HuMaQuest homo-binding prediction report for the submission number 1641

Submitted on Dec. 19, 2022, 7:47 a.m.

Current status: 49 of 49

As of Sun Dec 18 2022 20:54:32 GMT+0300 (EET)

49 out of **49** sequences have been processed

print Text

The full output for the job can be downloaded in plain text, once all sequences are processed here.

Results for the sequence(s) successfully processed:

1. sp|P05556|ICAM_HUMAN Complement 3,5 Ofcolibactin-saptein OXL#006 GAuC3 3TG1 ST=2

MEDPSSPWRMPRLWALLLLTLLLELSPAQIHAGSLNPMLDYFQQVERSKMAVLFGLTKKLAQLETEAGRQLQNVVEECRPMVSNSLNKDSLEEVSAWRQTVSSDEVLDSLEKILKTALPKKDSGCAQHALAAISLMNMASEEAGRYRSDLSTPNLPSTLQDLLVPEVTLAGFNLPPWTQPDTEAKIQEVTSPQPETLILKPDAVSLDVGKEQVFSVEIRVTPSIWVGVIYGFGSTDHMSKALVSLSTGLNCTEDVTLTLMPLDTVMDMLEVWLPGIYEVSSDAISHTMRTSDRPLAVGSSLGMIHVGLSSVAGWSQLTKEKSLEENPVSVNLPTMSKFSHYAVVIPRTGQEDAPASNTTKKVTQRSFPEELNMHMLNMCTPNIDMAYTCQPARSEEDAQYESVYLMTVDPKVNKRMAYRLDLSKVNFFSGLIPMLNTKSPFPHFRGVMTAVSLSPSATNRLLYHGDKFSQPLAQQVTSMHTSLDLGYVFLVNYTDYFGKMNVTLAQKQGRMKVDVDTPSMISEGKAKDEVLQAVFMLTRKDLFMDRVSNLPETMQNVKEYLQKSHVIAFTNCQENSSEKSQEDLVQECQLARQQMEVELEEVVSGSMAPFRFELQRTWGDHVMMVRKQMKELIFPAAREQQSFWEVLEGNMFIAMMDTLRQSALLDKDSISDANVNLTYLPVAEAASGLVMVHSLVQPEVEAPSFSLHFHMQMGTNVRDGGFLAALFPNSISVLELSDVPLAVHLQTASTQDPPSPGQLAVQLHNNPLLEVTGFSANWTFGLDFGKNKTHLFHPEPVCAPPCSEDLVNSLTHLCVLFSEKTSKHVPKQASPEDRCTVFAISSMYKPGASLQLQRRSNPGLLPVLHDVVQGAQPGETQEPSYVGSLTSVPGQLLPFARVPVTLQCSSNLPSLNCQVDKVNVKFKSMCRRMQGAWPSIKDVLELTTDVTVRGRNISSTPYFFYPKVNDTRSAQGDNLPFEAEEIQLERVVWYSVGLMASEGNKLAKEAGFLALVQALSQKEEPLDLYTVEGSGWVGARGELATAMEGQSSCLQLNLEAQKEIEISPVFVDLETEQVVTAFQPFLQDQLHPMVLGPGLLNLTLTNPLVLLNWTAGDQNSIWLEKCRGQSPGKVRCDWQKHLQELQKMQLLVSVGLVDQAEDAQLALGMHSVDSSLGFEGGNASSPTMQQKFVVDCSMRSAVNWGESVFKGNYTSKQPYMTHMALDPQALEFVDATDFFMTIVNRSSQPLSMLQIQSWLYTLFALEFPTSDQAQGQNFTVPVKGTYTLSPVCSGLLIPRHLNQEQQDKVHSFLSSVISRVDPSWTAGFSLQDVQEQLVAGLTQVQVNVLSMFQDSKDFDIPLLKYSDFPIQDLSVEQAQRLFKADIDGDGQVSMDEFQLVLKKISGMEDIFLPEQLGELFQGSDKSGDSSLEVEELARHLEGCEPARLEATLNTVYHRFQGEKGYIDQSDLAEVLKLLVGHPLGIRLEDLPMVGTLDHSKDGAVTFQGFLKSYVRKEMDTAAIFRTLDRVQEGVIRAHQVLTLSALFGVALLRPEQFLSRLSVGMDPVASRGNLTSVLAEVPVGLPAPSLPWFNEWRQVFLVPPLSQPGAAAGVSWGFVAPNASMEGTMVFLQVPEGLSGPSQSVQFQQDSGWLGSLVGLDSQDLSSCLSFSWSQLQGQPLIVTVTNDLKAQENFTKVVQPLLQNLCQKLGSTNVSCSQHLCPVSLRGLMKDTAKWEDTVTAWRDEHRGQELHPQKLCSCPQQAEKSFCHPDEECSKVLVESCHTQLKANPQGVDIAYWHSMDLQDQPESPVDCTLEPGCSPGTQNNATPGSVPTTCKSQEYVACQEQDPCEPNPVTGSRVVGGLVAKPGDFPWQVSLHVQGVAGAQFCGGSLIAEQWVLSAAHCFPEHHMKEVLARLQVVLRQHLQLFHEPHVSFPFMRPSCPMVMGDQRPLYIHKNGFVGSSHAATLSSGRSLTYSTFRTIHLPLASPEDLRNLCPTVGTNLFRTLRMDVVDPDGQSRYTVPYDSVLVFPSGIAHLEFRQDKRKEMEHLMLVAVDGAFRLQEDFHFSIDSLSLLSDVTHVSKSCLPEDPGFKSHPMIHSVNQPAPLFPRHHQAGEEPGLEPHTQQAEGPRPQLHKPVSAPLIPFDPDTIHITELEKDKFLMDLVPWDSWVSLETCDLDEERIAATEPSIFSFWSPDFEPLGSLDSCPQEASLNSSDWRFYHLQVPREMNQLSFGGCLLNVSVWDKAEPVEKLVFIAVRDDKKLMEEAIDIYTRHLIDEAGTFGLSFPSLYRVGQTLLSQGRRNLTLPPPEGTQKKEAQDKVFLDKTENTCHLEVFQVLPKECLLNSRCQVRPRMEPSGTQGPLVAGVLLYNPVDFTGMIGRIRLWVNETSLELRGGAQHDHCGLSLRSWFHVIPRTNSSGSDRGIAVTQQKEEVLFGSVHDLKLLGPKAQLLTKDNLILTVTRKEKGACGHPNPQAIECFSGNLTDTCGCFTECKEPRGEHWLEDDLLSMDINPCDNITRVVSSLSMYVGILFHKNQEQMLRDRETLRDGAHLAKMSPGSVKTAFRAAKVQPDPGGWVDRSGVDSRAGVTAFVPTLSEIELRLRSEKSGLWNQVSPQLEFTLSAESYLKGAAGQDPYTLYFYLQVPNVSVNCVNLTLEPETVKLGEVEEVQAVCQLRDAKEKTKEKLDFQLKLKSDLALVSTQVTFDPVEPTQNQHVKLKCQADSNSFHRLVCDGKLEFQKNWAEECQVKAEESVNLTCEVTNFLGAENVTLELPFHVVKHVQELSEKPVLMTLKVENEGQYEVLLDNAKGKNKGSISVWYKPPLQEDDKERHHIREAGLVTLFQGDTDSVTLPHDEYTTQGRLGSDAEFRLTEGHLTMLSPLGLSEVSGVWVQCNASTYPEEELTFQVSLQLNMAQESDMHILRCEAKNIKGYLQSTFSFAVRPFLNYRVENGHKISLIGEPIKEEPNLAYIFEDADGSVNTGRLSSERDFYMLPTFTQKGTVSFDFQEASQAFQLELSDASKPDNPDDSTEICLDVPVRNIPCVISDGDLKPGFQVVQKSSASFNLSLTEKNQGEYEVMIQHKNSDIIARRSIRVVLVPVGSLSVQMTVALETLRPSTHVIVAIFDISLSSITPETDRVFQSAIQSSCLPSQECQSYLQLTSSCQWQPRLSHVPKPLTLQLWDQMGSGKSLKPPNMTFSPGSEAIQKLIEGCLVDESLHPPVLEKETEECQSFTVSFQVQMTAECAGLAQEEVVPVEVVDAQVKELTEEKVESMLQCGQGRCTRETGRLVWEVVQVRRLVEEVTLEVHDKGNFSVDEGQDVRFQVTARDALGATRTLQPESEVQDNGDGTHSYSLTVKTKKPGSYEVNVPVASRPEVDKRQHTVKVFMNPFSPTHVQAKLSSQKSVCMLEEVVLKVTVCNLFGSYAETLVWEVPPGLELVEGKTRQRVDSPGSQSAFDLTVRASQVGRFPCSVYGLSCGQQPPSPRLCGVLRVEPSQLSLVLEPEGEQQVSAGVVGGSGNHTVYTFRVLDAGEVTISSLKPSCVVQDQKAEYEGSGTICLEVSTEKVPDLLDHLQGGRASLLTNLTIILDPNGGFLSSWSPRISVEGPLEVDSTLTLDLFHVAKAGLDRDFVPPDPRQVYCQYGSFCTHDCAPVKETSCSCRHGKVPPDCSPVCGSDGVTYDNECLLCAASVEKGDSIDVAYDGACKAISVVGAVISGLQITVPFFQLQISYSVQVPYTSSILIYICEDSGTRPAFRHDDIVGIQPVLKKELKRLKFTLSTVVEENIFSRNQKELQLKLNTDAKSARRQIRLTFNIRGVGQMVRGSLDESGLLEWVFSLDTKDHSMLYFHAFLDCVVRLIVEVTRKPSVQVTLSGHENNRVAQVGEAIPLKVLVTDQDEDPVQGVVNFYCSPANGPEQLSQDKDDDDGLAQVSITVGNKTQNVIFAVTDNALVGLQLTVEAPCSGQQGLESLWKVVPLNLTASSQPLSFRVYGLSRTKLTVCSNNHFLRPDAGEASMQVQAGYSCGVPQKSVEVVPEGAKDTYSAELILQTDSRTPCPLTVSEEQRQLEERAVQEVTGVFSLDPELLPTLHPGQQKGLVCQNVTWYQRPLKLFTEKSEGQLQTEGCRNIFNVNDKALFVYKPQREDVFQDDTVYLIYFNEVQDINVGCNLHDQEIDSMNIWVEGHQLSVDKAELVDGENRTLSLPRKSLWGRLVLRSKVDEDSGRLQGVQKVVLYVQDEDRFLSCLGFSIFVPVNSFAFVTLHDGSGTDSTKANSQREPGIITGSLGLVAGAPLLFLLRKRRQIKNLDLKEDDSFLDPRENYHLFGSPAIEFLRDLVAGFSYFKEIWTEEAEVIGRTCHGRLADVRAQMNRSVDLLKARLTSVAKSGSHCIPPPPAPKSLVLYIKPLEELTLRDNDRERDSFSVHGGFEADIQAPMKGMAIDIQPKSEARLDCLITSAVSSVSFMCVEFLLKDLRQKMVGLFYNDVDGTLVESRDGSIFKVELEGSTDFMHTSGFVELQLQESPCLGLRPEAVDGPRVNVSMALYDSFSSKDFQVYVNGYRVPPVVDSPSHKVSFEEPFAMEWTKPHSGRNQVQVAGQDLTSEVVQFANLTELPRSPKPFGLFNKGSISVTRQAHLALSQVKVVDDGYPRGSVDAFQEETCVEFEVSTPEKTGVGVVSVVIGNQRSEHHLYLDVFLEQFQESSFRVSVEAAPSVPICGVSSHPSSQDVLFTPNPIVFHEVPLNEPQNVQYEVGPLVEGGNSPCSLQWWLSGEVSAVEEKCFPVTVDKATIGNVICTVPSYMVGDQFVGEEENIGYLFTSPTGSLEQQAKLSKQSITCDKNEHVCIQFVDQVGDSWLFIKRSLKTPQYFLSSDGQKKTEAPEFPSKLVCVLAEECLPQSVGGLQQRLTLSRKNIDESGQFQVLVQGSLAGQEAGTVVQLNLQSRKSLEALLPVRIEKEDQLLSVPVMVDSQTNVTVRGSSFHETLQVTVPESVAEDTQRVQVNGSPSPSQLSFSSLKTKRSFHVRQEMAPASLSGTLVPVLHPLQKNEVNMPLTGATVCSEDGMPKSIIVFVRDLDKVLLGHSNASDGIFTFEFLTKDIVGTLIVQASLQDVQSEDVCSESFSIKQRGDLNLVILQPSLQQVAVNEKQNFTATVLGSSSQGVNWSVEEIGNSCSGLSVDSTTGKLHCTAVVPGPFVVIVKASKGQLTDSKKVNVVNWEKPKYLSLQKNQRQKLQAAGTPDIYHFDLFYNIPGCDKGEEQRKFRMYVESTSGSVMSSAIPGTKYSWRLDMDDVDFSNNLTLTVKAQGTDVLQGNKSEFEVIYIQVTDVLVSVNPSQNFVLQGGSQQMFTATGQNDKPVKVQFSIVSGPNKGKLEEKGLFTPDLEGPVTVQAVMISLEDPDVTATVNFELVIPKLNLSKEYLLWPTNSQNITLTLKNLLGCDWNTNIIFEENAEFFTSNQTQPVIQSILDSNHLKVFVLPLFAGQEKISGTVTLYLEEGKQLSTSLSFFVKVRASASVSLSGDRLEGNSPYTSIGQMAAFSVLLTDGRTNVSLSVDTWDFGDGSSETDDQAPKHTYTKPGDYTITLTVAGHNDVPNATAHVQVTIDVQPVNFHGSVNVDTSSAQPSPSVASLAGKATNFVAKVFSFSDPDAGDSHTVSLACGYGDGSPMMLVRRRDVLEASHTYLKPGEYTVSVTVSDDFEATTVQFRVCVYDALFVQSKASLVPTLEGRVGRGFVLTLSFAFLSGSTQSTARMACQEAPVLRWVSLQWGEVQPEWEDETQVSASQSSFTVKDVAEPGERYLCRLQVWLQGQGQPLSATTDIVFRTYLRMTVDEQGRDMIDDDITGNDNLKQWPTEDAPKAMEPSSFFQRISSGVLKVIQHPKVRWWQLSAPEMQREKSYSLRCTVCDQASRTVARSITLRPQKVQKVEEIQLQPGLWYNVLVQASTLYNETEVLLDSARTRFEVKKSLSVSKLSNLGAVFHWSLGPGSLQGQSTNPSSEHIIPIQTVSVKGFLVSLPRLIVEMAVNKSFFIDLNYPFSGEDVVFPGTKEYIYRVNENPGKFQLVEAEKGMSCDYVELSVPDNSFLSQTTGGVDHEAHSCLFIEIETRGQTVVQEDIDLCDVQCTDIIKPDSPLGMVAVQVNNSIPSSWTYEDITKHLVSTPSGVIQELAPRLPLVHMTNSSNSSMLVEWKEPQAPNGVLQGYRVFYTPDITRSVHMLNSTKTECTVGNLTKFTNYSVSVVAFTSIGDGPLSSNYTFSTLEDVPSKPPEVWAEAQSSTSITLKWKKPEYDGGAPVQKYIVEKQEKDSKRWLRAGLQPDTEYTVQGLKPNTEYEFRVVAVNGKGEGPPSSPSVGYKTLQAAPSQGPKLEVKDVTDTSVTLMWTPPESQVTGYRLTVGLTRRGQPRQYNVGPSVSKYPLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQVGSVIPYNTEVTVQVGDNVVLVPCTVYSSQNSQVCVEWSQQDQELACTMISLGNGSAELGLDLVGKSLMHYYSGLSLSVQNVTSLDHGLYVCSVSIFPSGNRNSKNITVRVNTCPEGKIKKKEGEGTLHLEEGEEAELVIPFQVYFFGIIFDEVTIHPNFIIQEVSEAFLGKQDVLKVPVGSVAEYTFRAPDVSPDSAYSLEVIGEWKLSRQKKPVSGAMYTFYLQPNAQVGSHSVNLKVSVNGAVSYEMCIQPGAVSASCECAGPGRLGTGLEAEVFIILSILSVDDKGEKVSPNEIVVFLPVPDPSGVSLSPAVVLEENTTMAHYYGSLPKDEHLGSGACVSVRVRPTEKTIAMSILKKDSKYRTNLQLEQSSRETPVFGFFTADRDQKSTCSGDEVVYHCQVKHSSLDMVTVKFFKNSQLSDQYNSKKFEQHPVGDTFFIVDKSDNNEGDYYCEVSAVTEVGKLQSEKAKISVRVHQKVVKFMDVNTTLAVGSTFNLTCLVTGNEVLVDFEMPEEEIQLFQGHQLPVLDLPSMHSSAGNKLCLQARLNTDVGEKKSSVVTVNIQDKIEGLVIYPSVPQGQYQMNKEAKLSVEGFNSCLVYGSTDVSFHWTLKDGSLLNATKTGRIEIRSTLSVLDLVVTEADDYTMEIEHESFQDAAAYPKLNVSLVDEVDSLMVFPTDSRDNSKCGGNQSLPVCDGYGRLSHLYTLGSCSIDETCLAGNSRCDPHPDQAIFSDSLPASKLCLGRPWKVFEGSTVRIPLKLSRVYNLTFHLRFKSSRSFGLLVDSEPVFEFSLKDVQNKIIIPDYVDKSSELIENWQSGYLSVAKGSHELKFVFLGRPKILSLPNDLAFVEVDFCSQVACLEREKTQKEECEDLLALDVVLSRTKAGLPSEYAWLPLSVGLVHGNSTRETLAEVESEHELACYTPRNVICSVEKPQSAPGTVHFTLEGAPFGFVEKDLKPVIAENNFLVLSAQIVEYLNQDLEESLELQVGRCECQGEAAPSVCQKVQGGLDCYSCGKHKEHLDKDCSQCFCQGATCGPKRGQCYAGKAIKGKKKEIFDIDSTVQYVFPNMAVLIEAKTTTEESVFEHVVKRIRSMFMSVSSILESSFDGFLRVTRGLVEFSLLEEPNIFRSLGLCVILHSKKEDFLTVQSFMGYDVDHVQELIERSRIAPTSIGSQLTLEYSTCHYKKEMSPPYDSSPVCEVIVQQYGSFTLGGTLSYKKGKSRNVVFPVSFVSMKNLEYEVQVKSRVFEEDQISLVVSDGNHKANVTLDHSGKMVKEVNMALELGPLSNVTMEIGYGLPFSAKGVAGMFQNVKLEEQEPLVHFEKCNSSNNRVEPGETFKVTCVAIDKNAAEPVQLPLSFEVVLWNYTTVYEDIKRSANASGNLPVSMTGTVRSRGEFNVIVIPKISEGATWHFDLEENLDFKVKLTSKRLRQNMSVANDLLVDYQFPEPSQSGCTLLVEESVLVLPELHTPCFSSEKDHYLIQNPQQQVLSVNVSLRSEVSPSILVTGYSIAYGFSEGSASLLCKELDSEDTAFKWYKGSWKDKNIVYFAIEDEIKSSMAYANFTSRHSIQVSQYGGNFSAEFLPVFQKAQSYFFSTQDIKNPVIQESLWVEVKGVVDTTNLTICIGTEGVWKCDHSLKDLKDQRSPQSIIVYFSIGGSVTGVVIVTILIALAMKKYYEDRKQNAIAMAQEKFQSVQSPTKATMSPNYAKNEIDFKDNIQKAKQENIEPGLPVNTNKHTPADEKKSIINVEEKNGGESQHSNDSKESAHRVLMSSRLSKTDQLVNAESSDFKENTIPAKTEDGIVGPVTAQSEHVVETEEDEEEEEEYKPNVTGVDDDMPDFYR

