2968;4647; True;True; 2992;4677; 18501;185! 9723;9724; 9724;1524!  
1030 1239;1240; True;True; 1248;1249; 7626;7627; 4112;4113; 4113;4124;  
73 11176 TRUE 11261 69407;694! 36876 36876  
82 1039;6414; True;True; 1046;6460; 6361;6362; 3409;3410; 3412;2107!  
460 3976 TRUE 4002 24653;246! 13019 13019  
652 1287;6476; True;True; 1296;6522; 7877;7878; 4255;4256; 4255;2127!  
659 10102 TRUE 10182 62553;625! 33196 33196  
1225 89;566;482 True;True; 89;568;486 524;525;52 277;278;18 278;1878;1  
93 3781 TRUE 3807 23456;234! 12428;124! 12430  
162 2273;7143; True;True; 2289;7202; 14098;140! 7486;2339! 7486;2339!  
386 709;2438;1 True;True; 715;2455;1 4319;4320; 2328;2329; 2330;8008;  
262 5187;7770; True;True; 5224;7832; 32086;320! 17192;254! 17192;254!  
758 3948;1149! True;True 3974;1158! 24467;244! 12922;379! 12922;379!  
1496 2708;3148; True;True; 2728;3172; 16864;168! 8887;1030! 8887;1030!  
1088 5994 TRUE 6037 37144;371! 19786 19786  
1578 229;1609;1 True;True; 229;1622;1 1388;1389; 758;5325;5 758;5326;5  
1297 1310;2349; True;True; 1319;2365; 8026;8027; 4335;7733; 4335;7733;  
143 657 TRUE 661 3977;3978; 2147;2148 2147  
429 3348;6477; True;True; 3373;6523; 20776;207! 10957;109! 10958;212!



1552 512;844;20 True;True; 513;851;20 3107;3108;1704;2753;1704;2753;  
 910 7;357;1093 True;True; 7;358;1100 45;46;47;41 18;19;20;2 19;1200;36  
 1591 11389 TRUE 11474 70705;707 37524;375 37525  
 1457 91;4190;84 True;True; 91;4217;85 530;531;53 280;281;13 280;13753;  
 1658 2391;9247 True;True 2408;9317 14880;148 7882;3010 7882;3010  
 1407 2864;4256;False;False 2887;4283;17880;178 9429;9430;9432;1397  
 1224 1454;1593;True;True; 1465;1606;8903;8904;4821;4822;4821;5276;  
 792 2084;8640 True;True 2100;8706 12912;129 6875;2813 6875;2813  
 1357 493;910;16 True;True; 494;917;16 2981;2982;1652;1653;1653;2952;  
 1151 1067;1152;True;True; 1074;1159;6534;6535;3503;3504;3504;3775;  
 1851 561;1164;1 True;True; 563;1173;1 3388;3389;1858;1859;1858;3824;  
 1944 2335;3933 True;True 2351;3959 14483;144 7687;7688;7687;1288  
 106 1560;1728;True;True; 1573;1741;9579;9580;5165;5166;5165;5662;  
 548 2402;3137;True;True; 2419;3161;14941;149 7911;7912;7912;1027  
 523 1051;2790 True;True 1058;2811 6441;6442;3458;9173;3458;9174  
 2083 1434;8091;True;True; 1445;8154;8783;8784;4757;4758;4759;2641  
 206 2523;3363 True;True 2542;3388 15692;156 8280;8281;8280;1100  
 271 3201;3529;True;True; 3226;3554;19891;198 10454;116 10454;116  
 1321 7464;1088 True;True; 7525;1097 46119;461 24443;244 24447;359  
 286 5395;8125 True;True 5433;8188 33409;334 17915;265 17915;265  
 454 380;7460;8 True;True; 381;7521;8 2296;2297;1267;1268;1269;2442  
 1925 1384;2972;True;True; 1394;2996;8461;8462;4567;4568;4567;9737;  
 2017 3146;7423;True;True; 3170;7483;19556;195 10294;102 10297;242  
 108 295;1229;3 True;True; 296;1238;3 1786;1787;985;4084;4985;4085;9  
 684 2808;4844 True;True 2829;4877 17510;175 9223;1599 9223;1599  
 1587 5641 TRUE 5682 34994;349 18658;186 18661  
 539 4953;5131 True;True 4990;5168 30577;305 16333;163 16340;170  
 403 4250 TRUE 4277 26317;263 13937;139 13938  
 1764 1234;6696;True;True; 1243;6743;7592;7593;4095;4096;4097;2199  
 2131 2173;5735 True;True 2189;5777 13508;135 7187;1896 7187;1896  
 1955 1234;2280;False;True; 1243;2296;7592;7593;4095;4096;4097;7504;  
 1629 1175;2914;True;True; 1184;2938;7204;7205;3864;3865;3864;9566;  
 1953 2137;8262 True;True 2153;8325 13271;132 7073;7074;7078;2697  
 2013 2211;7087;True;True; 2227;7144;13731;137 7287;2321 7287;2321  
 1785 6107;9683 True;True 6150;9758 37861;378 20115;316 20115;316  
 665 6892 TRUE 6940 42626;426 22637 22637  
 695 9980 TRUE 10057 61701;617 32735 32735  
 1730 587;3821;5 True;True; 589;3847;5 3527;3528;1935;1257 1935;1257  
 703 5890 TRUE 5933 36481;364 19472;194 19473  
 368 631;6510 True;True 635;6556 3815;3816;2067;2068;2073;2138  
 1948 3048;9407;True;True; 3072;9478;18977;189 10001;306 10001;306  
 1961 2239;7278;True;True; 2255;7337;13912;139 7390;2384 7390;2384  
 1802 2943;5217;True;True; 2967;5254;18348;183 9654;9655;9658;1732  
 214 742;5412 True;True 749;5450 4521;4522;2414;2415;2414;1795  
 1864 3285;3513;True;True; 3310;3538;20366;203 10738;107 10739;115  
 411 441;2073;3 True;True; 442;2089;3 2682;2683;1488;1489;1488;6840;  
 1337 3848;7617;True;True; 3874;7679;23873;238 12647;126 12648;249  
 1241 1270;1430;True;True; 1279;1441;7784;7785;4205;4206;4206;4749;  
 1358 78;700;822 True;True; 78;704;829 453;454;45 243;244;22 244;2277;2  
 1100 492;5990;8 True;True; 493;6033;8 2974;2975;1650;1651;1650;1977

+

1376 1443;2487;True;True;1 1454;2505;8846;8847;4795;4796;4798;8172;  
1605 8701;9053 True;True 8768;9121 53636;536 28339;283 28341;2948  
1902 3932;5561 True;True 3958;5601 24369;243 12883;183 12883;1838  
1543 1577;2386;True;True;1 1590;2403;9683;9684;5221;7872;5221;7872;  
484 3084;6508;True;True;1 3108;6554;19186;191 10115;101 10116;2137  
2138 2701;3652;True;True;1 2721;3678;16816;168 8867;1201 8867;12018  
2054 3111;7014;True;True;1 3135;7069;19355;193 10198;230 10198;2302  
978 292;307;98 True;False; 293;308;99 1768;1769;981;1031;3 981;1031;3  
944 414;415;12 True;True;1 415;416;12 2519;2520;1398;1399;1400;1404;  
1469 324;1242;1 False;False 325;1251;1 1957;1958;1086;1087;1086;4128;  
1470 307;324;89 True;True;1 308;325;90 1859;1860;1031;1086;1031;1086;  
1110 10;1632;17 True;True;1 10;1645;18 67;68;9991 25;5373;53 25;5374;58  
1748 360;1048;1 False;False 361;1055;1 2170;6412;1205;3441;1205;3443;  
1472 360;1048;1 True;True;1 361;1055;1 2170;6412;1205;3441;1205;3443;  
491 360;1049;1 False;True; 361;1056;1 2170;6426;1205;3448;1205;3450;  
1473 360;1048;1 False;False 361;1055;1 2170;6412;1205;3441;1205;3443;  
954 520;682;28 True;True;1 521;522;68 3142;3143;1717;1718;1727;2213;  
1601 520;681;27 False;True; 521;522;68 3142;3143;1717;1718;1727;2210;  
105 520;679;32 False;False 521;522;68 3142;3143;1717;1718;1727;2206;  
1474 679;1101;2 True;True;1 683;1108;2 4112;4113;2205;2206;2206;3636;  
1950 680;2452;3 True;True;1 684;2470;3 4120;1522 2209;8060;2209;8060;  
1690 1101;2088;False;True; 1108;2104;6756;6757;3634;3635;3636;6883;  
691 6855 TRUE 6903 42417;424 22552;225 22552  
389 4833;7041;True;True;1 4866;7096;29828;298 15928;230 15928;2308  
1610 1502;6584;True;True;1 1514;6630;9235;9236;4990;2160 4990;21605  
1516 10332 TRUE 10414 64088;640 34126 34126  
757 6243 TRUE 6286 38725;387 20547;205 20549  
1985 2292;9860 True;True 2308;9937 14203;142 7550;7551;7550;32358  
1360 884;9939;1 True;True;1 891;10016;5372;5373;2882;3261 2882;32610  
43 3825;5949;True;True;1 3851;5992;23720;237 12581;125 12584;1968  
1712 1928;9394;True;True;1 1944;9465;11931;119 6319;6320;6319;30598  
1557 5351 TRUE 5389 33133;331 17787 17787  
986 55;621;356 True;True;1 55;624;625 317;318;31 152;153;15 153;2038;1  
1554 4920;8728 True;True 4957;8795 30373;303 16235;284 16235;2841  
374 2806 TRUE 2827 17496;174 9217 9217  
1737 8422 TRUE 8486 51889;518 27411;274 27415  
2090 452;781;14 True;True;1 453;788;14 2743;2744;1523;2556;1523;2556;  
959 8048;9795;True;True;1 8111;9872;49654;496 26279;321 26279;3213  
1074 2614;3136;True;True;1 2634;3160;16269;162 8615;8616;8616;10267  
1347 7414;7554;True;True;1 7474;7615;45801;458 24273;247 24273;2471  
587 1506;5938;True;True;1 1518;5981;9259;9260;4999;1965 4999;19658  
971 1838;3645;True;True;1 1852;3671;11351;113 6047;6048;6051;11992  
716 3979;8940 False;True 4005;9008 24668;246 13025;291 13025;2910  
79 3393;1121 True;True 3418;1129 21023;210 11103;111 11103;3698  
984 3671;3822;True;True;1 3697;3848;22791;236 12078;125 12078;1257  
969 3979;1004 True;True 4005;1012 24668;246 13025;329 13025;3295  
768 3090;5419;True;True;1 3114;5458;19229;192 10138;101 10138;1797  
2040 8925;1049 True;True 8992;1058 54970;549 29049;346 29049;3469  
743 11104 TRUE 11189 68932;689 36651 36651  
1954 1906;6131;True;True;1 1921;6174;11773;117 6245;2019 6245;20198

2149 367;10152 True;True 368;10232 2198;2199;1215;3336;1215;3336;  
 2053 2506;2686 True;True 2525;2706 15574;155 8231;8232;8232;8820  
 800 335;2439;5 True;True; 336;2456;5 2019;2020;1115;1116;1116;8009;  
 787 616 TRUE 619 3714;3715;2023;2024; 2023  
 53 7510;9686 True;True 7571;9761 46385;463 24577;245 24577;3170  
 845 69;738;136 True;True; 69;745;137 397;398;39 203;204;24 203;2401;4  
 1881 3389;4244; True;True; 3414;4271;21006;210 11094;139 11094;1391  
 2127 11639 TRUE 11725 72297;722 38408;384 38409  
 297 3587 TRUE 3613 22299;223 11797 11797  
 2104 667;2460;3 True;True; 671;2478;3 4042;4043;2170;2171;2174;8091;  
 606 11605 TRUE 11691 72078;720 38290;382 38290  
 614 7321 TRUE 7380 45230;452 23975 23975  
 1263 2237;5197 True;True 2253;5234 13900;139 7382;1722 7382;17224  
 1049 3160;6980; True;True; 3184;7033;19649;196 10338;103 10339;2292  
 185 847;915;13 True;True; 854;922;13 5160;5161;2758;2759;2758;2965;  
 569 2368;3775 True;True 2385;3801 14739;147 7819;1240 7819;12403  
 1860 3346;4761 True;True 3371;4792 20768;207 10952;109 10954;1562  
 479 2283;3544; True;True; 2299;3569;14150;141 7518;1166 7518;11660  
 1456 1194;2176; True;True; 1203;2192;7312;7313;3930;3931;3930;7196;  
 514 1557;1584; True;True; 1570;1597;9573;9733;5162;5238;5162;5238;  
 747 3198;6557 True;True 3223;6603 19873;198 10451;215 10451;2153  
 1393 3554;6826; True;True; 3579;6874;22105;221 11690;116 11692;2247  
 152 4005 TRUE 4031 24826;248 13099;131 13099  
 1394 300;6105;9 True;True; 301;6148;9 1824;1825;1013;2011 1013;20112  
 638 2470;6139; True;True; 2488;6182;15343;153 8114;2021 8114;20213  
 1667 1115;1116; True;True; 1122;1123;6828;6829;3668;3669;3668;3669;  
 568 10725 TRUE 10810 66600;666 35459;354 35462  
 1103 299;645;64 True;True; 300;649;65 1816;1817;1006;1007;1011;2111;  
 1968 6013;6987 True;True 6056;7040 37256;372 19833;229 19833;2294  
 16 6345 TRUE 6391 39323;393 20849;208 20851  
 1848 6344;8501; True;True; 6390;8565;39307;393 20841;208 20844;2765  
 817 2699;3298; True;True; 2719;3323;16800;168 8861;8862;8861;10791  
 2055 735;2447;4 True;True; 742;2464;4 4483;4484;2397;8035;2397;8035;  
 1081 698;1665;8 True;True; 702;1678;8 4232;4233;2275;5481;2275;5481;  
 1166 2608;3173; True;True; 2627;3197;16218;162 8583;8584;8583;10383  
 1799 10627 TRUE 10712 65962;659 35131;351 35132  
 1835 8058 TRUE 8121 49709;497 26309 26309  
 304 3526;8641 True;True 3551;8707 21936;219 11600;116 11605;2813  
 425 1861;2705; True;True; 1875;2725;11483;114 6121;6122;6121;8876;  
 493 1590;1860; True;True; 1603;1874;9766;9767;5264;5265;5269;6117;  
 1562 308;2648;1 True;True; 309;2668;1 1864;1865;1032;1033;1033;8719;  
 76 5184;1149; True;True 5221;1157 32070;320 17187;378 17187;3785  
 1998 27 TRUE 27 157;158;15 71 71  
 543 7155 TRUE 7214 44196;441 23416 23416  
 582 6613 TRUE 6659 40935;409 21700;217 21704  
 1896 437;11355 True;True 438;11440 2653;2654;1480;1481;1480;37415  
 1005 7016;1094 True;True; 7071;1102 43381;679 23032;361 23032;3614  
 232 1363;2045; True;True; 1373;2061;8344;8345;4515;4516;4515;6752;  
 527 10050 TRUE 10128 62165;621 32975;329 32975  
 154 3957 TRUE 3983 24523;245 12951 12951

873	6678	TRUE	6725 41337;413;21949;219;	21952
44	3831;7255;	True;True;	3857;7314;23757;237;12595;237;12595;237;	
1351	907;1072;2	True;True;	914;1079;25510;5511;2949;3531;2949;3531;	
1689	72	TRUE	72 418;419;42218;219;22	221
835	2450;2478;	True;True;	2468;2496;15218;152;8056;8138;8056;8138;	
451	6947	TRUE	6998 42970;429;22813;228;	22813
1909	4890;4976;	True;True;	4923;5013;30153;301;16116;164;16116;164;	
829	3731;6152	True;True	3757;6195 23156;231;12276;202;12276;202;	
38	6834;6950	True;True	6882;7002 42288;429;22502;228;22502;228;	
147	668;3627;5	True;True;	672;3653;54049;4050;2176;1192;2176;1192;	
1812	11150	TRUE	11235 69230;692;36794;367;	36796
1299	419;606;94	True;True;	420;609;952556;2557;1420;1421;1422;1997;	
1742	110	TRUE	110 650;651	353 353
2062	3290;5802;	True;True;	3315;5844;20403;204;10766;107;10768;191;	
153	7107;9552;	True;True;	7165;9625;43903;439;23274;232;23275;312;	
2056	4439;6396;	True;True;	4468;6442;27336;396;14557;210;14557;210;	
875	10716	TRUE	10801 66530;665;35414;354;	35417
1668	161;6479;6	True;True;	161;6525;6958;959;96538;539;54541;21283;	
1951	7342;7361;	True;True;	7401;7420;45350;453;24030;240;24030;241;	
2064	1362;3930	True;False	1372;3956 8336;8337;4509;4510;4514;1287;	
868	3930;6442;	True;True;	3956;6488;24354;243;12872;128;12872;211;	
639	7285	TRUE	7344 45001;450;23866;238;	23866
279	10903	TRUE	10988 67682;676;35988;359;	35988
833	1757;7388;	True;True;	1770;7447;10770;107;5750;5751;5752;2418;	
1560	1818;6713;	True;True;	1832;6761;11214;112;5968;5969;5970;2204;	
3	964;3901;4	True;True;	971;3927;45855;5856;3122;1280;3122;1280;	
1075	389;867;12	True;True;	390;874;122350;5282;1301;2836;1301;2838;	
315	4375;1085;	True;True	4404;1093 26954;269;14329;143;14329;358;	
1788	575	TRUE	577 3466;3467;1901;1902;	1904
1098	2400;4199;	True;True;	2417;4226;14927;149;7901;7902;7902;1377;	
1262	1004;3594;	True;True;	1011;3620;6161;6162;3303;3304;3305;1181;	
2114	33;918;420	True;True;	33;925;422176;177;1782;2968;1382;2968;13	
1783	664;4975	True;True	668;5012 4024;4025;2166;1642;2166;1642;	
1136	8705	TRUE	8772 53655;536;28348;283;	28348
1228	1522;3887;	True;True;	1534;3913;9351;9352;5042;1275;5042;1275;	
250	1742	TRUE	1755 10689;106;5707;5708;	5709
1093	1130;4963;	True;True;	1137;5000;6915;6916;3717;3718;3717;1637;	
540	3322	TRUE	3347 20604;206;10870;108;	10871
480	465;6162;6	True;True;	466;6205;62816;2817;1559;2029;1559;2029;	
1216	260;879;50	True;True;	260;886;501573;1574;882;883;88883;2865;1	
828	950;2228;4	True;True;	957;2244;45779;5780;3095;7343;3095;7345;	
525	5908;7901;	True;True;	5951;7963;36606;366;19547;195;19548;258;	
824	1236;3975;	True;True;	1245;4001;7607;7608;4107;4108;4109;1301;	
68	4444;5941;	True;True;	4473;5984;27355;273;14570;196;14570;196;	
95	2762;7396;	True;True;	2782;7455;17186;171;9079;9080;9081;2420;	
1642	5422;8678;	True;True;	5461;8745;33575;335;17981;179;17982;282;	
774	1046;4521;	True;True;	1053;4551;6402;6403;3437;1483;3437;1483;	
1411	1585	TRUE	1598 9736;9737;5239;5240;	5245
598	2651	TRUE	2671 16516;165;	8723 8723
470	6540;9083	True;True	6586;9151 40532;405;21482;295;21482;295;	