Actual or candidate predicted by WEKA

Rank	conf. confirmed	Next conf.	Tier changed	Comment	Predicted By (pH)
#1	0.9999999	0.9			
#2	0.9	0.8333333	1		3TG1
#3	0.8333333	0.7142857	1		3TG1
#4	0.7142857	0.5555556	1		3TG1
#5	0.5555556	0.5	1		3TG1
#6	0.5	0.4285714	1		3TG1
#7	0.4285714	0.3333333	1		3TG1
#8	0.3333333	0.2857143	1		3TG1
#9	0.2857143	0.2	1		3TG1
#10	0.2	0.1666667	1		3TG1
#11	0.1666667	0.1428571	1		3TG1
#12	0.1428571	0.1111111	1		3TG1
#13	0.1111111	0.1	1		3TG1
#14	0.1	0.0909091	1		3TG1
#15	0.0909091	0.0833333	1		3TG1
#16	0.0833333	0.0769231	1		3TG1
#17	0.0769231	0.0714286	1		3TG1
#18	0.0714286	0.0666667	1		3TG1
#19	0.0666667	0.0625	1		3TG1
#20	0.0625	0.0588235	1		3TG1
#21	0.0588235	0.0555556	1		3TG1
#22	0.0555556	0.0526316	1		3TG1
#23	0.0526316	0.05	1		3TG1
#24	0.05	0.0476191	1		3TG1
#25	0.0476191	0.0454546	1		3TG1
#26	0.0454546	0.0434783	1		3TG1
#27	0.0434783	0.0416667	1		3TG1
#28	0.0416667	0.04	1		3TG1
#29	0.04	0.0384616	1		3TG1
#30	0.0384616	0.0370371	1		3TG1
#31	0.0370371	0.0357143	1		3TG1
#32	0.0357143	0.0344828	1		3TG1
#33	0.0344828	0.0333334	1		3TG1
#34	0.0333334	0.0322581	1		3TG1
#35	0.0322581	0.03125	1		3TG1
#36	0.03125	0.0303031	1		3TG1
#37	0.0303031	0.0294118	1		3TG1
#38	0.0294118	0.0285715	1		3TG1
#39	0.0285715	0.0277778	1		3TG1
#40	0.0277778	0.0270271	1		3TG1
#41	0.0270271	0.0263159	1		3TG1
#42	0.0263159	0.0256411	1		3TG1
#43	0.0256411	0.025	1		3TG1
#44	0.025	0.0243903	1		3TG1
#45	0.0243903	0.0238096	1		3TG1
#46	0.0238096	0.0232559	1		3TG1
#47	0.0232559	0.0227274	1		3TG1
#48	0.0227274	0.0222223	1		3TG1
#49	0.0222223	0.0217392	1		3TG1
#50	0.0217392	0.0212766	1		3TG1
#51	0.0212766	0.0208334	1		3TG1
#52	0.0208334	0.0204082	1		3TG1
#53	0.0204082	0.02	1		3TG1
#54	0.02	0.0196079	1		3TG1
#55	0.0196079	0.0192309	1		3TG1
#56	0.0192309	0.0188681	1		3TG1
#57	0.0188681	0.0185186	1		3TG1
#58	0.0185186	0.0181819	1		3TG1
#59	0.0181819	0.0178572	1		3TG1
#60	0.0178572	0.0175439	1		3TG1
#61	0.0175439	0.0172415	1		3TG1
#62	0.0172415	0.0169492	1		3TG1
#63	0.0169492	0.0166668	1		3TG1
#64	0.0166668	0.0163935	1		3TG1
#65	0.0163935	0.0161291	1		3TG1
#66	0.0161291	0.0158731	1		3TG1
#67	0.0158731	0.0156251	1		3TG1
#68	0.0156251	0.0153847	1		3TG1
#69	0.0153847	0.0151516	1		3TG1
#70	0.0151516	0.0149254	1		3TG1
#71	0.0149254	0.0147059	1		3TG1
#72	0.0147059	0.0144928	1		3TG1
#73	0.0144928	0.0142858	1		3TG1
#74	0.0142858	0.0140846	1		3TG1
#75	0.0140846	0.0138889	1		3TG1
#76	0.0138889	0.0136987	1		3TG1
#77	0.0136987	0.0135137	1		3TG1
#78	0.0135137	0.0133334	1		3TG1
#79	0.0133334	0.0131579	1		3TG1
#80	0.0131579	0.0129871	1		3TG1
#81	0.0129871	0.0128206	1		3TG1
#82	0.0128206	0.0126583	1		3TG1
#83	0.0126583	0.0125001	1		3TG1
#84	0.0125001	0.0123457	1		3TG1
#85	0.0123457	0.0121952	1		3TG1
#86	0.0121952	0.0120482	1		3TG1
#87	0.0120482	0.0119048	1		3TG1
#88	0.0119048	0.0117648	1		3TG1
#89	0.0117648	0.0116281	1		3TG1
#90	0.0116281	0.0114947	1		3TG1
#91	0.0114947	0.0113637	1		3TG1
#92	0.0113637	0.0112361	1		3TG1
#93	0.0112361	0.0111112	1		3TG1
#94	0.0111112	0.0109892	1		3TG1
#95	0.0109892	0.0108697	1		3TG1
#96	0.0108697	0.0107528	1		3TG1
#97	0.0107528	0.0106384	1		3TG1
#98	0.0106384	0.0105265	1		3TG1
#99	0.0105265	0.0104169	1		3TG1
#100	0.0104169	0.0103097	1		3TG1
#101	0.0103097	0.0102048	1		3TG1
#102	0.0102048	0.0101021	1		3TG1
#103	0.0101021	0.0100015	1		3TG1
#104	0.0100015	0.0099029	1		3TG1
#105	0.0099029	0.0098062	1		3TG1
#106	0.0098062	0.0097114	1		3TG1
#107	0.0097114	0.0096184	1		3TG1
#108	0.0096184	0.0095272	1		3TG1
#109	0.0095272	0.0094377	1		3TG1
#110	0.0094377	0.0093499	1		3TG1
#111	0.0093499	0.0092637	1		3TG1
#112	0.0092637	0.0091791	1		3TG1
#113	0.0091791	0.0090961	1		3TG1
#114	0.0090961	0.0090146	1		3TG1
#115	0.0090146	0.0089346	1		3TG1
#116	0.0089346	0.0088561	1		3TG1
#117	0.0088561	0.0087791	1		3TG1
#118	0.0087791	0.0087035	1		3TG1
#119	0.0087035	0.0086294	1		3TG1
#120	0.0086294	0.0085566	1		3TG1
#121	0.0085566	0.0084853	1		3TG1
#122	0.0084853	0.0084152	1		3TG1
#123	0.0084152	0.0083465	1		3TG1
#124	0.0083465	0.0082791	1		3TG1
#125	0.0082791	0.0082129	1		3TG1
#126	0.0082129	0.0081479	1		3TG1
#127	0.0081479	0.0080841	1		3TG1
#128	0.0080841	0.0080215	1		3TG1
#129	0.0080215	0.0079601	1		3TG1
#130	0.0079601	0.0078998	1		3TG1
#131	0.0078998	0.0078406	1		3TG1
#132	0.0078406	0.0077825	1		3TG1
#133	0.0077825	0.0077255	1		3TG1
#134	0.0077255	0.0076696	1		3TG1
#135	0.0076696	0.0076147	1		3TG1
#136	0.0076147	0.0075608	1		3TG1
#137	0.0075608	0.0075079	1		3TG1
#138	0.0075079	0.0074559	1		3TG1
#139	0.0074559	0.0074049	1		3TG1
#140	0.0074049	0.0073548	1		3TG1
#141	0.0073548	0.0073056	1		3TG1
#142	0.0073056	0.0072573	1		3TG1
#143	0.0072573	0.0072098	1		3TG1
#144	0.0072098	0.0071632	1		3TG1
#145	0.0071632	0.0071174	1		3TG1
#146	0.0071174	0.0070724	1		3TG1
#147	0.0070724	0.0070282	1		3TG1
#148	0.0070282	0.0069847	1		3TG1
#149	0.0069847	0.0069421	1		3TG1
#150	0.0069421	0.0069001	1		3TG1
#151	0.0069001	0.0068589	1		3TG1
#152	0.0068589	0.0068184	1		3TG1
#153	0.0068184	0.0067786	1		3TG1
#154	0.0067786	0.0067395	1		3TG1
#155	0.0067395	0.0067011	1		3TG1
#156	0.0067011	0.0066634	1		3TG1
#157	0.0066634	0.0066263	1		3TG1
#158	0.0066263	0.0065898	1		3TG1
#159	0.0065898	0.0065539	1		3TG1
#160	0.0065539	0.0065187	1		3TG1
#161	0.0065187	0.0064841	1		3TG1
#162	0.0064841	0.0064501	1		3TG1
#163	0.0064501	0.0064167	1		3TG1
#164	0.0064167	0.0063838	1		3TG1
#165	0.0063838	0.0063515	1		3TG1
#166	0.0063515	0.0063197	1		3TG1
#167	0.0063197	0.0062885	1		3TG1
#168	0.0062885	0.0062578	1		3TG1
#169	0.0062578	0.0062276	1		3TG1
#170	0.0062276	0.0061979	1		3TG1
#171	0.0061979	0.0061688	1		3TG1
#172	0.0061688	0.0061401	1		3TG1
#173	0.0061401	0.0061119	1		3TG1
#174	0.0061119	0.0060842	1		3TG1
#175	0.0060842	0.0060569	1		3TG1
#176	0.0060569	0.0060301	1		3TG1
#177	0.0060301	0.0060037	1		3TG1
#178	0.0060037	0.0059778	1		3TG1
#179	0.0059778	0.0059523	1		3TG1
#180	0.0059523	0.0059272	1		3TG1
#181	0.0059272	0.0059025	1		3TG1
#182	0.0059025	0.0058782	1		3TG1
#183	0.0058782	0.0058543	1		3TG1
#184	0.0058543	0.0058308	1		3TG1
#185	0.0058308	0.0058076	1		3TG1
#186	0.0058076	0.0057848	1		3TG1
#187	0.0057848	0.0057624	1		3TG1
#188	0.0057624	0.0057403	1		3TG1
#189	0.0057403	0.0057186	1		3TG1
#190	0.0057186	0.0056972	1		3TG1
#191	0.0056972	0.0056761	1		3TG1
#192	0.0056761	0.0056554	1		3TG1
#193	0.0056554	0.0056349	1		3TG1
#194	0.0056349	0.0056148	1		3TG1
#195	0.0056148	0.0055949	1		3TG1
#196	0.0055949	0.0055754	1		3TG1
#197	0.0055754	0.0055561	1		3TG1
#198	0.0055561	0.0055371	1		3TG1
#199	0.0055371	0.0055184	1		3TG1
#200	0.0055184	0.0055	1		3TG1

2. sp|P05362|ICAM_HUMAN Complement 3,5 Ofcolibactin-saptein OXL#006 GAuC3 3TG1 ST=2

MEDPSSPWRMPRLWALLLLTLLLELSPAQIHAGSLNPMLDYFQQVERSKMAVLFGLTKKLAQLETEAGRQLQNVVEECRPMVSNSLNKDSLEEVSAWRQTVSSDEVLDSLEKILKTALPKKDSGCAQHALAAISLMNMASEEAGRYRSDLSTPNLPSTLQDLLVPEVTLAGFNLPPWTQPDTEAKIQEVTSPQPETLILKPDAVSLDVGKEQVFSVEIRVTPSIWVGVIYGFGSTDHMSKALVSLSTGLNCTEDVTLTLMPLDTVMDMLEVWLPGIYEVSSDAISHTMRTSDRPLAVGSSLGMIHVGLSSVAGWSQLTKEKSLEENPVSVNLPTMSKFSHYAVVIPRTGQEDAPASNTTKKVTQRSFPEELNMHMLNMCTPNIDMAYTCQPARSEEDAQYESVYLMTVDPKVNKRMAYRLDLSKVNFFSGLIPMLNTKSPFPHFRGVMTAVSLSPSATNRLLYHGDKFSQPLAQQVTSMHTSLDLGYVFLVNYTDYFGKMNVTLAQKQGRMKVDVDTPSMISEGKAKDEVLQAVFMLTRKDLFMDRVSNLPETMQNVKEYLQKSHVIAFTNCQENSSEKSQEDLVQECQLARQQMEVELEEVVSGSMAPFRFELQRTWGDHVMMVRKQMKELIFPAAREQQSFWEVLEGNMFIAMMDTLRQSALLDKDSISDANVNLTYLPVAEAASGLVMVHSLVQPEVEAPSFSLHFHMQMGTNVRDGGFLAALFPNSISVLELSDVPLAVHLQTASTQDPPSPGQLAVQLHNNPLLEVTGFSANWTFGLDFGKNKTHLFHPEPVCAPPCSEDLVNSLTHLCVLFSEKTSKHVPKQASPEDRCTVFAISSMYKPGASLQLQRRSNPGLLPVLHDVVQGAQPGETQEPSYVGSLTSVPGQLLPFARVPVTLQCSSNLPSLNCQVDKVNVKFKSMCRRMQGAWPSIKDVLELTTDVTVRGRNISSTPYFFYPKVNDTRSAQGD

N/Ns	Count_residue	Start_residue	Net_charge	Comment	Predicted K_D (pM)
1	Y113	R.KPVTQDY.-	2+1		7.03
2	Y113	R.KPVTQDY.-	2+1		7.03
3	Y113	R.RSSTQDY.-	2+1		7.03
4	D110	S.RSSTQDY.-	2+1		7.03
5	D110	S.RSSTQDY.-	2+1		7.03
6	D110	S.RHSTQDY.-	2+1		7.03
7	D110	S.RHSTQDY.-	2+1		7.03
8	D110	S.RHSTQDY.-	2+1		7.03
9	D110	S.RHSTQDY.-	2+1		7.03
10	D110	S.RHSTQDY.-	2+1		7.03
11	D110	S.RHSTQDY.-	2+1		7.03
12	D110	S.RHSTQDY.-	2+1		7.03
13	D110	S.RHSTQDY.-	2+1		7.03
14	D110	S.RHSTQDY.-	2+1		7.03
15	D110	S.RHSTQDY.-	2+1		7.03
16	D110	S.RHSTQDY.-	2+1		7.03
17	D110	S.RHSTQDY.-	2+1		7.03
18	D110	S.RHSTQDY.-	2+1		7.03
19	D110	S.RHSTQDY.-	2+1		7.03
20	D110	S.RHSTQDY.-	2+1		7.03
21	D110	S.RHSTQDY.-	2+1		7.03
22	D110	S.RHSTQDY.-	2+1		7.03
23	D110	S.RHSTQDY.-	2+1		7.03
24	D110	S.RHSTQDY.-	2+1		7.03
25	D110	S.RHSTQDY.-	2+1		7.03
26	D110	S.RHSTQDY.-	2+1		7.03
27	D110	S.RHSTQDY.-	2+1		7.03
28	D110	S.RHSTQDY.-	2+1		7.03
29	D110	S.RHSTQDY.-	2+1		7.03
30	D110	S.RHSTQDY.-	2+1		7.03
31	D110	S.RHSTQDY.-	2+1		7.03
32	D110	S.RHSTQDY.-	2+1		7.03
33	D110	S.RHSTQDY.-	2+1		7.03
34	D110	S.RHSTQDY.-	2+1		7.03
35	D110	S.RHSTQDY.-	2+1		7.03
36	D110	S.RHSTQDY.-	2+1		7.03
37	D110	S.RHSTQDY.-	2+1		7.03
38	D110	S.RHSTQDY.-	2+1		7.03
39	D110	S.RHSTQDY.-	2+1		7.03
40	D110	S.RHSTQDY.-	2+1		7.03
41	D110	S.RHSTQDY.-	2+1		7.03
42	D110	S.RHSTQDY.-	2+1		7.03
43	D110	S.RHSTQDY.-	2+1		7.03
44	D110	S.RHSTQDY.-	2+1		7.03
45	D110	S.RHSTQDY.-	2+1		7.03
46	D110	S.RHSTQDY.-	2+1		7.03
47	D110	S.RHSTQDY.-	2+1		7.03
48	D110	S.RHSTQDY.-	2+1		7.03
49	D110	S.RHSTQDY.-	2+1		7.03
50	D110	S.RHSTQDY.-	2+1		7.03
51	D110	S.RHSTQDY.-	2+1		7.03
52	D110	S.RHSTQDY.-	2+1		7.03
53	D110	S.RHSTQDY.-	2+1		7.03
54	D110	S.RHSTQDY.-	2+1		7.03
55	D110	S.RHSTQDY.-	2+1		7.03
56	D110	S.RHSTQDY.-	2+1		7.03
57	D110	S.RHSTQDY.-	2+1		7.03
58	D110	S.RHSTQDY.-	2+1		7.03
59	D110	S.RHSTQDY.-	2+1		7.03
60	D110	S.RHSTQDY.-	2+1		7.03
61	D110	S.RHSTQDY.-	2+1		7.03
62	D110	S.RHSTQDY.-	2+1		7.03
63	D110	S.RHSTQDY.-	2+1		7.03
64	D110	S.RHSTQDY.-	2+1		7.03
65	D110	S.RHSTQDY.-	2+1		7.03
66	D110	S.RHSTQDY.-	2+1		7.03
67	D110	S.RHSTQDY.-	2+1		7.03
68	D110	S.RHSTQDY.-	2+1		7.03
69	D110	S.RHSTQDY.-	2+1		7.03
70	D110	S.RHSTQDY.-	2+1		7.03
71	D110	S.RHSTQDY.-	2+1		7.03
72	D110	S.RHSTQDY.-	2+1		7.03
73	D110	S.RHSTQDY.-	2+1		7.03
74	D110	S.RHSTQDY.-	2+1		7.03
75	D110	S.RHSTQDY.-	2+1		7.03
76	D110	S.RHSTQDY.-	2+1		7.03
77	D110	S.RHSTQDY.-	2+1		7.03
78	D110	S.RHSTQDY.-	2+1		7.03
79	D110	S.RHSTQDY.-	2+1		7.03
80	D110	S.RHSTQDY.-	2+1		7.03
81	D110	S.RHSTQDY.-	2+1		7.03
82	D110	S.RHSTQDY.-	2+1		7.03
83	D110	S.RHSTQDY.-	2+1		7.03
84	D110	S.RHSTQDY.-	2+1		7.03
85	D110	S.RHSTQDY.-	2+1		7.03
86	D110	S.RHSTQDY.-	2+1		7.03
87	D110	S.RHSTQDY.-	2+1		7.03
88	D110	S.RHSTQDY.-	2+1		7.03
89	D110	S.RHSTQDY.-	2+1		7.03
90	D110	S.RHSTQDY.-	2+1		7.03
91	D110	S.RHSTQDY.-	2+1		7.03
92	D110	S.RHSTQDY.-	2+1		7.03
93	D110	S.RHSTQDY.-	2+1		7.03
94	D110	S.RHSTQDY.-	2+1		7.03
95	D110	S.RHSTQDY.-	2+1		7.03
96	D110	S.RHSTQDY.-	2+1		7.03
97	D110	S.RHSTQDY.-	2+1		7.03
98	D110	S.RHSTQDY.-	2+1		7.03
99	D110	S.RHSTQDY.-	2+1		7.03
100	D110	S.RHSTQDY.-	2+1		7.03

23. sp|P00174-HSA1_HUMAN Isoform 4 of Complement decay-accelerating factor OS=Homo sapiens OX=9606 GN=CD55

MTVARPSVPAALLVLGALFWLSPVGGLQEATCYGPVSNETLARLESPVAPVEEECVHNQIDDYKNDLKWWEFQHCAKKLTEVTYGTCSLAEQCPNLEHRSLYSRGVQETWTGNCNLTKCSTLENDVHSFFLDMNVFLMLTAFDPSKEAFKTVACEVCADGLIGMLQMFCQQIWVEPTLEQWQTMDKVEIQEMSKLPVQEILAQSPTYLEVDMSLDCVGLTSLETSICEEMNLPSPQNLTEELWSNNITEKTLLGNFYIPGPPGIPDSLDFSTSIVRIPQPLGFFILHSKMSTIHEFTHEIFNRGVNETWRMCSVNHEGMNTSLEQFKLQISVSSCEMYGNMSPYVQTTSHQWLLFTRTEGSLFWDTVDGFFSLTGLYLMAIGSHMKEGDETPKEQLTEENVSLLMSHIHLQVKERYIVTPVFPRGEFGENCDMKLTTCIVNVLFKDKTSKDGFSIFYGDCEMIHTAASSENSKMYLGLMPGDSIGSSLQPELASQEERYLSYYSLKHVEKFDMLKGTHHKLVTLNVSPDYNEPLHIDNKVRSPNDTLRSQMAVGRTMETIRWISEDSKDPVAIVDARTGHLNQVLKSHQDQPVAVFGIQIKSKSHDPKEDGKVQAIELNAVLIPDFKNISMKIGNTYYLSVNNVLPVSSKIPECELSNKTKCSFNKAQVVSQLEYDSFLCKDAVSPVQAHLPLCNNSRVFGTWIPVTMMDAHSGNDGEDLILFSNTEIQLPVSESYLNSLEMNLSCLGLVSTLGT

Species with HeMoQuest predicted HBMs

>sp|P01024|CO3_HUMAN Complement C3 OS=Homo sapiens OX=9606 GN=C3 PE=1 SV=2
MGPTSGPSLLLLLLTHLPLALGSPMYSIITPNILRLESEETMVLEAHDAQGDVPVTVTVH
DFPGKKLVLSSEKTVLTPATNHMGNVTFTIPANREFKSEKGRNKFVTVQATFGTQVVEKV
VLVSLQSGYLFIQTDKTIYTPGSTVLYRI**FTVNHKLLP**VGRTVMVNIENPEGIPVKQDSL
SSQNQLGVLPLSWDIPELVNMGQW**KIRAYYENS**PQQVFSTEFEVKEYVLPSFEVIVEPTE
KFYYIYNEKGLEVTITARFLYGKKVEGTAFVIFGIQDGEQRISLPESLKRIPIEDGSGEV
VLSRKVLLDGVQNPRAEDLVGKSLYVSATVILHSGSDMVQAERSGIPIVTS**PYQIHFTKT**
PKYFKPGMPFDLMVFVTNPD**GSPAYRVPV**AVQGEDTVQSLTQGDGVAKL**SINTHPSQK**PL
SITVRTKKQELSEAEQATRTMQALPYSTVGNSNNYLHLSVLRTELRPGETLNVNFLLR**MD**
RAHEAKIRYYTYLIMNKGRLLKAGRQVREPGQDLVVLPLSITTDFIPSFRLVAYYTLIGA
SGQREVVADSVWVDVKDSCVGSLVVKSGQSEDRQPVPGQQMTLKIEGDHGARVVLVAVDK
GVFVLNKKNKLTQSKIWDVVEKADIGCTPGSGKDYAGVFSDAGLTFTSSSGQQTAQRAEL
QCPQPAARRRRSVQLTEKRMDKVGKYPKELRKCCEDGMRENPMRFSCQRRTRFISLGEAC
KKVFLDCCNYITE**LRRQHARASHLGLA**RSNLDEDIIAEENIVSRSEFPESWLWNVEDLKE
PPKNGISTKLMNIFLKDSITTWEILAVSMSDKKGICVADPFEVTVMQDFFIDLRLPYSVV
RNEQVEIRAVLYNYRQNQELKVRVELLH**NPAFCSLATTKRRHQQTV**TIPPKSSLSVPYVI
VPLKTGLQEVEV**KAAVYHHFISD**GVRKSLKVVPEGIRMNKTVAVRTLDPERLGREGVQKE
DIPPADLSDQVPDTESETRILLQGTPVAQMTEDAVDA**ERLKHLIVT**PSGCGEQNMIGMTP
TVIAVHYLDETEQWEKFGLEKRQGALELIKKGYTQQLAFRQPSSAFAAFVKRAPSTWLTA
YVVKVFSLAVNLIAID**SQVLCGAVK**WLILEKQKPDGVFQEDAPVIHQEMIGGLRNNNEKD
MALTAFVLISLQEAKDICEEQVNSLPGSITKAGDFLEANYMNLQRSYTVAIAGYALAQMG
RLKGPLLNKFLTTAKDKNRWEDPGKQLYNVEATSYALLALLQLKDFDFVPPVVRWLNEQR
YYGGGYGSTQATFMVFQALAQYQKDAPDHQELNLDVSLQLPSRSSKI**THRIHWESA**SLLR
SEETKENEGFTVTAEGKGQGTLSVVTMYHAKAKDQLTCNKFDLKVTIKPAPETEKRPQDA
KNTMILEICTRYRGDQDATMSILDISMMTGFAPDTDDLKQLANGVDRYISKYELDKAFSD
RNTLIIYLDKVSHSEDDCL**AFKVHQYFNVE**LIQPGAVKVYAYYNLEESC**TRFYHPEKE**DG
KLNKLCRDELCRCAEENCFIQKSDDKVTLEERLDKACEPGVDYVYKTRLVKVQLSNDFDE
YIMAIEQTIKSGSDEVQVGQQRTFISPIKCREALKL**EEKKHYLMW**GLSSDFWGEKPNLSY
IIGKDTWVEHWPEEDECQDEENQKQCQDLGAFTESMVVFGCPN

>sp|P00751|CFAB_HUMAN Complement factor B OS=Homo sapiens OX=9606 GN=CFB PE=1 SV=2
MGSNLSPQLCLMPFILGLLSGGVTTTPWSLARPQGSCSLEGVEIKGGSFRLLQEGQALEY
VCPSGFYPYPVQTRTCRSTGSWSTLKTQDQKTVRKAE**CRAIHCPRP**HDFENGEYW**PRSPY**
YNVSDEISFHCYDGYTLRGSANRTCQVNGRWSGQTAICDNGAGYCSNPGIPIGTRKVGSQ
YRLEDSVTYHCSRGLTLRGSQRRTCQEGGSWSGTEPSCQDSFMYDTPQEVAEAFLSSLTE
TIEGVDAEDGHGPGEQQKRKIVLDPSGSMNIYLVLDGSDSIGASNFTGAKKCLVNLIE**KV**
ASYGVKPRYGLV**TYATYPKIW**VKVSEADSSNADWVTKQLNEI**NYEDHKLKS**GTNTKKALQ
AVYSMMSWPDDVPPEGWNRTRHVIILMTDGLHNMGGDPITVIDEIRDLLYIGKDRKNPRE
DYLDVYVFGVGPLVNQVNINALASKKDNEQHVFKVKDMENLEDVFYQMIDESQSLSLCG**M**
VWEHRKGTDYHKQPWQAKISVIR**PSKGHESCM**GAVVSEYFVLTAAHCFTVDDKEHSIKVS
VGGEKRDLEIEVVLFHPNYNINGKKEAGIPEFYDYDVALIKLKNKLKYGQTIRPICLPCT
EGTTRALRLPPTTTCQQQKEELLPAQDIKALFVSEEEKKLT**RKEVYIKNG**DKKGSCERDA
Q**YAPGYDKVK**DISEVVTPRFLCTGGVSPYADPNTCRGDSGG**PLIVHKRSR**FIQVGVISWG
VVDVCKNQKRQK**QVPAHARDF**HINLFQVLPWLKEKLQDEDLGFL

>sp|P00751-2|CFAB_HUMAN Isoform 2 of Complement factor B OS=Homo sapiens OX=9606 GN=CFB
MGSNLSPQLCLMPFILGLLSGGVTTTPWSLARPQGSCSLEGVEIKGGSFRLLQEGQALEY
VCPSGFYPYPVQTRTCRSTGSWSTLKTQDQKTVRKAE**CRAIHCPRP**HDFENGEYW**PRSPY**
YNVSDEISFHCYDGYTLRGSANRTCQVNGRWSGQTAICDNGAGYCSNPGIPIGTRKVGSQ
YRLED**SVTYHCSRG**LTLRGSQRRTCQEGGSWSGTEPSCQDSFMYDTPQEVAEAFLSSLTE

TIEGVDAEDGHGPGEQQKRKIVLDPSGSMNIYLVLDGSDSIGASNFTGAKKCLVNLIE**KV**
ASYGVKPRYGLV**TYATYPKIW**VKVSEADSSNADWVTKQLNEI**NYEDHKLKS**GTNTKKALQ
AVYSMMSWPDDVPPEGWNRTRHVIILMTDGLHNMGGDPITVIDEIRDLLYIGKDRKNPRE
DYLDVYVFGVGPLVNQVNINALASKKDNEQHVFKVKDMENLEDVFYQMIDESQSLSLCG**M**
VWEHRKGTDYHKQPWQAKISVIR**PSKGHESCM**GAVVSEYFVLTAAHCFTVDDKEHSIKVS
VGKDATEGPGLHLCSPGNTSHFLQI**LHSTHPQCS**PIPCTPDQSGMGEDVKLGMTRGQRQE
AAHKEVVPTLLLQEGRSGTWR