1781 1248;9172 True;True 1257;9241 7677;7678;4136;2986;4136;2986  
2073 1786 TRUE 1800 11001;1105851;5852 5852  
1023 736;1238;1 True;True; 743;1247;14490;7619;2398;4111;2398;4111;  
1022 1637;2603; True;True; 1650;2622;10034;1005396;5397;5397;8566;  
1064 2225;3424; False;True; 2241;3449;13827;1387338;7339;7338;11220  
2147 4412;9338 True;True 4441;9408 27175;27114452;30414452;3042  
465 3512;7412 True;True 3537;7472 21838;21811548;24211548;2426  
1825 2863 TRUE 2886 17876;1789428 9428  
282 936;986;23 True;True; 943;993;245691;5692;3049;3229;3049;3229;  
866 5;5646 True;True 5;5687 33;34;35;315;18672;115;18672  
1901 473;532 True;True 474;534 2855;2856;1583;1743;1583;1744  
1934 1285;5687; True;True; 1294;5729;7868;7869;4253;18804253;18803  
561 6073;9852 True;True 6116;9929 37619;37620012;20020012;3232  
1717 2722 TRUE 2742 16942;1698933;8934; 8935  
388 4708 TRUE 4738 28964;28915450;15415450  
1795 1447;3361 True;True 1458;3386 8871;8872;4809;4810;4810;11000  
560 1342;7964; True;True; 1352;8027;8223;8224;4452;26034452;26038

Oxidation ( Oxidation (M) site positions

5;11971;12023;12387;35319;35381;36581

12017;12637;14780;15814;25119;30076;30758;35738

58 218

58 221

58 223

58 223

58 188

58 218

58 218

24162

3

8978;10556;18832;33432;33449

6801;21832

434;9393;9444;11433;24950

3420;33417;36558

5;17921;18351;33953

4;16727;19904

11092;13590;14775;14930;15625;17817;26691;30146

2;15040;19031;35754

25760;32276;33012;35480

441;7097;8944;22369;22513;31380;33258;38087

);19412;20789;22803;34203

13218;19012;29685;30731

6058;10096;14116;18492;20723;22181;27990;28147;34698;37918

10543;16799;30184

53

53;28888;36811

2;25293

26

);18153;23196;36413

55

3;36556;37806

5;19390

);20632;35799

7

7;24404

3

5

24

47;32715

16

8237;9905;10436;14815;18901;20184;20293;21485;22120;24051;26155;29704;34983;36610;37124;37

13646

33;19399;19710;22141;25172

54

39;25129

5

16

59

51

32830

12027;13570;17897;22074;22172;33750;34064

4

4247;17478;25076

6624;6984;6991;16080;24399;26479;26985;35315

3;19551;22114;25641;30545;36550

7;12643;12657;19936;21984

286;15021;15022;32303;35044

3;14066;17344;23124;28523;37023

12004;12919;20255;25375

19686;20161;26980;33728;33733

3;26958;35032;35348;38219

11953;14650;20086;27173;35370;35783

149;11448;13370;20409;21508;29492;33312

5;32398

22850;27075;33242

12135;33537

34;32777

20762

2;24054

21767;22334

7

32

24;8130;8531;10074;10260;11408;12415;16171;17980;30985;32521

4763;19267;19947;19982;20592;23080;23587;32733;34458;36505

14255;17102;21562;21853;21864;25473;30859;35588;37136;37139

);17517;21937;25713;35676;37063

83 32

3;32042;34346

5546;16931;18868;20095;21945;21947;23564;26904

11;15459;17747;18892;19304;19905;22998;26888

617;10921;20569;28142;28146;38372

85;4895;5689;7228;7412;9410;10902;11710;12682;13075;15330;15789;18896;19126;20540;24618;246

13

19

51 495

4103;7269;12142;12813;13382;15683;32614

12;17664;17815;18555;23946;35009

59 52

6408;9453;10652;10858;16001;18168

5307;35227

307;35227

14259;14361;15419;25675

5;17706;18572;25272;29964;33650

18361;23111;23349;27029;34424;38075

22086;33705

34;26345;28976;35340;37649

5;16274;23423;26894;27254;38186

12;32180;32186

15178;29728;34181

11

3

);16808;20823

39;22509;35706

1;17751;26092;34248;34488

);13988;17572;37675;38396

13;36810;38244

10;31226;37572

38;26738;27297;33015

5

4864;9007;10225;10722;14043;15434;19155;24432;28528;28937;32982;32988;33376;33437

36;29087;31471;33770

23675;27305

0455;13044;30341

17350;21711;27067;27205

38

7914;15081;24507

38052

59

3;32886;38285

2;15048;15050;15059;22974;24047;25124;25385;25391;26486;28317;29269;37134

2;14106;15067;24834;25938;27004;34682;37841

8111;11006;14179;14279;14280;14288;14901;35136;37329;38450;38451

5;17501;26063;30243;32795



14535;18081;18107;20091;22919;23805;26668;30784;30787;32202;35817;36615

3703;17520;34669

l;23210;31561;31641

54

12275;22269;25364;27366;33827;34755;36544;37535

5

02

52;53 148;196

10;28701;30607;34875;38265

53;36573

2

9;13068;19733;23758;25720

28718;36078

18

4;10536;17346;24880;25997;29541;34670;37107

76;77;78;79;44;47;153;227;283;305;325

76;77;78;79;44;47;153;227;283;305;325

78;79;80 45;48;326

2;25990;27692;29399;30008

13737;14197;18728

24825;30109

5;23551;37426

0638;35286

10467;13485;20828;21423;24064

12320

7045;9203;10204;18759;20812;34514

11

17

55;16427;18521;21429

14

45;36867

31

9;33287;34813;35369

32079

00

8096

31

3237;5207;9804;12315;15623;17843;25686;28633;33391;33698;35744;36968;38058

3618;21089;24161;25605

7

15576;35575;37569

2

);22648;31952;36489

8758;13859;14505;16286;21417;24735;30840;34287;35863

30;19308;20288;20402;27121

35

250

844;11210;11387;12507;12783;20400;23085;26062;30649;31045;37424

5;33471

5;19536;23002;24050;25806

34;19536

5;19536;25808;35921

41;19723

);32885

);7

27226;27283;36230

25;26 72;79

35

16997;17494;26141;28476;34525

23135;29298

14924;15793

7424;8277;8850;8851;9694;12497;14637;14662;15232;15920;15923;18949;20344;31666;36360;37394

5;36360;37394

10

16

10

16

39;18364;20655;26221;26986;32224;37687

26;32742;33483;33708

9252;9606;10083;12309;16328;26939;31631;37540

);2

536;1917;3014;4382;4863;5168;5334;5683;7757;8429;9187;9661;12324;13763;14348;14450;14812;14

26;1530;1917;3014;4382;5164;5683;6996;7757;8429;9289;9661;12332;13763;14347;14349;14450;148

49;22957;35199;35634

40

94

);7

5;24788;31679;33474;37299

);3;16146;23715

);2;17363;33206

40;30393

668;2963;4229;34590

55

8910;9351;30062;34131;34332;37108

525;10293;26918;34131;36110

44;2361;3917;4259;5470;11527;12069;13348;13492;16108;17767;23378;23386;23487;25238;25735;27

10503;11847;13564;27874;27989

44 240

4967;5448;6749;12243;14569;25762;27667;27816;28797;28804

19;10452;11272;12519;12525;16919;25761;27663;35512

56;12541;13441;22506;23770;25849;27809;28532;35470;36914

7578;11267;11849;19756;20564;25212;27820;31875;31876

12246;16111;27818;27991;29859;30293;32030;34447

668;5477;7352;7358;10937;18800;26086;26707;27778;29826;32309;32607;32684

50

5424;17024;18539;20519;24039

2119;23410

4;17987;18539;19801;24039

70;29476

39

3;15006;15079;18808;31071;37337

2

50

25164;38228

28;31244

149;8568;16740;18338;27354;31315;35546

13631;17560;20140;21431;28372;36899

17378;20672;23552;27548;34234;35036

16076;18631;19350

15202;15293;17640;20630

16;34654;35633

7579;11085;14580;15296;17480;24150;24368;25480;30759;32507;34539

003;9101;9620;10352;10717;11919;15445;15476;17460;19262;20928;21290;24438;26380;26596;3271

30

19646;29748

34

58;29067

32;18493;18886;25695;29599;37514

57 51

36;37;38;39;113;145;408;478

5;18229;24193;27418;30301;35886;38282

3

3

26;34274  
2420;14142;17403;21902;23250;23518;28007;31521  
58;22338;28082;30909;33367;37180  
2;26717;27159  
4;17136;26520;30529;37041

20  
38;24987;25235  
50

3655;5290;6972;7149;7659;10220;12076;15417;17951;19685;19713;21876;26035;27381;28264;31533  
4;32190;34407  
08;25029;31204  
7976;9527;10944;12349;23005;23764;25011;28055;31204;32135;37797  
17415;29187;32080  
33;37934  
33472  
;1682;5093;6653;7682;8184;10464;12316;16105;16688;17663;18477;19219;19588;20776;21176;21558  
7;10380;10522;12150;12161;13131;14572;18746;34782  
11990;15903;16697;24257;26695;27763;35814  
3  
7;23671;24949;29380;31331  
12400;13325;14000;16053;16110;23034  
5 352

3;25880;33401;35836;35903  
3

5;35923  
5  
33 15

7879;20588  
20232  
54;17010;17954;27042;27952;29693;34051  
20030;21033;21038;37927

07;29716;31547  
8759  
27;35613

2;28524  
2;14971  
26;37189  
6124;9015;10978;12749;16229;17662;17704;20754;20775;22032;24278;24605;24711;25929;27462;28  
)

6631;18757;23223;23893;24313;26956;28362;28786;32071;36464;38344

3

12;32240;35658

3

05

50

3;19477;29447

);25221;25273

1292;11516;11777;13641;17394;17712;18370;18773;25973;30916;30925;32413;38420

5;32870;36834

64;7100;7441;10448;14262;15813;18104;18395;19417;19573;21519;24827;25923;28506;30198;32714

59

4;22055;26106

56;31671

102 370

05;20527;26277;26689;31404

097;14511;17180;17911;22981

6900;17499;30424;30940

607;4071;4083;4870;7952;12688;13395;16329;17168;17171;17585;17819;17967;25505;31343;32266;3

20;30849;31531

36;18751;19082;22601;26185;27141;37817

33;24584;27140;28351;37854

3;21421;27936;27937

3909;5271;12620;12979;29108;33225

60 257

7;31111

39;35256

36;28091;33065

);36513;37249

9552;10208;12225;13024;16036;19401;27997;29341;29736;36617

7639;11344;17225;21735;29305;29511

3;14926;15864;16363;20328;27474;31831;37761

20624;20704;28041;32043

5;33078

73

06

3

49

7;1211;5627;10546;10846;21604;24310

38;16054;19991;36380;37861

28;14503;17154;18474;19198;19895;20511;23439;24215;24917;25075;25658;25799;26077;27507;295

3;22330;29429;32115;32681;33341

5;13227;13765;14552;22138;25818;27544;28189;28728;29147;29612;30358;38077

9786;26783;32126;36175  
2;30741  
10880;11434;21622;28683;30359;35798  
7947;8835;14148;14867;26892;38384  
7  
59;32156  
58;29832  
35  
24 189  
21356  
51;32525  
41;38150  
36  
51  
73;35317;36675  
30768;37103;38392  
49;19672;22231  
3  
4785;11881;32611  
96 168  
30  
36  
  
2079;17804;26190  
5;13662;15409;18221;19812;24774;35170;37882  
25;30142

18;22065;28981;34171;36942

6722;11890;12693;14155;17264;29111;36622  
1975;2744;3753;4303;4717;9128;9334;10500;10680;13031;14390;14589;15481;16732;17229;17411;17  
8936  
3  
59  
5;34438

4  
37;31656  
39;12928;32317

839;26582;27025  
37;35590  
3;34811  
218;10947;37240

4586;5860;11811;12344;20343;22180;24294;31800

7;25128;35411;38365  
933;13598;19212;20867;26184;31126;34485;36732  
3;19408;24753;27797;35306;36418  
l;21098  
30254;31810  
3598;8002;13921;13925;18076;19594;22988;24007;24009;29889;29890;37152

8630;20765;33716

57;25930  
12865;20341;20545  
17327;21157;24789;25581;26594;27865;28510;34511;37068  
2234;9489;23216;34182;34196;34197

5;31587;34431  
33;35545

3910;26652;27146;29547;30776;33327  
3  
3  
34  
5;16810;22529;23579;26715;29403;29840;33490;34151  
3  
745;4034;13668;23566;23571;23890;26653;28452

54  
09;23658;28502;36447;37400

32555;34712  
33;32850  
4

5  
3;12252;12516;37619  
75;31090

19761;21871;30222;33295;35005  
52;19164;23040;29351  
08;16689;18262;19288;35973

32;34832

3;12461;13787;27442;33217  
48

79;32444

33

517;6646;7916;8640;9422;10903;14132;14611;18696;23310;23499;37661

8716;12203;20936;21696;22000;23466;26752;29042;31553;36888;37274

3;28416

)

13463;21409;28310

32

36;27017

11;36596

27723;35674

46

12434;17741;22275

23611;36818

5;25157

34

29

49

36

1

5;13326;30297

81;3463;5442;5628;7256;9584;10153;10569;12379;13437;14143;15842;16236;16544;16546;18314;186

223

15;33084

10;32904;38209

5757;9000;14360;15124;16722;18415;19035;20952;21165;25878;25971;26553;26671;27774;28515;30

30;31688

59

12775;31392;32997

57

5726;12025;13383;23435;25586;31871;35291;36206

18;29501

46

42

20

53;25299;35737

28363

);14474;19490;21974

59;37201;38094

21

7498;8573;9688;13002;18532;19724;20784;22936;23014;26040;34315;34751;36082

34;29000



31;14753;15278;30858

5;26826;35632

7;15910;24936;25883;28970;31778;33626;35122;36411;36631;36757

13333;15045;17114;17319;18296;22449;28986;34843;35749;35969

2402;2817;9260;9265;10441;11258;12002;12356;12600;13772;14325;15133;15757;16608;16794;1709

4183;13900;13994;13995;22988;37145

53

3765;24176;32128

9;16107;35768;35808

12691;19566;24973;25526;32214;34213

)

5;22097;27444;28047

3;15134;15443;17336;22517;26012;26569;37749

25963;26733;29197

5;21250;28051;36869

71;26788

33;18434;34314

9120;9122;9798;12402;13479;13482;26368;32644;32657;37250

15617;20029;30166;30213;32320;33489

846;10222;19532;19804;32697;32723;32808;35723;38108

);19567;26414;27885;32658;36097;38342

l;12779;13250;14755;23148;23291;26044;26891;27710;27711;28605;28759;29431;29576;30532

968;8528;12993;16199;19252;24014;24274;26045;26466;28185;33298;37638

7;10457;11723;11883;14468;15194;15781;18669;18742;24800;26982;28074;32511

3;14835;20837;23432

346;3860;4094;4241;5684;6155;8366;8917;11051;12223;12646;13784;14003;14375;15925;16284;1699

59

5

33

4

l;26099

28;26187;36136

l9;35535

7016;24539

5;10695;31843

19942;34868

3;33764

23507;23514

7;38250

5

3;20866;24888;29802;30504;32074;38215

3352;5451;6462;6591;10630;10961;11616;13977;14887;18362;21010;23962;24992;27728;28765;3098

16952;21347;21516;23007;24549;29192;31394;37590;37599

16574;27347

5;10307;11146;31409

9

4

4;37855

9

1

33223

57;26876

50;37625

5;32724

0

4506

06;37978

06;37978

13643

70

4501;6446;6447;7686;7848;7850;8369;10103;10106;10126;11585;16078;24674;24726;26434;28221;28

8775;9862;10951;24452;26972

07;19749;20900;21976

0;12199

51

0;23614

8;9370;21443;34480;35892

37

4;19297;19881;28595;37830

9623;24943;28788;32161;35498

20;19234;19579;27622;31715

12251;15129;19712;20840;21681;31480;34368;37185

15359;20924;26270;26730;30094;34348;37196

40;29286;29782;30403

11117;13703;14771;28563;28674;29783

11117;13703;14771;26624;28563;29783

8;6026;10591;15994;17462;17685;17848;18814;22628;25620;26811;29977;29978;31158

3815;4058;4270;5591;5600;6327;7270;7619;7712;7716;9297;10864;11684;12017;12168;12904;16168;

11;20711;28114;37458

17;37442

910;8142;8373;11485;11639;11641;12347;13448;14545;15807;17703;18179;20135;31615;32826;3321

3;15211;33282;37969

28;25651

5;21425;23687;26732;27559;32462

11288;11645

9866;11303;15880;26005;28949

23998;27602;32206;33803

79;34380

6892;7130;7364;7858;7876;8319;8324;9143;9405;9653;10713;12475;13671;17387;17636;19779;19926

4

33239

15801;28972;35499

72;26449;29998

7778;8644;14831;17333;19459;28679

02;4319;6040;8028;8554;9040;10813;11544;12700;12861;13210;13261;15521;16382;16998;19324;219

9473

2;18615;25758;27161;32515

36

10849;12021;17695;37791

4

35;31291

33;38340

24

6712;20345;30262

2;20345;21474;30262;33606

9790;16143;19483;20278;21314;25853;26971;27100;37835;38138

35

6138;7451;8155;11861;12201;12369;12372;13760;17660;17773;18114;20790;21233;22833;25949;341

9259;12369;12372;18114;23065;34121

1;19197;22702;25300;30277;30528

39;29512;35708;37398;38403

3

18938

3;30981;36667;38404

9421;15199;22518;31300;32630

5;14929;17244;18748;19915;28065;34706

5

8911;10558;12822;15405;15761;19200;23923;24319;32011

3;12180;13411;17089;24173;36363;38433

9925;19745;27052;27920;36716

27;19493;24121;31944;33408;37065;37810;37947

46;23497;25914;26325;29587;35504

12;37198

8135;36384

24277;33851

12140;14493;17113;19287;22472;26091;28218;30440

3

43;23837;26247;34495;36080;36774

467;7138;7545;8580;10468;10733;12830;14051;21156;23898;25274;26860;30615;34394

5

);31406;33542

11794;13238;31376;32897

2

17203;18176;20872;20873;34806;37277

59;20040;20440;27745

1;20674;24744;26725

2;16653;35147

36

33

7517;9130;17412;26283;26400;32709;34057

;5614;17190;20435;20521;24168;26348;27335;35038;37219

3

6066;9999;12782;19767;21862;26282;31691;32021;35935

2700;5872;8510;15346;19313;21108;26251;26314;27037;27038;28391;29519

692;7436;8116;14399;14814;23680;35524;38296

098;9780;11164;13722;16436;17141;19274;34013

7600;10291;10914;15086;20376

599;10241;10916;20376

);19237;22123;27620;28344;29481;30040;30261;37242

48;15365;16539;16556;16589;20174;23313;27457;28587;33574;35750

1;13032;14396;15353;15631;16589;17814;22963;26208;30265;35752;35933;35954

38;16560;16589;22855;23312;23889;27111

4;35465

3;17860;20698;24883;26513

);18018;18151;21396;22092;23508;25232;25998;26150;34665;35577;36329;37037;37405;37691;37753

52;4493;4525;5113;5171;6025;6083;6443;6976;7232;8847;9730;9752;10644;12271;12690;12754;1338

5;32541;32852

);25037

14189;14626;16085;24952;37601

36;16279;20350

5;22845;25059;26440;32743

95

1

8;948;949;1127;1375;1476;1500;1542;1631;2016;2188;2982;3214;3736;3774;3898;4431;4439;4633;46

0;1375;1483;1513;1594;2021;2543;2582;4212;4678;5546;6936;7115;10506;11251;11282;11589;12208

5;25978;26340;36739;37027

2;21085;23649;25247  
3;17084;35982;36319  
5;26046;26813;30516;33848

8029;18130;21171;35001  
38

88;2131;4411;5100;8497;10786;12269;13697;15342;17595;21291;21302;25564;26298;26970;27064;36  
13692;17595;26970;33990;37173;37174  
;15153;15160;15368;17385;19799;20660;28291;33354

2;20798;24716;28094  
277;10499;20748;20852;28120;35995  
19  
27586;38221  
35  
1;36052  
5;16276;16551;20084;21743;22010;30978;32819  
5  
6015;6294;7691;14522;17737;25252;26712;27703;31242;37624

9637;9884;27104;28512;30129;35770  
)

38

2;31159;31787;37433  
8656;12130;12982;13798;15218;17973;20783;21141;23997;24846;32542;34618;35948  
2;16307;22976;24346;29258;29340;31197;31792;34448  
5845;7071;9006;9110;9243;16023;19602;19888;22486;25397;28744;28894;33047;37345  
3918;4155;4826;5484;11853;14036;15505;15507;16728;17718;23292;24216;25200;30501;37972;3822  
27