>sp|P05156|CFAI_HUMAN Complement factor I OS=Homo sapiens OX=9606 GN=CFI PE=1 SV=2
MKLLHVFLLFLCFHLRFCKVTYTSQEDLVEKKCLAKKYTHLSCDKVFCQPWQRCIEGTCV
CKLPYQCPKNGTAVCATNRRSFPTYCQQKS**LECLHPGTK**FLNNGTCTAEGKFS**VSLKHGN**
TDSEGIVEVKLVDQDKTMFICKSSWSMREANVACLDLGFQQGADTQRRFKLSDLSINS**TE**
CLHVHCRGLETSLAECTFTKRRTMGYQDFADVVCYTQKADSPMDDFFQCVNGKYISQMKA
CDGINDCGDQSDELCCKACQ**GKGFHCKSG**VCIPSQYQCNGEVDCITGEDEVGCAGFASVT
QEETEILTADMDAERRRIKSLLPKLSCGV**KNRMHIRRK**RIVGGKRAQLGDLPWQVAIKDA
SGITCGGI**YIGGCWILT**AAHCLR**ASKTHRYQI**WTTVVDWIHPDLKRIVIEYVDRIIFHEN
YNAGTYQNDIALIEMKKDG**NKKDCELPR**SIPACVPWSPYLFQPNDTCIVSGWGREKDNER
VFSLQWGEVKLISNCSKFYGNRFYEKEMECAGTYDGSIDACKGDSGGPLVCMDANNVTYV
WGVVSWGENCGKPEFPGVYTKVANYF**DWISYHVGRP**FISQYNV

>sp|P00746|CFAD_HUMAN Complement factor D OS=Homo sapiens OX=9606 GN=CFD PE=1 SV=5
MHSWERLAVLVLLGAAACAAPPRGRILGGREAEAHARPYMASVQLNGAHLCGGVLVAEQW
VLSAAHCLEDAADGKVQVLLGAHSLSQPEPSKRLYDVLRAVPHPDSQPDTIDHDLLLLQL
SEKATLGPAVRPLPWQRVDRDVAPGTLCDVAGW**GIVNHAGRR**PDSLQHVLLPVLDRATC**N**
RRTHHDGAITERLMCAESNRRDSCKGDSGGPLVCGGVLEGVVTSGSRVCGNRKKPGIYTR
VASYAAWIDSVLA

>sp|P27918|PROP_HUMAN Properdin OS=Homo sapiens OX=9606 GN=CFP PE=1 SV=2
MITEGAQAPRLLLPPLLLLLTLPATGSDPVLCFTQYEESSGKCKGLLGGGVSVEDCCLN**T**
AFAYQKRSGGLCQPCRSPRWSLWSTWAPCSVTCSEG**SQLRYRRCV**G**WNGQCSGKV**APGTL
EWQLQACEDQQCCPEMGGWSGWGPWEPCSVTCSKGTRTRR**RACNHPAPKCGGHCPGQ**AQE
SEACD**TQQVCPTHG**AWATWG**PWTPCSASCHGGPHEPKE**TRSRKCSAPEPSQKPPGKPC**PG**
LAYEQRRCTGLPPCPVAGGWGPWGPVSPCPVTCGLGQTMEQ**RTCNHPVPQ**HGGPFCAGD**A**
TRTHICNTAVPCPVDGEWDSWGEWSPCIRRNMKSISCQEIPGQQSRGRTCRGR**KFDGHRC**
AGQQ**QDIRHCYSIQHCPLK**GSWSEWSTWGLCMPPCGPNPTRARQRLCTP**LLPKYPPTV**SM
VEGQGEKNVTFWGRPLPRCEELQGQKLVVEEK**RPCLHVPAC**KDPEEEEL

>sp|P08603|CFAH_HUMAN Complement factor H OS=Homo sapiens OX=9606 GN=CFH PE=1 SV=4
MRLLAKIICLMLWAICVAEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLG
NVIMVCRKGEWVALNPLRKCQK**RPCGHPGDT**PFGTFTLTGGNVFEYGVKAVYTCNEGYQL
LGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNS
GYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMG
YEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQC**RNGFYP**
ATRGNTAKCTSTGWI**PAPRCTLKP**CDY**PDIKHGGLYHENMRRPYFPVAVGKYYSYY**CDEH
FETPSGSYWDHIHCTQDGWSPAVP**CLRKCYFPYL**ENG**YNQNYGRKF**VQGKSIDVACHPGY
ALPKAQTTVTCMENGWSPTPRCI**RVKTCSKSS**IDIENGFISESQYTYALKEKAKYQCKLG
YVTADGETSGSITCGKDGWSAQPTCIKSCDIPVFMNARTKNDFTWFKLNDTLDYECHDGY
ESNTGSTTGSIVCGYNGWSDLPICYERECELPKIDVHLVPDRKKDQYKVGEVLKFSCKPG
FTIVGPNSVQCYHFGLSPDLPICKEQVQSCGPPPELLNGNVKEKTKEEYGHSEVVEYYCN
PRFLMKGPNKIQCVDGEWTTLPVCIVEESTCGDIPELEHGWAQLSSPPYYYGDSVEFNCS
ESF**TMIGHRSIT**CIHGVWTQLPQCVAID**KLKKCKSSN**L**IILEEHLKNK**KEFDHNSNIRYR
CRGKEGWIHTVCINGRWDPEVNCSMA**QIQLCPPPP**QIPNSHNMTTTLNYRDGEKVSVLCQ

ENYLIQEGEEITCKDGRWQ**SIPLCVEKI**PCSQPPQIEHGTINSSRSSQESYAHGTKLSYT
CEGGFRISEENETTCYMGKWSSPPQCEGLPCKSPPEISHGVVAHMSDSYQYGEEVTYKCF
EGFGIDGPAIAKCLG**EKWSHPPSCIKTDCLSLP**SFENAIPMGEKKDVYKAGEQVTYTCAT
YYKMDGASNVTCINSRWT**GRPTCRDTSCVNPP**T**VQNAYIVSR**QMSKYPSGERVRYQCRSP
YEMFGDEEVMCLNGNWTEPPQCKDSTGKCGPPPPIDNGDITSFPLSVYAPASSVEYQCQN
LYQLEGNKRITCRNGQWSEP**PKCLHPCVI**SREIMENYNIALRWTA**KQKLYSRTG**ESVEFV
CKRGYRL**SSRSHTLRTTCWDGK**LEYPTCAKR

>sp|P08603-2|CFAH_HUMAN Isoform 2 of Complement factor H OS=Homo sapiens OX=9606 GN=CFH
MRLLAKIICLMLWAICVAEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLG
NVIMVCRKGEWVALNPLRKCQK**RPCGHPGDT**PFGTFTLTGGNVFEYGVKAVYTCNEGYQL
LGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNS
GYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMG
YEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQC**RNGFYP**
ATRGNTAKCTSTGWI**PAPRCTLKP**CDY**PDIKHGGLY**HEN**MRRPYFPVAVGKYYSYY**CDEH
FETPSG**SYWDHIHCT**QDGWS**PAVPCLRKCYFPYL**ENG**YNQNYGRKF**VQGKSIDVACHPGY
ALPKAQTTVTCMENGWSPTPRCIRVSFTL

>sp|P15529|MCP_HUMAN Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46 PE=1 SV=3
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVLPPSSTKPPALSHS
VSTSSTTKSPASSASG**PRPTYKPPV**SNYPGYPKPEEGILDSLDVWVIAVIVIAIVVGVAV
ICVVPYRYLQRRKKKGTYLTDETHREVKFTSL

>sp|P15529-2|MCP_HUMAN Isoform B of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVLPPSSTKPPALSHS
VSTSSTTKSPASSASGPRPTYKPPVSNYPGYPKPEEGILDSLDVWVIAVIVIAIVVGVAV
ICVVPYRYLQRRKKKGKADGGAEYATYQTKSTTPAEQRG

>sp|P15529-11|MCP_HUMAN Isoform C of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVSTSSTTKSPASSAS
G**PRPTYKPPV**SNYPGYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKKK
GTYLTDETHREVKFTSL

>sp|P15529-3|MCP_HUMAN Isoform D of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVSTSSTTKSPASSAS

G**PRPTYKPPV**SNYPGYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKKK
GKADGGAEYATYQTKSTTPAEQRG

>sp|P15529-12|MCP_HUMAN Isoform E of Membrane cofactor protein
OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSG**KPPICEKVL**CTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKG**PRPTYKPPV**SNYPG
YPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKKKGTYLTDETHREVKFT
SL

>sp|P15529-4|MCP_HUMAN Isoform F of Membrane cofactor protein
OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSG**KPPICEKVL**CTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKG**PRPTYKPPV**SNYPG
YPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKKKGKADGGAEYATYQTK
STTPAEQRG

>sp|P15529-13|MCP_HUMAN Isoform G of Membrane cofactor protein
OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVLPPSSTKPPALSHS
VSTSSTTKSPASSASGYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKK
KGTYLTDETHREVKFTSL

>sp|P15529-5|MCP_HUMAN Isoform H of Membrane cofactor protein
OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKATV**MFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVLPPSSTKPPALSHS
VSTSSTTKSPASSASGYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKK
KGKADGGAEYATYQTKSTTPAEQRG

>sp|P15529-14|MCP_HUMAN Isoform I of Membrane cofactor protein
OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVSTSSTTKSPASSAS
GYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKKKGTYLTDETHREVKF
TSL

>sp|P15529-6|MCP_HUMAN Isoform J of Membrane cofactor protein
OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV

DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVSTSSTTKSPASSAS
GYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKKKGKADGGAEYATYQT
KSTTPAEQRG

>sp|P15529-15|MCP_HUMAN Isoform K of Membrane cofactor protein
OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSG**KPPICEKVL**CTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKATV**MFECDKGFYLDGSDTIVCDSNSTWDPPVPK**CLKGYPKPE**EGILDSLDV
WVIAVIVIAIVVGVAVICVVPYRYLQRRKKKGTYLTDETHREVKFTSL

>sp|P15529-7|MCP_HUMAN Isoform L of Membrane cofactor protein
OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSG**KPPICEKVL**CTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKATV**MFECDKGFYLDGSDTIVCDSNSTWDPPVPK**CLKGYPKPE**EGILDSLDV
WVIAVIVIAIVVGVAVICVVPYRYLQRRKKKGKADGGAEYATYQTKSTTPAEQRG

>sp|P15529-8|MCP_HUMAN Isoform M of Membrane cofactor protein
OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVSTSSTTKSPASSAS
G**PRPTYKPPV**SNYPGYPKPEEGILDSLDVWVIAVIVIAIGKQMVELNMPLTRLNQPLQQS
REAE

>sp|P15529-9|MCP_HUMAN Isoform N of Membrane cofactor protein
OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCKKGYFYIPPLATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSG**KPPICEKVL**CTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKATV**MFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKG**PRPTYKPPV**SNYPG
YPKPEEGILDSLDVWVIAVIVIAIGKQMVELNMPLTRLNQPLQQSREAE

>sp|P15529-10|MCP_HUMAN Isoform 2 of Membrane cofactor protein
OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVLPPSSTKP**PALSHS
TTK**SPASSASGPRPTYKPPVSNYPGYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVP
YRYLQRRKKKGTYLTDETHREVKFTSL

>sp|P15529-16|MCP_HUMAN Isoform 3 of Membrane cofactor protein
OS=Homo sapiens OX=9606 GN=CD46

MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSGETCPYIRDPLNGQAVPANGTYEFGYQM
HFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEVFEY
LDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQISGF**G**
KKFYYKATVMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVLPPSSTKPPALSHSVST
SSTTKSPASSASGPRPTYKPPVSNYPGYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICV
VPYRYLQRRKKKGKADGGAEYATYQTKSTTPAEQRG

>sp|P08174|DAF_HUMAN Complement decay-accelerating factor OS=Homo sapiens OX=9606 GN=CD55 PE=1 SV=4
MTVARPSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPNAQPALEGRTSFPEDTV
ITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFCNRSCEVPTRLNSAS**LKQPYITQN**YFP
VGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGI
LFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQ**GER**
DHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRGKSLTSKVPPTVQKPT
TVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVSRT**TKHFHETTP**NKGSGTTSGTTRLLS
GHTCFTLTGLLGTLVTMGLLT

>sp|P08174-2|DAF_HUMAN Isoform 1 of Complement decay-accelerating factor OS=Homo sapiens OX=9606 GN=CD55
MTVARPSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPNAQPALEGRTSFPEDTV
ITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFCNRSCEVPTRLNSAS**LKQPYITQN**YFP
VGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGI
LFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQ**GER**
DHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRGKSLTSKVPPTVQKPT
TVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVS**RTTKHFHETTP**NKGSGTTSGTTRLLS
GSRPVTQAGMRWCDRSSLQSRTPGFKRSFHFSLPSSWYYR**AHVFHVDRF**AWDASNHGLAD
LAKEELRRKYTQVYRLFLVS