1;36202  
9883;10835;13289;18149;22599;35426;36148;37131  
9138;13754  
12952;16077;28410;28702  
7

2;19611;28064  
23685  
56;19010;20425;20677;22961  
48 92  
34 88

9531;18318;22317;25183;27841;33008  
33  
36;29813;33107;38051

3;36359

14;22613;26262;28121;32318;35373

4253;23851;28301;30443;36707

716;18289;21620;31062

39;26487

3

16816;22586

5;26087;29505

35

31

3

9805;24724;25253

36

14185;22234;24287;25077;33738

36

9574;14756;15601;19285;20369;22805

9575;14758;15611;19285;20369;22805

1;27605;27606;30612

19435;19933;20560;27845;36046

7476;19933;20560;27849;27855;31223;36046

14874;15606;16909;19285;20369;22805

34

3;25590;35485

30

5216;6562;10841;12144;14200;22475;22495;32148;36730;36734;38361;38432

33

3

30897;33306

16169;19819;25918;32807

664;12339;12676;17120;22264;23307;27948;34405

6 550

1366;4483;8524;8536;10350;11393;18002;18975;21603;23201;23531;23868;24080;27769;29189;3005

5930;9912;15660;17051;20444;30035;32847;34239

4297;4657;7921;9755;9916;12845;14540;15634;15648;17051;20444;23317;24650;24659;24742;24927

5694;8393;10218;11093;11393;18000;18109;20528;20628;22567;22812;23530;24636;27027;29536;30

7731;7732;8302;8331;13903;18861;22343;29273;30802;37372;38369

5285;12971;18196;18581;19283;25396;25769;26350;31729;35794;36132;38311

226;5949;6183;7299;7738;7745;8112;8309;8312;8337;8338;8619;11115;13681;13990;14114;14131;14

47 466

9916;15634;15648;17051;20444;24927;29931;32847;35978  
5;29735;35406  
J4  
J;27266;37930

12 33

J;35709  
7;32755

J;14858;17726;27483  
79;22665;29679;29682;31658  
J;22726;22827  
J;19334;19420;28243  
11781;15128;19336;24609;27945;27947;28409;29760;29761  
11783;15123;15257;22785;29766;36919  
10064;11790;11960;15265;37571  
L9;37573  
14374;17041;25363;26566;29842;31013;34793;36315;37456  
12607;14413;29218;29997;31526;34793;36313;37453  
12606;14413;29244;29997;31526;34793;37448  
5181;7924;14223;29988;34788  
J;11959;13151;13319;14859;15622;15679;15739;19371;20349;23430;24248;24855;27079;27083;30943  
J;18663;20800;22593;23661;24551;27506;28636;29854;30907;34484;37533;38441  
1;1146;9437;9949;9954;10176;11395;12231;12760;16233;19570;19750;22836;22842;22858;22873;22885  
5626;6229;7547;8852;11792;18188;19431;20614;22551;24127;27271;31483;36274;37483  
7549;8692;11792;18191;19431;20610;24129;27271;31483;31888;36277;37485  
5354;5722;8109;13770;13849;17497;17555;17567;20268;20270;20791;21031;22649;23088;23820;23871;28246  
020;5696;7632;10655;21117;22322;23608;23814;25211;28182;28183;29654;37993

56 193

17212;18057;20051;20052;22934;23387;23640;26164;27198;27668;27760;34053;35829  
4017;11177;11183;14095;27345;30022;34280  
3222;4333;10442;10552;11178;11183;14090;19775;21400;22105;32877;32907  
57  
79;17789;19544;23224  
24

L;26475;29843

15574;25311  
L

58;37465;38435  
58;31042;34597  
13364;17468;17506;17530;17936;27965;28378;28380  
13364;17506;17530;17931;27970;28378;28380  
13364;17508;17548;23887;27979  
4  
5;23619;23623;36356

11487;14165

5;23619;32581

31;32 60;63

31;32 60;63

31;32 60;63

31;32 60;63

l;27338;29951;38120

84 85

1649;14267;20811;32363;32889;34964;37932

l1;32363;32889;34802;34964

5124;5128;9831;10217;13816;17729;17735;30322;36857;37435

5124;5128;9831;10217;13816;17729;17735;23370;30322;36857

3

5124;5136;9834;23370;30334;36839

5124;5128;9821;10217;23364;30334;36839

5124;5128;9821;10217;23364;30331

9528;18374;18885;25811;33344

8254;19707;21045;26921;29090;30961

11477;31116;31290

35

3;23045;24730;25367;31459;36401;38306

);20338;28156;30534

09;30353;32124;34890

991;19697;22570;31870;33082;33488

5;20314;24095;24320;24485;25107;30051;31472

22595;25069;35947

7

13985;18245;20284;21286;25414;27683;29168;29684;31794;33144;33336;33353;35117

54;20512;23067;27142;29916;33320;33720;34836;35891

3;27619;35479

09

4

35

25

5

0

2305;13122;13795;14405;34842;37688;38367

75

7052;11055;12725;14016;18185;24191;26987;32707;33583;37342

3;18042;19413;32744;34953

3;23305;28602

2;28207;36304

4368;4804;15438;16014;20756;24422;25616;30059;30135;32544;33982;36534;37197

32948;37833;38345

552;4929;7627;10160;14997;15060;19224;19850;20408;20818;21368;23981;24842;27441;27712;3050



10159;29674;30009

2

5960;9712;10687;11437;11749;12190;20069;21435;27375;28214;28845;33099

6657;6781;6994;7708;8702;10211;11608;14515;16769;18692;20235;21737;22049;22148;22661;25023

5

3;27765

4;38090

7;15317;18613;18652

52;24595;26473;34831;35071;35401;36891

3740;4200;7102;7250;8776;13811;14392;15277;19349;20766;24582;28270;28486;35100;35255;35384

8727;14967;25112;29262;32423;36982

19494

4754;13724;15743;16735;19861;24020;27687;27800;28477;34244;36452

7;19163;19346;21191;22542;22866;24442;30280;31059;34283;35285

7087;10387;17971;30536;38274

091;12280;14240;14457;18305;20412;20424;20816;22324;22330;23713;24120;27308;32118;33341;35

7332;9808;16993;21388;22093;35041;36298

1;18558;26626;26635;28900;29634

15;17;18 313;341;416

4064;8986;9330;11069;16141;18558;19137;20092;28906;30974;32564;34946;35157;37336

3051;9239;12042;12053;12614;17232;18126;18560;18931;20211;25530;25665;26641;27058;28775;28

14;15 259;316

5;12101;18558;28244

32;24109;26096;28714;31900;37262;37304

10359;11906;20216;24153;37262

19 297

89;2860;6479;9570;9685;10353;12730;13189;16772;20216;24109;24153;25743;25844;26202;26423;30

60;6479;9570;9685;10353;13189;16772;20216;24109;24153;25743;25844;26423;30471;37088;37262;3

16 249

13 406

58;28346

12;30225;35625;35938

30;22546;27258;27357;32514

639;22302;24745

33;27143;33214

)

20;24304;26875;26967;28682;31809

2;12921;20082;24683;25283;27877;29878;29894;34881;37551

4;12921;13868;20082;22779;24683;25283;27166;27877;29894;34219;37551

5;31130;36518

4396;4401;4560;6151;7437;9045;9534;15115;15333;16530;17813;18469;18635;20223;21172;21360;21

987;2249;2253;3361;4386;4393;5623;6571;7673;8217;8674;8818;12450;13089;16715;19100;19203;20

57;14587  
1192;19221;33279;34292;38067  
19691;24876;29506  
3952;7113;13028;18307;23155

9707;13475;29390;37865  
16017  
1851;11566;27238  
);21126  
5  
2  
30041;33425;36460  
1579;2246;4503;4682;7804;8082;8901;11550;12734;15478;16507;16892;18745;19487;19847;20410;21  
14585;23726;27362

7;31801  
5519;21267;22016;22262;22409;33442  
7;28076;28304;30010  
74;37393  
l;19788;33277  
3;30123  
7218;25290;27386;36879  
51;22910;26540;26564;27115;32442;37570  
);13727;14789;16670;21548;23746;26625;27837;29504;34775;37999  
);29851  
6147;6743;10244;11698;22190;26882;27250;31885;34809;34901;36376  
97;12666;15496;17153;19843;27245;28667;34901  
40;17306;26245;31039;38199  
7;26199;37834  
5;13455;14103;15473;20356;21073;21582;24902;34547;35410;36950  
73;21582;30517;34546  
);29388  
);24042;25134;28042

39;37874  
5;13120;15553

3;15843;16260;20876;20880;27012;36450  
30;38029  
);8  
15373

54;23926

28394;32966  
5  
l5  
l2  
25569;36050

34;36163  
30;18242;32204

7  
3238;8434;12856;12898;14546;19402;20475;25647;33609  
10973;19790;25016;35039  
7881;10992;11402;13802;14061;15220;16495;21913;22978;24779;29530;31621;33684;33860;35717;3  
7;21692;29227

3;18352;19711;28661;31954

9844;11465;12790;12887;12916;13814;15429;17103;18691;24875;28101;29499;29523;30964;36559  
30;36719;37135  
4629;32273;32277;32278;32280;32311  
21 76

7  
7746

11134;12412  
2;12501;27019

15847;18731  
58  
3  
32387;36717  
7;26704;37935  
3

14;27430  
3  
53;17112;19114;31951;36922

36714

34  
4  
464;33418;36425;38174

197;12210;12747;13711;16946;18065;21468;26662;27791;27835;28566;30853;32706;38235

39  
54 517  
17926;17983;19078;22034;23972;26010  
56;32875

37

100

301

418;21840;24996

58;36042

20623;37658

34;26769;29137;35289;35385

39;19710;34803

34

10

30

5;15850;34450;36257;37227

1237;22491;26090

);29703;33081

7;13307;22606;23144;26349;27106;32290;32298

62;8767;12572;24968;25739;27522

5;29907

14021;21753;25506;30145

32;30078;32165

7

14;24370;32252;33677

3

33;36090

2450;2784;2811;2812;7034;7216;9046;11137;15346;16637;16906;18150;19313;26251;27038;28383;30

21251

5

4534;29821;34510

3;29443

136;9511;12853;30296;34261;36688

38

5999;8879;9668;12801;17992;18062;19989;20308;20439;29276;29296;29455;36827

7

3;24552;27962

5

31;4995;5251;5338;5785;6190;6776;7452;8406;9596;9598;10178;10653;11868;12295;12392;12447;13

6128;6902;14495;16124;24074;27536;35167

6900;8385;10891;12769;20709;23429

72

90

70 372

8785;9819;17652;17687;18468;23546;26300  
62;63;64;65;86;137;162;329;365;627;879;941;1489;1594;1910

5  
9;6951;7439;11584;11720;35608

52  
3  
9104;10231;10257;10570;14781;16028;17300;18894;26523;30096;32000  
13983;19344  
441;33494  
9;20036;32621  
12712;15125

5

19

12957;30072;30074;30207

35;29436  
24548;37346  
72  
9

9;22184  
9  
3;624;652;662;747;761;820;913;914;2429;2451;2464;2548;3059;3524;4832;5358;7574;10179;10190;10191

53;27905  
735;4954;5989;8782;10039;10728;10765;12553;14856;18793;21477;23078;24533;25222;26989;28259  
735;4954;5989;8782;10039;10728;10765;12553;14856;18793;21477;23078;24533;25222;26018;26989  
1  
12823;19706;23980;27478;27871;29958;30442  
14;36259;36782  
14;31213;35809

98;26496  
18764  
13;30617;32105  
6092;6095;6668;30082;36832;37831

9;16612;17034;29773;35979  
5;30920  
3711;4428;9677;10142;12358;19428;22915;25555;26518;27074;34254

14;21246;23107  
54;38119  
7594;19464;29422;30419

17;28481  
1;22806;30733

1;24298  
55;21196;21415;34198  
;2641;2703;3071;3367;3650;4736;6200;6213;6878;8121;8269;10727;11760;14339;17850;18036;18120  
53;28225;33202;34442;35326  
10392;12598;15041;18217  
25;24999;28282;32884;37413  
12616;13577;16821;16897;19826;22520;24781;25467;29884;33623;38393  
5;20534;20934;27725;28116;38159  
6067;10897;16597;18472;20165;21739;37917  
);25219;26023;32820

7;12953;18516;30111  
11;20770;21899;22274;24269;29784  
1862;24217;28598;29010  
37033  
);34692;36976

3536;23110;30922;34569  
18402;21635;24036  
7;36514

7338;11224;23895;25184;25192;27125;27133;30191  
);22655  
1;33402;33445;35991  
72;24822;35907

4610;17874;18400;19005;21005;21608;26583;31906

)7

1;14847;15632;18485;21480;30075;35316;36649;38021  
2;15695;17810;20758;21137;21457;29582;32509;33252  
11  
230;7082;7502;7605;8146;8872;13658;15468;19769;21666;23696;27499;27584;30130;31171;37021  
32;32347  
7044;9069;10200;11827;12185;12631;12632;13064;13736;17693;18108;19107;23643;24815;26024;28

41;42      65;81

39;32263

3;28609;29410;31881  
1;35252  
3;21397;35931;36443  
8234;8451;9971;12182;13072;17876;18750;23958;26037;27136;29517;32039

1;24002;31144;35542  
11494;24006;27425;31144;35542;37931  
3;37193  
62;27906  
1

3;26592

9638;17309;22556;32024;34667

9670;12378;12565;18092;20977;33114;33482;35354

7;13876;17670;37402

57;25104

);37463  
1458;14245;23103;27323;30498;33358;36735;36737  
5  
3  
85 76  
85;86 61;136  
6416;6557;10573;14568;15308;32925;34888;35206

3;13177;30941  
20;27030  
15  
34;27775  
3729;7861;9846;9935;19156;21071;22503;32486;34610;35388

3

79  
52  
12427;14776;19721;19737;27779;30279  
35241  
199;5445;12490;14008;14011;15372;18015;20645;22288;25985;26130;30156;31549  
2;17673;21422;22294;26130;27065;30152;30831  
);14008;14012;16389;16797;22296;25268;26113;30156;32561;36180  
31;20102;31516;34560;35626  
5415;18443;20889;21494;25334;33627;36542

20

3741;4021;11323;14801;14964;16695;19669;21311;23911;25557;29069;29183;33657;35393;36606

5;17046;18473;28072;28686;35521;36692

7

40;36511

672;14125;19928;23978;28417;30522;32821;33318

19

40;13466;16620;20969;23199;32946;35518

12757;22516;24686;37031

12900;29619

37;28297;30070

13061;35412

5825;28210;28482;31575;32440;37260

623;2009;10209;11424;17072;17079;19510;24488;31387;31391;35338;36107;38188

10779;10781;14007;14566;24198;27174;30355;37117;37118

3

79

3876;4846;10181;11378;15663;26886

3;34246

13

2

13551;20470;24194;25275;30177;32861;38195

57;32688

9812;17950;17986;25336;26998;27103;27202;27757;29707

39;20714;29064;32414;38455

5;7678;8054;10795;13314;14489;16724;17879;19111;21581;22967;23670;25154;31036;36748;37128;3

3562;3765;5152;16264;17879;19111;21581;22967;23669;25943;36743;37128;38006;38308

52;23321;30589;37129

449;1571;2125;2599;2643;2659;2757;2771;2849;2876;3818;3984;4192;4412;4505;4694;4827;5758;610

33

1;13865;16590;21198;34779

3032;11939;12093;12377;14722;21202;22047;24671;25522;26550;27512;31859;32833;36510;36639

14698;15742;16250;18990;22448;25957;35571

14701;15740;16250;22440;25471;26047

17434;25611;26678;28471;34711;36471



10127;10828;11826;11829;13782;17667;23798;23799;24143;24571;25400;25642;28369;28652;28851;

10832;11826;11831;25400;28851

49

53

7846;15588;17893;19240;25602;28110;35537;35538

1119;14485;23877;25084;28258;36731;36877

l;32375

13069;14328;14658;17909;21525;21997;23856;24482

8658;21997;22609;24170;24479;29598

5;31746

09;2731;2733;2789;2910;5588;6833;6835;7644;14945;17020;18023;18261;18636;18919;20031;20223;

5;17373;18154;25860;28881;29701;31990;36252;36423

38

15;8980;9947;14005;19178;19257;36944

2966;5416;5944;7895;8948;14001;14903;16132;20247;21959;24510;28296;30520;37892

3;29194;31032;31793;34341

7

7;21813;26476;27520;30987;32729

5;19007;26048

7572;15108;19077;32064

10409;11214;11238;12298;12941;15860;16449;22282;24873;32439;32734;35311

5 330

43;5345;27219;30179;30492

l

5;19108;20546;23220;23876;28748

57

5 253

22

l

5;26589

5

9180;18147;18882;25660;27137

3;23396;24701;24706;29008;30412;32242;37053

5;27751;34759

49

15248;18347;22160;27753;33319

6283;7869;7871;17566;29722;30003;31206;32076

04;18381;18437;20145;30218;30253

7

39;7590;9747;15249;17853;25082;25482;26755;26837;34451;35358

734;9166;9591;10502;13156;15366;16941;17277;19652;20359;23038;26759;31556;35367;35434

759;10735;20584;23137;24124

668;9750;11475;12179;13918;17131;22216;22851;22924;26039;27894;29007;31629;33480

42;21106;26197;27379;28085

14;38436

71;35519

11447;13146;25847;27680;28958;30595

1

36;32368

14152;17714;21839

5

5;14654;31371;32970;36545

40

16718;17338;31033

42;32958

50

3;20152;20678;34236

14109;17014;20181;26676;37566

9227;14204;15497;20121;22368;24668;25827;31490;32482

3;34492

7435;12936;13628;17134;19391;20643

16058;17797;22039;22573;23967;25199;38364

2;20509

11385;24393;33027

59

05

59

12721;12885;13835;14053;27028

15;32867

4

22

39;35253

046;31302;34156;34891;36948

0

3

5;23880;27690;31680

20

30587

7823;11231;36430;36432

31;25005;28464;36775

57;19882;21144;22071;24714;25798;26490;29313

43 425

61 434

9875;11725;11728;14840;18451;22668;26233;26996;32450;33788;36156;37497

2;13175;13269;13273;15241;18249;24156;24159;24677;24841;31275;34554

);24290;28314

75 377

5

5;13960

19834;22629;29352;31299

23273

2438;6029;6237;7372;7403;7494;7816;8958;10318;10592;12448;13239;15943;17642;18564;18601;215

24;28688

59

37

3

35

3;30306;31006;32973

30

8632;22594;25417;28427;28501;30596;37439

10732;35481

5

37

9256;13351;26268

3976;6043;6697;8344;12973;21101;21374;26132;32168;32382

5220;6467;12792;24179;37447

4531;6236;15030;36390

5

25452

6039;16939

2;23807;27325;28122

54

33828;38132;38135

52  
9687;36197  
8914;8916;14877;20696;20697;34378  
20874;29078

4  
04;25047;25380  
58

15570;33226  
56;32857

17577;19937;35939  
17;37766  
5;26935;27496  
5;24871;29397;31270;36435;37410  
1;35295  
3;14351;19470;21967;24850;34955  
7;15396;38386  
19681;20752;33493;35250;36371;37113  
32

94            1

87;88;89    276;404;410  
4388;15013;16656;28623;29021;37361;37365;37611  
16656;28891;34951;37361  
5;34738  
57

5  
46;34313

7;8            101;107  
22  
00;5060;10237;13401;32716;34216  
0;33884  
16159;36309;36657

55            360  
55            360

11061;22576;23047;23262;24586;25248;26263;30813;33247;36278;37593  
56;34464  
42;30601;30836

8391;11350;18309;19051;19112;20759;26778;29667;29903;34982  
3;31812  
10473;11163;20935;26934;29862;31188;35568