>sp|P08174-3|DAF_HUMAN Isoform 3 of Complement decay-accelerating factor OS=Homo sapiens OX=9606 GN=CD55
MTVARPSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPNAQPALEGRTSFPEDTV
ITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFCNRSCEVPTRLNSAS**LKQPYITQN**YFP
VGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGI
LFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQ**GER**
DHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRGKSLTSKVPPTVQKPT
TVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVSRT**TKHFHETTP**NKGSGTTSGTTRLLS
ALQVRPFEV**SGSSHISSK**KMMCIL

>sp|P08174-4|DAF_HUMAN Isoform 4 of Complement decay-accelerating factor OS=Homo sapiens OX=9606 GN=CD55
MTVARPSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPNAQPALEGRTSFPEDTV
ITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFCNRSCEVPTRLNSAS**LKQPYITQN**YFP
VGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGI
LFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQ**GER**
DHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRGKSLTSKVPPTVQKPT
TVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVS**RTTKHFHETTP**NKGSGTTSGTTRLLS
VLFM

>sp|P08174-5|DAF_HUMAN Isoform 5 of Complement decay-accelerating factor OS=Homo sapiens OX=9606 GN=CD55
MTVARPSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPNAQPALEGRTSFPEDTV
ITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFCNRSCEVPTRLNSAS**LKQPYITQN**YFP
VGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGI
LFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQ**GER**
DHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRGKSLTSKVPPTVQKPT
TVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVS**RTTKHFHETTP**NKGSGTTSGTTRLLS

ETVFHRVIQDGLDLLA**SRSACLGLPKCWDYRREPPHLARAHVFHVDRF**AWDASNHGLADL
AKEELRRKYTQVYRLFLVS

>sp|P08174-6|DAF_HUMAN Isoform 6 of Complement decay-accelerating factor OS=Homo sapiens OX=9606 GN=CD55
MTVARPSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPNAQPALEGRTSFPEDTV
ITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFCNRSCEVPTRLNSAS**LKQPYITQN**YFP
VGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGI
LFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQ**GER**
DHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRGKSLTSKVPPTVQKPT
TVNVPTTEVSPTSQKTTTKTTTPNAQGTETPS**VLQKHTTEN**VSATRTPPTPQKPTTVNVP
ATIVTP**TPQKPTTINV**PATGVSSTPQRHTIVNVSATGTLPTLQKPTRANDSATKSPAAAQ
TSFISKTLSTKTPSAAQNPMMTNASATQATLTAQKFTTAKVAFTQSPSAAPTRSTPVS**RT**
TKHFHETTPNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT

>sp|P08174-7|DAF_HUMAN Isoform 7 of Complement decay-accelerating factor OS=Homo sapiens OX=9606 GN=CD55
MTVARPSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPNAQPALEGRTSFPEDTV
ITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFCNRSCEVPTRLNSAS**LKQPYITQN**YFP
VGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGI
LFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQ**GER**
DHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRGKSLTSKVPPTVQKPT
TVNVPTTEVSPTSQKTTTKTTTPNAQGTETPS**VLQKHTTEN**VSATRTPPTPQKPTTVNVP
ATIVTPTPQKPTTINVPATGVSS**TPQRHTIVNV**SATGTLPTLQKPTRANDSATKSPAAAQ
TSFISKTLSTKTPSAAQNPMMTNASATQATLTAQKFTTAKVAFTQSPSAARKSTNVHSPV
TNGLKSTQRFPSAHITATRSTPVS**RTTKHFHETTP**NKGSGTTSGTTRLLSGHTCFTLTGL
LGTLVTMGLLT

>sp|P17927-E|CR1_HUMAN Complement receptor type 1 OS=Homo sapiens OX=9606 GN=CR1 PE=1 SV=3
MGASSPRSPEPVGPPAPGLPFCCGGSLLAVVVLLALPVAWGQCNAPEWLPFARPTNLTDE
FEFPIGTYLNYECRPGYSGRPFSIICLKNSVWTGAKDRCRRKSCRNPPDPVNGMVHVIKG
IQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTITNGDFIST
N**RENFHYGSV**VTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTP
PNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS**CSRVCQPP**
PDVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDD
FMGQLLNGRVLFPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIF
CPSPPVIPNGRHTGKPLEVFPFGKTVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNGVW
SSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYEC**RPEYYGRPF**SITCLDNL
VWSSPKDVCKRKSCKTPPDPVNGMVHVITDIQVGSRINYSCTTGH**RLIGHSSAE**CILSGN
AAHWSTKPPIC**QRIPCGLPP**TIANGDFISTN**RENFHYGSV**VTYRCNPGSGGRKVFELVGE
PSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGF
VMKGPRRVKCQALNKWEPELPS**CSRVCQPPP**DVLHAERTQRDKDNFSPGQEVFYSCEPGY
DLRGAASMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF
QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKAVNYTC
DPHPDRGTSFDLIGESTIRCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNA
SDFPIGTSLKYEC**RPEYYGRPF**SITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVHVITD
IQVGSRINYSCTTGH**RLIGHSSAE**CILS**GNTAHWSTKPPICQRIP**CGLPPTIANGDFIST
N**RENFHYGSV**VTYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSG**PAPQCIIPN**KCTP
PNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS**CSRVCQPP**
PEILHGE**HTPSHQDNF**SPGQEVFYSCEPGYDLRGAASLHCTPQGDWSP**EAPRCAVKS**CDD
FL**GQLPHGRVL**FPLNLQLGAKVSFVCDEGFRLKGSSVSHCVLVGMRSLWNN**SVPVCEHIF**
CPNPPAILNGRHTGTPSGDIPYGKEISYTCDPHPDRGMTFNLIGESTIRCTSDPHGNGVW
SSPAPRCELS**VRAGHCKTP**EQFPFASPTIPINDFEFPVGTSLNYECRPGYFGKMFSISCL
ENLVWSSVEDNCRRKSCGPPPEPFNGMVHINTDTQFGSTVNYSCNEGFRLIGSPSTTCLV
SGNNVTWDKKAPICEIISCEPPPTISNGDFYSNN**RTSFHNGTV**VTYQCHTGPDGEQLFEL

VGERSIYCTSKDDQVGVWSS**PPPRCISTN**KCTAPEVENAIRVPGNRSFFSLTEIIRFRCQ
PGFVMVGSHTVQCQTNGRWG**PKLPHCSRVCQPPP**EILHGE**HTLSHQDNF**SPGQEVFYSCE
PSYDLRGAASLHCTPQGDWSP**EAPRCTVKS**CDDFL**GQLPHGRVL**LPLNLQLGAKVSFVCD
EGFRLKGRSASHCVLAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPFGDIPYGKEIS
YACDTHPDRGMTFNLIGESSIRCTSDPQGNGVWSSPAPRCELSVP**AACPHPPKI**QNGHYI
GGHVSLYLPGMTISYICDPGYLLVGKGFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISK
ELEM**KKVYHYGDYVTLK**CEDGYTLEGSPWSQCQADDRWDPPLAKC**TSRTHD**

>sp|P17927-T|CR1_HUMAN Complement receptor type 1 OS=Homo sapiens OX=9606 GN=CR1 PE=1 SV=3
ALIVGTLSGTIFFILLIIFLSWIIL

>sp|P17927-C|CR1_HUMAN Complement receptor type 1 OS=Homo sapiens OX=9606 GN=CR1 PE=1 SV=3
KHRKGNNAHENPKEVAIHLHSQGGSSVHPRTLQTNEENSRVLP

>sp|Q03591|FHR1_HUMAN Complement factor H-related protein 1 OS=Homo sapiens OX=9606 GN=CFHR1 PE=1 SV=2
MWLLVSVILISRISSVGGEATFCDF**PKINHGILY**DEEKYKPFSQVPTGEVFYYSCEYNFV
SPSKSFWTRITCTEEGWSPTPK**CLRLCFFPF**VENGHSESSGQTHLEGDTVQIICNTGYRL
QNNENNISCVERGWSTPPKCRSTDTSCVNPPT**VQNAHILSR**QMSKYPSGERVRYECRSPY
EMFGDEEVMCLNGNWTEPPQCKD**STGKCGPPP**PIDNGDITSFPLSVYAPASSVEYQCQNL
YQLEGNKRITCRNGQWSEP**PKCLHPCVISR**EIMENYNIALRWTA**KQKLYLRTG**ESAEFVC
KRGYRL**SSRSHTLRTTCWDGK**LEYPTCAKR

>sp|P36980|FHR2_HUMAN Complement factor H-related protein 2 OS=Homo sapiens OX=9606 GN=CFHR2 PE=1 SV=1
MWLLVSVILISRISSVGGEAMFCDF**PKINHGILY**DEEKYKPFSQVPTGEVFYYSCEYNFV
SPSKSFWTRITCAEEGWSPTPK**CLRLCFFPF**VENGHSESSGQTHLEGDTVQIICNTGYRL
QNNENNISCVERGWSTPPKCRSTISAEKCGPPPPIDNGDITSFLLSVYAPGSSVEYQCQN
LYQLEGNNQITCRNGQWSEPPKCLDPCVISQE**IMEKYNIKL**KWTN**QQKLYSRTG**DIVEFV
C**KSGYHPTKSHSFRA**MCQNGKLVYPSCEEK

>sp|P36980-2|FHR2_HUMAN Isoform Short of Complement factor H-related protein 2 OS=Homo sapiens OX=9606 GN=CFHR2
MWLLVSVILISRISSVGGEAMFCDF**PKINHGILY**DEEKYKPFSQVPTGEVFYYSCEYNFV
SPSKSFWTRITCAEEGWSPTPK**CLRLCFFPF**VENGHSESSGQTHLEGDTVQII**CNTGYRL**
QNNENNISCVERGWSTPPKCRSTSSSVEYQCQNLYQLEGNNQITCRNGQWSEPPKCLDPC
VISQE**IMEKYNIKL**KWTN**QQKLYSRTG**DIVEFVC**KSGYHPTKSHSFRA**MCQNGKLVYPSC
EEK

>sp|Q02985|FHR3_HUMAN Complement factor H-related protein 3 OS=Homo sapiens OX=9606 GN=CFHR3 PE=1 SV=2
MLLLINVILTLWVSCANGQVKPCDF**PDIKHGGLF**HEN**MRRPYFPVAVGKYYSYY**CDEHFE
TPSGSYWDYIHCTQNGWSPAVPC**LRKCYFPYL**ENG**YNQNYGRKF**VQGNSTEVACHPGYGL
PKAQTTVTCTEKGWS**PTPRCIRVR**TCSKSDIEIENGFISESSSIYILNKEIQYKCKPGYA
TADGNSSGSITCLQNGWSAQPICINSSEKCGPPPPISNGDTTSFLLKVYVPQSRVEYQCQ
PYYELQGSNYVTCSNGEWS**EPPRCIHPCIITE**ENMNKNNIKLKGR**SDRKYYAKTG**DTIEF
MCKLGYNANTSILS**FQAVCREGI**VEYPRCE

>sp|Q02985-2|FHR3_HUMAN Isoform 2 of Complement factor H-related protein 3 OS=Homo sapiens OX=9606 GN=CFHR3
MLLLINVILTLWVSCANGQVKPCDF**PDIKHGGLF**HEN**MRRPYFPVAVGKYYSYY**CDEHFE
TPSGSYWDYIHCTQNGWSPAVPC**LRKCYFPYL**ENG**YNQNYGRKF**VQGNSTEVACHPGYGL
PKAQTTVTCTEKGWSPTPRCIRVNSSEKCGPPPPISNGDTTSFLLKVYVPQSRVEYQCQP
YYELQGSNYVTCSNGEWS**EPPRCIHPCII**TEENMNKNNIKLKGR**SDRKYYAKTG**DTIEFM