3282;5304;7307;7430;8890;9003;9874;10011;10700;12617;15279;16310;17083;18247;19648;19688;19  
40  
4840;14075;18801;21955;25520;32993;37783  
4840;18467;18801;25520;32993;37783  
33  
);20361;23939;32410;32949  
11375;13415;14190;23701;24029;24477;28567;30026;36584  
0462;11173;15573;17432;17840;21990;24314;27449;30131;31296;37632  
);2;16032;18379;18810;23633;30737  
16609;18158;20361;22902;23525;26895;31579;31705;37167  
20361;22899;23106;26895;31579;31705;36503;37167  
2940;36594  
L  
  
11165;21185;27450;30603;37635  
5897;6302;21213  
7  
  
);22225;23750;25703;30562;37575  
47;26847;30007;33323  
4915;6020;7012;10707;11197;22410;23480;23484;24462;25886;25888;31804;32670;34914  
);3;35514  
);4;31579  
);3;4952  
);3;4963;35050  
);4;26901;35047;37255;37259  
36685;37251  
);5;22458  
);8;26854;36453  
  
);3;23589  
);0  
0694;28149  
29066;35636  
);3;20838;28331;29131;33607;35772;36636  
23037  
  
);36  
);4;20692  
);2;32891;35745;36571  
);19  
);25  
);3;22816  
  
);1  
);38;14904;16973;17178;21868;31100;31102;37626  
);1;34852  
);75;14272;17939;22756;27525;38205

36  
3;32828  
3;18426;23061;36701  
7  
28553  
2  
24;19151;24538;35748

1;16667;17916;22213  
9556;20045;33103;37776  
8544;18744;19160;21556;27463;35148;35665;36842  
3;27285  
843;12587  
11;23601  
11;23557;25420

880;4959;4962;8005;10018;17511;27199;27625;27632;28334;29423;32227;33146;35888  
12;20105;36720  
8349;34529;35937  
36185

4588;35088;36362  
1;18641;28075;32763;36955;37104  
25;13872;14144;19434;27076  
14;33748  
55;36718;37056  
2  
33  
36;24052;31507  
4733;6876;8808;9281;9476;12807;14127;21262;21731;26294;28432;28505;30168;30527;32498  
5;18409;26101;28630

6333;11787;12022;12926;17204;19328;27592;34125;34302  
3146;15269;16291;21470;32522;32528;34871;38180  
3;30583;34871  
19479

101 732  
8057;19944;27929  
75  
5;15111;30805;31335;32990;35278  
3;23207  
82;11478;12064;25786  
361;11596;31399

10  
31;29696;34470;35101  
3  
59  
30 201

3;35135;35172  
07;27767  
3615;7984;12512;13359;15802;18825;25576;30542;35784;38255  
609;6683;11057;13361;13428;16639;17768;30954;32471;32768;36823  
04;30777;32552;37770  
17  
4566;5487;5493;7455;7521;9526;11336;13331;14398;15386;16640;23115;23415;24372;25177;28968;2  
544;15853;18287;23871;27917;27919;30316  
545;15853;18287;24350;27917;27919

5;21983;28896  
4;34147

5;26908;30462

91;92;93 121;326;358  
5  
258;12444;13729;13857;16165;16683;19475;19922;27307;28295;31352;35220;38155  
55;21907;27558  
14218;20450;36552;36697;37549  
0

5451;29384;29475;29888;30459;30657;32203;32219;32321;32328;32335  
5292;6945;17441;28406;36695  
4

5;34014;34577;37481  
24558;24559  
4;20686  
4;25626;28248;32142  
24558;24563;34267;36833  
6939;9899;17451;28407;35511  
08  
5

08;20482;27600;30214

08  
16;21664;21968;22597;24135;27834;30903;32574;35111;35210  
70;36928  
21139;25142;26124;29330;38170  
24989;25236;25345  
0;13890;15184;17395;20745;37538;38028  
0;13890;14816;15184;17297;17395;38028;38114

l2

27 1

2770;13890;15184;17395;25103;38028

57;32911;36709;37261

7;31559;37823

39

39;21934;38446

514;6596;8252;8253;11546;14102;15559;16117;21632;28956;30932;33749

09;24177;27433;28231;31444

4909;6428;13683;14117;17929;21181;22523;27286;27314;27315;31364

2;22784

31

l9

22847;24201;28198;36872

22;25650;25993;29818;37662

32

70;36972

3;19802;28271

33;37403

70;32641;35313

05

40;25427;36244

11558;24912;27200;34204

19310

0;34078

10360;20323;28737

06;28194;34702

29

5

72

09;26988

30;33589;35283

3;14201;15228;23050

25;18630

15;34895

56

8;3402;3545;4173;5209;5538;5867;6188;9492;12367;13558;14646;17195;19929;20724;21520;23917;2

6211;33572

50;27608

5

13;30573

3;17272;23102

74



75;31096

205;15411;19125;20864;33485;37975

17033;21594;28359

24

34

32

304;10736;16777;23333;24598;29561;32262;36154

793;5574;5649;5781;5790;6641;6836;7013;7056;7065;8441;8701;13567;16988;19314;21167;21399;22

7974;8977;9364;9699;16214;22011;22340;22377;29588;30530;30555;32470;32535;33701;34886

28;30812

12400;13325;16053;16110;23034;23592;35620

32;28604;33040

);30957

4;37026;37929

1;17356;30242;30986;31505;35357;35905;36874

6809;18295;18501;34602

3;14040;14084;17262;23154;23795;32394;33056;37399

30

11;35579;36895

19335;19593;28479;30160

430;9671;9701;10150;12722;16701;19423;19426;22853;25514;26001;27071;28692;29428;37461

3;37507

6733;7598;13027;17743;19398;22864;26804;32517;38110

33;28530

2903;8746;10180;10182;10185;13016;20992;23519;25814;27367;27370;32538;32540;33110;37501

790;6862;9425;19026;19763;24229;25935;27694;28924;29769;33395;35026;35725;36708

9171;28400;28632

70

6075;13629;13745;25007

3141;3384;6608;6610;9126;25676

73

370

78;2274;4277;4792;6070;6804;8188;13892;14571;18651;19934;20586;31912;33259

4

10959;26497;31574;31636

16261;16283;23666

3;22771;32888

10936;14229;15535;21970

659;14865;24940;33276;34741;36051

39;22158;26027

38;16244;17210;29311

57;16240;19067

12717;23337;23852;29982  
37;22885  
15449;18122;18170;25478;26359;27182;30468;32692;34533;37115

23;24524

4  
33;32099  
11570;14072;38083  
3;23667;28750

30;21773;25678

59  
76;34374  
3  
8439  
10284;18846;19559;20537;26424;27162;31048

52  
35  
321;13506;20945;25216;30950;32956;35333  
39

5  
5  
4  
2  
3  
10048;22564;23881;25460;28475;28938;29030;34985  
10048;22564;23881;25460;28475;28938;29030;34985  
18;2904;3698;16775;25830;32108;34564;35508  
19  
39;12335;17918;26601;32606  
24700;28199;28253;30799  
3;19095;31147;35580;35852

54;32499

8865;9700;11324;14594;14792;19789;22788;23062;25637;28934;29591;29790;32578;37647;38069  
743;7127;10730;11347;14038;16021;18612;19595;19597;19883;23988;25801;28864;33221;35494  
5371;9225;10808;12206;14853;15407;17895;22185;25294;30905;31258;32018;34857  
10745;14595;14657;16704;18884;20595;23063;28862;36705  
4406;11947;20911;26191;30098;31191;32111;37945  
3428;8024;8288;12307;14451;16371;17320;17716;24258;25035;31897;35965;37061  
3461;5353;5849;8257;9197;9635;11637;13282;13989;14788;16016;18567;19444;25000;26127;30519;3  
7729;11926;12196;12680;14448;15721;31078;35128  
19;19838

5  
57  
3;36620  
05;35565  
46;31140  
3

48  
22959;30525;34587  
07  
38;36224  
14622;19343;21256;31791;33808;33819  
36;35574;36555;36704;36912  
6707;12495;13334;14173;30174  
7;15230;27914;29045;34772  
7;34113;35023  
7554;20941;26322;31567;37938  
51

25416;26500;28843;37019  
97 1  
09;4146;10369;10463;10532;11879;17400;19109;23736;24790;26232;26819;31689;35661;36885  
5;10990;12116;12867;13426;14987;16133;18681;26863;31708

30  
7479;8955;9058;13165;18084;22732;25448;29413;30972  
3915;4032;4446;7342;11968;12850;22182;25738;34465;35598  
2377;6395;18148;19700;22786;23153;29237;31155

);25753;26909;29653;30215;36025  
29945  
2 6936  
3;32660;35780;37871

l;27862;28544;29595;32340

5911;19610;20316;21662;36958

4;23602;27212;31326  
33293  
24;31868;31869  
l5  
3;27392;30288

478;13936;17156;18791;21590;21764;23095;26015;29932  
31168

73;37759

6633;6640;10374;22471;29382;35623  
 06;4950;6209;6966;11923;14271;16056;18499;18609;18855;19320;20422;22005;22465;26771;27276;2  
 27641;37518  
 3  
 4;15286;17916;22213  
 6538;8689;11343;12852;16444;23864;25015;26388;31920  
 1  
 5301;6508;7224;8455;9091;9303;9387;10112;11484;12060;13588;18342;18837;19087;19502;20016;22  
 4684;9179;12345;14334;15510;15830;17830;18809;19722;22802;23139;24805;25622;30255;32702;35  
 5565;7208;7391;20579;21668;35011;35093  
 4  
 7247;7919;12391;14104  
 2;18758  
  
 3;31670;38178  
 3  
 21;13354  
 42;38112  
 31  
 3;28984  
 14425;18858;25442;37982  
 31;37429  
 973;17011;17253  
 1  
  
 07  
  
 3;22611;26285  
 5  
 26370  
 16327  
 4  
 3;24087  
 33  
  
 29                      1  
  
 4;17757;29733  
  
 5  
 47;32710;38262  
 2;25877;28645;38015  
 2;27209  
 3  
 49;27698;28599  
 12726;12843;13233;17492;18552;18853;20885;29289;31369;31379;34570;34687;35476  
 41;32505  
  
 74                      215  
 688;2689;5037;6828;10524;17519;18206;19132;22242;25149;32283;34674  
 3;26816;27296

14480;14778;15746;18040;26588;27035;29260;30644;33478;34839;35731;36382;36575

32

33

10206;11097;11237;15835;16040;21274;21653;23081;24497;25036;27796;37341

77;31573

3;12711;14774;18273;22248;24144;30410

17;29150;37672

220;16580;16583;18565;18985;26207;27036;28469

4254;7421;8582;8790;14082;16580;16583;16632;16633;17829;18565;18985;22797;27036;31564;3821

4130;7468;14082;16440;16580;16583;17824;18565;18985;27036;28734;31566

2920;4128;4130;7468;14082;16580;16583;18565;18985;26775;27036;28734;31566

59;6195;23213;25250

90 267

90 302

23 372

90 287

3;4;45;46 55;215;239;312

3;4;45;46 73;233;257;330

3;4 420;604

4;45;46 233;257;330

4 257

4 257

32;25594

5;31009;37623

3

);34179;34635

33;32241;32570;34180

3;37229

49;50 41;62

14

4905;9948;12037;15709;18284;21244;26785;27435;27589

31;32524;34282;34880

7;13897;19822;21874;22875;26216;28347

13;33784

3;27289

2;19582;23358;27155;37226

17

30

76;21732;23461

57

75;22577;24564

30

3;27875;35976;36053

2

17970

36

518;4965;5351;12772;22512;23486;23973;24689;25295;29017;31368;32072;34273;34507;36973  
15;32900

10706;24529;26266

4

26;29556;36349;36969;37805  
4472;9758;11722;12383;25398;27168

3

24

);16596;20542  
7718;9159;16489;31695;32002  
12819;30085  
31  
70;23541

2;32139;37409

3;37082;38024

20213;37082

2112;3695;4912;5940;12816;15502;15504;17978;18357;18840;21315;23694;23894;24011;26291;2645  
47

55;36421

1;14790;15187;16106;16218;18236;35287;36437  
13128;15930;17256;20733;30499;31569;34172;38401  
28086;29326  
3;16625;24597;37567

37

10401;11518;15613;18941;18968;19690;20768;22249;25736;28019;28785;28963;28965;29668;35610;  
11629;15526;19751;20462;20477;24573;31849;35691;36381;37812  
34417  
37

5

41;36231

14221

18;28066  
8973;14891;16051;24632;25859;31997

37327

23;16641;20751;25479;27739

54

25

5;17100;21375;35925

3089;7761;8264;8513;9977;9978;10111;11837;12277;12364;15206;18527;24541;27644;28062;28211;3

73;21365;22801;26825;34263;36167

12;33011

13;28892

21448;30011

11;24283

2

51;28985;33129;34316

2;33388

2;22267;23555;37066

1;14821;15068;17215;22154;31003;34889

3997;6078;8535;11658;13033;13563;17798;20118;22612;23039;23212;23260;24612;26083;28805;316

53

4;17886;19216;21817;21822;21880;25056;27902;30820;31757;35642;36326;36414;37001;37076;38098

3;21826;21831;21896;24448;25401;27472;31261;33726;34666;35648;35651;36330;36859;36986;38102

779;21617;23857;27464;33759;35641

2

9;18512;30560;33044;34720;35149

7;16401;23810;26154;27301;28323;32417

5;22557

6587;18792

13148

52;25897;26227;26344

7;14784;18566;30406;34412;37163

55;31054;33629;36284

4;37109

56;36943

2;27867;35736

5

6185;7369;8768;9306;10003;14100;19369;21865;30937;31053;31857;33831;35035;37539  
9318;9319;10948;15919;16135;19742;24070;27077;27637;30980;31165  
);23895;25264;29471;30191

22

52

7898;29002;29792

3;37811

23

)

3;35667







522;29023;29502;33409;33460;34942;36865



935;15810;17576;18511;20281;21565;22362;23018;23330;25174;25926;26984;31195;31653;34312;3405;17583;18511;21488;21564;22359;23019;23331;23839;25921;25969;26206;31195;31653;34780;351

7720;27827;32232;35168;36822

9;34505;37492

;31639;32752;33786;36386

3;25430;26465;29905;32853;35962;38061;38100

687;29028;31004;31397;33690

;34483;35275

32427;36890;37230

52;30729;32727;34907



7694;18303;18545;18953;19806;20389;20574;21025;21760;24279;24470;24490;26983;27110;30165;30



556;19598;21145;23053;24945;25797;27204;28068;28534;29414;31914;32577;32619;32754;33355;344

042;30196;30724;33615;35917

4;18962;20194;20206;20208;20471;20663;21011;21104;21555;22033;22070;24590;24786;26308;2633

91;17659;18327;18708;19680;19692;20114;20212;20469;20701;20987;21019;21136;21472;22804;2322

4;31638;32919;33382;33384;34835;36207

3588;31286;31408;37602

17354;17641;23320;24402;25456;25920;27614;29248;30045;31437;34414;34499;35607;37388;38117

0;37298

5;19967;21554;21796;24200;28356;28386;28508;30809;31113

981;22927;23882;24140;25203;27091;29441;30899;32314;35257;37910;38162

21;35305;36609

};37889;38257  
0;13403;13517;13739;13762;19276;19818;20483;20868;21348;21495;21577;22782;23355;25872;2683

38;4680;4729;5230;5232;5505;5546;6507;6930;7117;7406;7833;9633;10077;10516;11274;12390;1267  
;12675;15162;15180;15414;16344;16600;18879;20340;22357;22376;22701;22715;28160;29356;29360

3994;35666;37173;37174;38316



0;35130

;26710;26991;28127;28527;29571;29931;32847;33191;33752;35978

230;34165;35261;37960

210;14387;16656;19629;22424;24514;26963;28996;30930;32095;34951;37361;37365;37611;38462

}

389;22908;24219;25980;34713

91;29435;29755;30769;36063;36064;37963



;25304;25894;27473;27486;30745;31517;32448;32633;32766;33567;33711;33986;35431;35453;35846

;35870;37334

456;36184;36292

840;29970;33121;34845;35068;35079;36647;37381

3471;37088;37262;37317;38352  
37304;38352

1598;21630;21631;22143;22537;24631;24784;24921;26057;26172;28776;28784;29141;32813  
223;21598;22621;24493;26810;27068;28017;33085

l353;22133;22764;23048;23294;24199;25098;27443;29252;29798;30231;30456;33062;33116;34479

6174

0566;30569;32468

006;14354;16313;16323;16961;17418;17880;18003;18741;19013;19021;19128;19913;19964;20780;21

3306;10798;10799;10861;11289;11665;11668;11670;11673;11674;11678;11680;12033;12087;12113;12

;28569;30752;30754;36161;36266;36565;37437;38127

;28259;28569;30752;30754;36266;36565;37437;38127



;18408;19089;19614;19748;20431;21077;21243;21263;21611;21741;24722;25450;25677;25783;25823

585;30952;31340;34217;36404;36406



38004

06;6107;6111;6113;6291;6392;7079;7760;8315;8813;9024;10656;11432;11809;11942;11978;12464;125

35569

21129;21197;21313;21354;21600;22131;23189;24065;24766;26328;26411;28154;28768;29153;30200;



547;21618;26470;32887



901;21026;21728;21774;25008;26094;26362;26573;27187;28653;29241;29335;30339;31891;31955;33





29116;31443;34042;34586

4417;24816;25951;29317;32589;34020;36934;37340;37546

041;24589;24926;25772;27216;28973;29687;29808;35239;38299





28370;29739;34383;36041;37990

2713;23271;26701;36845  
177





7;29005;37233;37412

36177;37813;38001

32421;32592;35839

90;33520;34037;35386;36930

3  
2











780;35145  
38









0246;31989;32656;33533;33996;34603;34999;35526;36166;36961;37354;37356;37622



139;35330;35407;35604;35987;36255;37183;38301

9;26491;26828;27032;29122;29579;30176;31425;31828;32106;35912;36210;37384;37455

!7;23727;24018;24213;24511;25756;25765;26118;26120;26398;28484;28830;28957;29050;29545;3257







2;27154;28123;28936;29032;31308;31454;34517;34565;35193;36758;36821;36979;37096;38183

2;13034;13435;14688;14982;16355;16600;17222;17596;17709;18873;20340;20964;21333;21588;2235  
;29375;29379;30639;31115;33695;33978;34372;34461;35240;35402;36217;36263;36618









;36200;37324;38428







867;23361;23501;24327;27539;28696;28826;28929;32322;32473;34608;36140;36924;36962;38309

2120;12128;12868;12869;12882;12888;12891;12895;12931;12944;12986;13164;13180;13229;14954;14

;25924;27337;28735;31272;33575;33621;34281;34339;35207;36138;38407



579;12667;13721;13773;13840;15703;18210;18279;18491;18972;19963;20124;20127;20190;20199;202

30553;31822;33053;33660;33675









3871;37490;38092



















































'6;33002;34840;36280;36634;37195;37948;38025





7;22370;22584;22698;23653;27294;29366;29496;29711;31185;31462;31491;32249;33526;33597;3360



















1958;15073;15774;16397;16677;16779;16785;16823;16825;16833;16835;16851;16853;16856;16860;16







202;20303;21051;21110;21122;21194;21510;21698;21714;21724;22867;23293;24322;25874;26178;261



































































5;33976;34300;34404;34787;34822;34828;35713;35879;35981;36212;36459;36788;37160;37477;3748





















866;16868;16872;16873;16874;16878;18753;19025;19027;19052;19055;19246;20057;20077;20806;20





l83;26225;26288;26336;26488;26694;26698;26773;26833;26937;27045;27530;27768;27847;28547;286





































































6;37487;37942;38322;38434



















1986;20999;21161;21334;22656;22754;22793;23131;23132;23138;23141;23217;29345;29448;29726;32































































































!350;33897;33900;33901;33905;33908;33910;33912;33925;33929;33937;33948;33955;33961;33965;33







73;35966;36379;36572;37015

























































































971;34060;34068;34072;34081;34088;34096;34101;34102;34111;34208;34324;34632;34656;34766;34































































































785;35062;35711;35898;36030;36033;36085;36142;36143;36188;36225