CKLGYNANTSILS**FQAVCREGI**VEYPRCE

>sp|Q92496|FHR4_HUMAN Complement factor H-related protein 4 OS=Homo sapiens OX=9606 GN=CFHR4 PE=1 SV=3
MLLLINVILT**LWVSCANGQ**EVKPCDFPEIQHGGLYYKS**LRRLYFPAA**AGQSYSYYCDQNF
VTPSGSYWDYIHCTQDGWSPTVP**CLRTCSKSD**VEIENGFISESSSIYILNEETQYNCKPG
YATAEGNSSGSITCLQNGWSTQPICIKFCDMPVFENSRAKSNGMWFKLHDTLDYECYDGY
ESSYGNTTDSIVCGEDGWS**HLPTCYNSS**ENCGPPPPISNGDTTSFPQKVYLPWSRVEYQC
QSYYEL**QGSKYVTCS**NGDWSEPPRCISMKPCEF**PEIQHGHLYYE**N**TRRPYFPVA**TGQSYS
YYCDQNFVTPSGSYWDYIHCTQDGWLPTVP**CLRTCSKSD**IEIENGFISESSSIYILNKEI
QYKCKPGYATADGNSSGSITCLQNGWSAQPICIKFCDMPVFENSRAKSNGM**RFKLHDTLD**
YECYDGYEISYGNTTGSIVCGEDGWSHFPTCYNSSEKCGPPPPISNGDTTSFLLKVYVPQ
SRVEYQCQSYYELQGSNYVTCSNGEWS**EPPRCIHPCII**TEENMNKNNIQLKGK**SDIKYYA**
KTGDTIEFMCKLGYNANTSVLSFQAVCREGIVEYPRCE

>sp|Q92496-2|FHR4_HUMAN Isoform 2 of Complement factor H-related protein 4 OS=Homo sapiens OX=9606 GN=CFHR4
MLLLINVILTLWVSCANGQVKPCDFPEIQ**HGGLYYKSLRRLYFPAA**AGQSYSYYCDQNFV
TPSGSYWDYIHCTQDGWSPTVP**CLRTCSKSD**VEIENGFISESSSIYILNEETQYNCKPGY
ATAEGNSSGSITCLQNGWSTQPICIKFCDMPVFENSRAKSNGMWFKLHDTLDYECYDGYE
SSYGNTTDSIVCGEDGWSHLPTCYNSSENCGPPPPISNGDTTSFPQKVYLPWSRVEYQCQ
SYYEL**QGSKYVTCS**NGDWSEPPRCISMKPCEF**PEIQHGHLYYE**N**TRRPYFPVA**TGQSYSY
YCDQNFVTPSGSYWDYIHCTQDGWL**PTVPCLRTCSKSD**IEIENGFISESSSIYILNKEIQ
YKCKPGYATADGNSSGSITCLQNGWSAQPICIKFCDMPVFENSRAKSNGM**RFKLHDTLD**Y
ECYDGYEISYGNTTGSIVCGEDGWSHFPTCYN**SSEKCGPPP**PISNGDTTSFLLKVYVPQS
RVEYQCQSYYELQGSNYVTCSNGEWS**EPPRCIHPCII**TEENMNKNNIQLKGK**SDIKYYAK**
TGDTIEFMCKLGYNANTSVLSFQAVCREGIVEYPRCE

>sp|Q92496-3|FHR4_HUMAN Isoform 3 of Complement factor H-related protein 4 OS=Homo sapiens OX=9606 GN=CFHR4
MLLLINVILT**LWVSCANGQ**EVKPCDFPEIQ**HGGLYYKSLRRLYFPAA**AGQSYSYYCDQNF
VTPSGSYWDYIHCTQDGWSPTVP**CLRTCSKSD**IEIENGFISESSSIYILNKEIQYKCKPG
YATADGNSSGSITCLQNGWSAQPICIKFCDMPVFENSRAKSNGM**RFKLHDTLD**YECYDGY
EISYGNTTGSIVCGEDGWSHFPTCYNSSEKCGPPPPISNGDTTSFLLKVYVPQSRVEYQC
QSYYELQGSNYVTCSNGEWSEP**PRCIHPCII**TEENMNKNNIQLKGK**SDIKYYAKTG**DTIE
FMCKLGYNANTSVLS**FQAVCREGI**VEYPRCE

>sp|Q9BXR6|FHR5_HUMAN Complement factor H-related protein 5 OS=Homo sapiens OX=9606 GN=CFHR5 PE=1 SV=1
MLLLFSVILISWVSTVGGEGTLCD**FPKIHHGFLY**DEEDYNPFSQVPTGEVFYYSCEYNFV
SPSKSFWTRITCTEEGWSPTPKCLRMCSFPF**VKNGHSESS**GLIHLEGDTVQIICNTGYSL
QNNEKNISCVERGWS**TPPICSFTKGECHVPIL**EANVDAQPKKESYKVGDVLKFSCRKNLI
RVGSDSVQCYQFGWSPNFPTCKGQVRSCGPPPQLSNGEVKEIRKEEYGHNEVVEYDCNPN
FIINGPKKIQCVDGEWTTLPTCVEQVKTCGYIPELEYGYVQPSVPPYQHGVSVEVNCRNE
YAMIGNNMITCINGIWTELPM**CVATHQLKR**CKIAGVNIKTLLKLSG**KEFNHNSRI**RYRCS
DIFRYRHSVCINGKWNPEVDCTEKREQFCPPPPQIPNAQNMTTTVNYQDGEKVAVLCKEN
YLLPEAKEIVCKDGRWQ**SLPRCVEST**AYCGPPPSINNGDTTSFPLSVYPPGSTVTYRCQS
FYKLQGSVTVTCRNKQWSEPPRCLDPCVVSEENMNKNNIQLKWRNDGKLYAKTGDAVEFQ
CKFPHKAMISSPPFRAICQEGKFEYPICE

>sp|P04003|C4BPA_HUMAN C4b-binding protein alpha chain OS=Homo sapiens OX=9606 GN=C4BPA PE=1 SV=2
MHPPKTPSGALHRKRKMAAWPFSRLWKVSDPILFQMTLIAALLPAVLGNCGPPPTLSFAA
PMDITLTETRFKTGTTLKYTCLPG**YVRSHSTQT**LTCNSDGEWVYN**TFCIYKRCRHPGEL**R
NGQVEIKTDLSFGSQIEFSCSEGFFLIGSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPPD
IRNGRHSGEENFYAYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSPPTCEKITCR

KPDVSHGEMVSGFGPIYNYKDTIVFKCQKGFVLRGSSVIHCDADSKWNPSPPACEPNSCI
NLPDIPHASWETYPRPTKEDVYVVGTVL**RYRCHPGYK**PTTDEPTTVICQKNLRWTPYQGC
EALCCPEPKLNNG**EITQHRKSRPANHCVYFY**GDEI**SFSCHETSR**FSAICQGDGTWSPRTP
SCGDICNFP**PKIAHGHYKQSSSYSFFK**EEIIYECDKGYILVGQAK**LSCSYSHWS**APAPQC
KALCRKPELVNGRLSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNRTWYPEVPKCEW
ETPEGCEQVLTGKRLMQCLPNPEDVKMALEVYKLSLEIEQLELQRDSARQSTLDKEL

>sp|P20851|C4BPB_HUMAN C4b-binding protein beta chain OS=Homo sapiens OX=9606 GN=C4BPB PE=1 SV=1
MFFWCACCLMVAWRVSASDAEHCPELPPVDNSIFVAKEVEGQILGTYVC**IKGYHLVGK**KT
LFCNASKEWDNTTTE**CRLGHCPDP**VLVNGEFSSSGPVNVSDKITF**MCNDHYILK**GSNRSQ
CLEDHTWAPPFPICKSRDCDPPGNPVHGYFEGNNFTLGSTISYYCEDRYYLVGVQEQQCV
DGEWSSALPVCKLIQEAPKPECEKALLAFQESKNLCEAMENFMQQLKESGMTMEELKYSL
ELKKAELKAKLL

>sp|P20851-2|C4BPB_HUMAN Isoform 2 of C4b-binding protein beta chain OS=Homo sapiens OX=9606 GN=C4BPB
MFFWCACCLMVAWRVSASDEHCPELPPVDNSIFVAKEVEGQILGTYVC**IKGYHLVGK**KTL
FCNASKEWDNTTTE**CRLGHCPDP**VLVNGEFSSSGPVNVSDKITF**MCNDHYILK**GSNRSQC
LEDHTWAPPFPICKSRDCDPPGNPVHGYFEGNNFTLGSTISYYCEDRYYLVGVQEQQCVD
GEWSSALPVCKLIQEAPKPECEKALLAFQESKNLCEAMENFMQQLKESGMTMEELKYSLE
LKKAELKAKLL

16 unique entries/genes
46 sequences

Species with detected HBM variations

>sp|P01024|CO3_HUMAN Complement C3 OS=Homo sapiens OX=9606 GN=C3 PE=1 SV=2

MGPTSGPSLLLLLLTHLPLALGSPMYSIITPNILRLESEETMVLEAHDAQGDVPVTVTVH
DFPGKKLVLSSEKTVLTPATNHMGNVTFTIPANREFKSEKGRNKFVTVQATFGTQVVEKV
VLVSLQSGYLFIQTDKTIYTPGSTVLYRIFTVNHKLLPVGRTVMVNIENPEGIPVKQDSL
SSQNQLGVLPLSWDIPELVNMGQWKIRAYYENSPQQVFSTEFEVKEYVLPSFEVIVEPTE
KFYYIYNEKGLEVTITARFLYGKKVEGTAFVIFGIQDGEQRISLPESLKRIPIEDGSGEV
VLSRKVLLDGVQNPRAEDLVGKSLYVSATVILHSGSDMVQAERSGIPIVTSPYQIHFTKT
PKYFKPGMPFDLMVFVTNPDGSPAYRVPVAVQGEDTVQSLTQGDGVAKLSINTHPSQKPL
SITVRTKKQELSEAEQATRTMQALPYSTVGNSNNYLHLSVLRTELRPGETLNVNFLLRMD
RAHEAKIRYYTYLIMNKGRLLKAGRQVREPGQDLVVLPLSITTDFIPSFRLVAYYTLIGA
SGQREVVADSVWVDVKDSCVGSLVVKSGQSEDRQPVPGQQMTLKIEGDHGARVVLVAVDK
GVFVLNKKNKLTQSKIWDVVEKADIGCTPGSGKDYAGVFSDAGLTFTSSSGQQTAQRAEL
QCPQPAARRRRSVQLTEKRMDKVGKYPKELRKCCEDGMRENPMRFSCQRRTRFISLGEAC
KKVFLDCCNYITELRRQHARASHLGLARSNLDEDIIAEENIVSRSEFPESWLWNVEDLKE
PPKNGISTKLMNIFLKDSITTWEILAVSMSDKKGICVADPFEVTVMQDFFIDLRLPYSVV
RNEQVEIRAVLYNYRQNQELKVRVELLHNPAFCSLATTKRRHQQTVTIPPKSSLSVPYVI
VPLKTGLQEVEVKAAVYHHFISDGVRKSLKVVPEGIRMNKTVAVRTLDPERLGREGVQKE
DIPPADLSDQVPDTESETRILLQGTPVAQMTEDAVDAERLKHLIVTPSGCGEQNMIGMTP
TVIAVHYLDETEQWEKFGLEKRQGALELIKKGYTQQLAFRQPSSAFAAFVKRAPSTWLTA
YVVKVFSLAVNLIAIDSQVLCGAVKWLILEKQKPDGVFQEDAPVIHQEMIGGLRNNNEKD
MALTAFVLISLQEAKDICEEQVNSLPGSITKAGDFLEANYMNLQRSYTVAIAGYALAQMG
RLKGPLLNKFLTTAKDKNRWEDPGKQLYNVEATSYALLALLQLKDFDFVPPVVRWLNEQR
YYGGGYGSTQATFMVFQALAQYQKDAPDHQELNLDVSLQLPSRSSKITHRIHWESASLLR
SEETKENEGFTVTAEGKGQGTLSVVTMYHAKAKDQLTCNKFDLKVTIKPAPETEKRPQDA
KNTMILEICTRYRGDQDATMSILDISMMTGFAPDTDDLKQLANGVDRYISKYELDKAFSD
RNTLIIYLDKVSHSEDDCLAFKVHQYFNVELIQPGAVKVYAYYNLEESCTRFYHPEKEDG
KLNKLCRDELCRCAEENCFIQKSDDKVTLEERLDKACEPGVDYVYKTRLVKVQLSNDFDE
YIMAIEQTIKSGSDEVQVGQQRTFISPIKCREALKLEEKKHYLMWGLSSDFWGEKPNLSY
IIGKDTWVEHWPEEDECQDEENQKQCQDLGAFTESMVVFGCPN

VAR_070941, CA213419, RCV000077796, RCV000202831, RCV000765476, RCV000963525, RCV001130000, RCV001130001, RCV001130002, rs147859257, 155, K>Q, ARMD9; results in resistance to proteolytic inactivation by CFH and CFI (UniProt), MACULAR DEGENERATION, AGE-RELATED, 9, SUSCEPTIBILITY TO (ClinVar), Age related macular degeneration 9 (ClinVar), Atypical hemolytic-uremic syndrome with C3 anomaly (ClinVar), Complement component 3 deficiency (ClinVar)
VAR_063215, CA9129171, COSM3797670, rs117793540, 735, R>W, AHUS5 (UniProt), urinary tract (Cosmic)
CA9129168, RCV001129557, RCV001129558, RCV001129559,rs578116271, 736, R>Q, Age related macular degeneration 9 (ClinVar), Atypical hemolytic-uremic syndrome with C3 anomaly (ClinVar), Complement component 3 deficiency (ClinVar)
RCV001136442, RCV001136443, RCV001136444, rs1967565177, 873, C>R, Age related macular degeneration 9 (ClinVar), Atypical hemolytic-uremic syndrome with C3 anomaly (ClinVar), Complement component 3 deficiency (ClinVar)
CA403633250, RCV001328277, RCV001880191, rs1443451793, 881, R>H, Variant assessed as Somatic; 0.0 impact. (NCI-TCGA), Atypical hemolytic-uremic syndrome (ClinVar)

CA9128779, RCV000311409, RCV000350872, RCV000398615, RCV001859955, rs750654763, 1100, L>P, Age related macular degeneration 9 (ClinVar), Atypical hemolytic-uremic syndrome with C3 anomaly (ClinVar), Complement component 3 deficiency (ClinVar)
AR 063220, 1464, H>D, Hemolytic uremic syndrome atypical 5 (AHUS5) (UniProt)

>sp|P00751|CFAB_HUMAN Complement factor B OS=Homo sapiens OX=9606 GN=CFB PE=1 SV=2
MGSNLSPQLCLMPFILGLLSGGVTTTPWSLARPQGSCSLEGVEIKGGSFRLLQEGQALEY
VCPSGFYPYPVQTRTCRSTGSWSTLKTQDQKTVRKAE**CRAIHCPRP**HDFENGEYW**PRSPY**
YNVSDEISFHCYDGYTLRGSANRTCQVNGRWSGQTAICDNGAGYCSNPGIPIGTRKVGSQ
YRLEDSVTYHCSRGLTLRGSQRRTCQEGGSWSGTEPSCQDSFMYDTPQEVAEAFLSSLTE
TIEGVDAEDGHGPGEQQKRKIVLDPSGSMNIYLVLDGSDSIGASNFTGAKKCLVNLIE**KV**
ASYGVKPRYGLV**TYATYPKIW**VKVSEADSSNADWVTKQLNEI**NYEDHKLKS**GTNTKKALQ
AVYSMMSWPDDVPPEGWNRTRHVIILMTDGLHNMGGDPITVIDEIRDLLYIGKDRKNPRE
DYLDVYVFGVGPLVNQVNINALASKKDNEQHVFKVKDMENLEDVFYQMIDESQSLSLCG**M**
VWEHRKGTDYHKQPWQAKISVIR**PSKGHESCM**GAVVSEYFVLTAAHCFTVDDKEHSIKVS
VGGEKRDLEIEVVLFHPNYNINGKKEAGIPEFYDYDVALIKLKNKLKYGQTIRPICLPCT
EGTTRALRLPPTTTCQQQKEELLPAQDIKALFVSEEEKKLT**RKEVYIKNG**DKKGSCERDA
Q**YAPGYDKVK**DISEVVTPRFLCTGGVSPYADPNTCRGDSGG**PLIVHKRSR**FIQVGVISWG
VVDVCKNQKRQK**QVPAHARDF**HINLFQVLPWLKEKLQDEDLGFL

CA136894909, RCV001155151, RCV001155152, rs374738591, 306, K>R, Macular degeneration (ClinVar), Atypical hemolytic-uremic syndrome with B factor anomaly (ClinVar)
CA3728362, RCV000282119, RCV000405241, rs138207668, 508, H>Q, Macular degeneration (ClinVar), Atypical hemolytic-uremic syndrome with B factor anomaly (ClinVar)

>sp|P00751-2|CFAB_HUMAN Isoform 2 of Complement factor B OS=Homo sapiens OX=9606 GN=CFB
MGSNLSPQLCLMPFILGLLSGGVTTTPWSLARPQGSCSLEGVEIKGGSFRLLQEGQALEY
VCPSGFYPYPVQTRTCRSTGSWSTLKTQDQKTVRKAE**CRAIHCPRP**HDFENGEYW**PRSPY**
YNVSDEISFHCYDGYTLRGSANRTCQVNGRWSGQTAICDNGAGYCSNPGIPIGTRKVGSQ
YRLED**SVTYHCSRG**LTLRGSQRRTCQEGGSWSGTEPSCQDSFMYDTPQEVAEAFLSSLTE
TIEGVDAEDGHGPGEQQKRKIVLDPSGSMNIYLVLDGSDSIGASNFTGAKKCLVNLIE**KV**
ASYGVKPRYGLV**TYATYPKIW**VKVSEADSSNADWVTKQLNEI**NYEDHKLKS**GTNTKKALQ
AVYSMMSWPDDVPPEGWNRTRHVIILMTDGLHNMGGDPITVIDEIRDLLYIGKDRKNPRE
DYLDVYVFGVGPLVNQVNINALASKKDNEQHVFKVKDMENLEDVFYQMIDESQSLSLCG**M**
VWEHRKGTDYHKQPWQAKISVIR**PSKGHESCM**GAVVSEYFVLTAAHCFTVDDKEHSIKVS
VGKDATEGPGLHLCSPGNTSHFLQI**LHSTHPQCS**PIPCTPDQSGMGEDVKLGMTRGQRQE
AAHKEVVPTLLLQEGRSGTWR

CA136894909, RCV001155151, RCV001155152, rs374738591, 306, K>R, Macular degeneration (ClinVar), Atypical hemolytic-uremic syndrome with B factor anomaly (ClinVar) [By similarity]
CA3728362, RCV000282119, RCV000405241, rs138207668, 508, H>Q, Macular degeneration (ClinVar), Atypical hemolytic-uremic syndrome with B factor anomaly (ClinVar) [By similarity]

>sp|P05156|CFAI_HUMAN Complement factor I OS=Homo sapiens OX=9606 GN=CFI PE=1 SV=2
MKLLHVFLLFLCFHLRFCKVTYTSQEDLVEKKCLAKKYTHLSCDKVFCQPWQRCIEGTCV
CKLPYQCPKNGTAVCATNRRSFPTYCQQKS**LECLHPGTK**FLNNGTCTAEGKFS**VSLKHGN**

TDSEGIVEVKLVDQDKTMFICKSSWSMREANVACLDLGFQQGADTQRRFKLSDLSINS**TE**
CLHVHCRGLETSLAECTFTKRRTMGYQDFADVVCYTQKADSPMDDFFQCVNGKYISQMKA
CDGINDCGDQSDELCCKACQ**GKGFHCKSG**VCIPSQYQCNGEVDCITGEDEVGCAGFASVT
QEETEILTADMDAERRRIKSLLPKLSCGV**KNRMHIRRK**RIVGGKRAQLGDLPWQVAIKDA
SGITCGGI**YIGGCWILT**AAHCLR**ASKTHRYQI**WTTVVDWIHPDLKRIVIEYVDRIIFHEN
YNAGTYQNDIALIEMKKDG**NKKDCELPR**SIPACVPWSPYLFQPNDTCIVSGWGREKDNER
VFSLQWGEVKLISNCSKFYGNRFYEKEMECAGTYDGSIDACKGDSGGPLVCMDANNVTYV
WGVVSWGENCGKPEFPGVYTKVANYF**DWISYHVGRP**FISQYNV

CA357865066, RCV001328252, rs1478686846, 98, T>A, Atypical hemolytic-uremic syndrome (ClinVar)
VAR 063666, CA278398, rs141853578, 119, G>R, AHUS3 and ARMD13; the mutant is both expressed and secreted at lower levels than wild-type protein; mediates C3 degradation to a lesser extent than that of controls (UniProt)
VAR 063667, CA3042233, RCV000973356, rs75612300, 183, H>R, Hemolytic uremic syndrome atypical 3 (AHUS3) (UniProt)
CA3042231, RCV000778715, RCV001856163, rs368615806, 187, R>*, Atypical hemolytic-uremic syndrome with I factor anomaly (ClinVar)
CA3042230, COSM1309619, RCV001148815, RCV001858976, rs143366614, 187, R>Q, Atypical hemolytic-uremic syndrome with I factor anomaly (ClinVar), urinary tract (Cosmic)
CA3042165, RCV001148813, rs547901965, 261, G>S, Atypicalhemolytic-uremic syndrome with I factor anomaly (ClinVar)
RCV001328246, rs759676430, 336, R>*, Atypical hemolytic-uremic syndrome (ClinVar)
CA3042011, RCV000386149, rs763931500, 371, G>V, Atypicalhemolytic-uremic syndrome with I factor anomaly (ClinVar)
CA357858724, RCV001029951, rs1579173999, 373, C>S, Atypical hemolytic-uremic syndrome with I factor anomaly (ClinVar)
CA357857740, RCV001029952, rs1373768125, 387, T>I, Atypical hemolytic-uremic syndrome with I factor anomaly (ClinVar)
CA357857713, RCV000786883, rs1292929833, 389, R>C, Atypical hemolytic-uremic syndrome with I factor anomaly (ClinVar)
CA3041835, RCV000505641, RCV001865643, rs200973120, 570, S>T, Atypical hemolytic-uremic syndrome with I factor anomaly (ClinVar)

>sp|P00746|CFAD_HUMAN Complement factor D OS=Homo sapiens OX=9606 GN=CFD PE=1 SV=5
MHSWERLAVLVLLGAAACAAPPRGRILGGREAEAHARPYMASVQLNGAHLCGGVLVAEQW
VLSAAHCLEDAADGKVQVLLGAHSLSQPEPSKRLYDVLRAVPHPDSQPDTIDHDLLLLQL
SEKATLGPAVRPLPWQRVDRDVAPGTLCDVAGW**GIVNHAGRR**PDSLQHVLLPVLDRATC**N**
RRTHHDGAITERLMCAESNRRDSCKGDSGGPLVCGGVLEGVVTSGSRVCGNRKKPGIYTR
VASYAAWIDSVLA

CA9026370, RCV000767925, rs373019471, 155, I>V, Recurrent Neisseria infections due to factor D deficiency (ClinVar)

>sp|P27918|PROP_HUMAN Properdin OS=Homo sapiens OX=9606 GN=CFP PE=1 SV=2
MITEGAQAPRLLLPPLLLLLTLPATGSDPVLCFTQYEESSGKCKGLLGGGVSVEDCCLN**T**
AFAYQKRSGGLCQPCRSPRWSLWSTWAPCSVTCSEG**SQLRYRRCV**G**WNGQCSGKV**APGTL

EWQLQACEDQQCCPEMGGWSGWGPWEPCSVTCSKGTRTRRRACNHPAPKCGGHCPGQAQE
SEACDTQQVCPTHGAWATWGPWTPCSASCHGGPHEPKETRSRKCSAPEPSQKPPGKPCPG
LAYEQRRCTGLPPCPVAGGWGPWGPVSPCPVTCGLGQTMEQRTCNHPVPQHGGPFCAGDA
TRTHICNTAVPCPVDGEWDSWGEWSPCIRRNMKSISCQEIPGQQSRGRTCRGRKFDGHRC
AGQQQDIRHCYSIQHCPLKGSWSEWSTWGLCMPPCGPNPTRARQRLCTPLLPKYPPTVSM
VEGQGEKNVTFWGRPLPRCEELQGQKLVVEEKRPCLHVPACKDPEEEEL

VAR 002002, CA121395, COSM296671, RCV000011932, rs132630259, 100, R>W, Properdin deficiency (PFD);Three phenotypes have been reported: complete deficiency (type I), incomplete deficiency (type II), and dysfunction of properdin (type III); type II (UniProt), Properdin deficiency, type II (ClinVar), large intestine (Cosmic), Variant assessed as Somatic; impact. (NCI-TCGA), endometrium (Cosmic)
CA121391, RCV000011931, rs132630258, 161, R>*, Properdin deficiency, X-linked (ClinVar), Properdin deficiency, x-linked (cfpd) (Ensembl)
CA121401, RCV000011934, rs132630260, 206, S>*, Properdindeficiency, X-linked (ClinVar), Properdin deficiency, x-linked (cfpd) (Ensembl)
VAR 083039, 244, E>K, PFD; type II; decreases expression, inhibits oligomerization and fails to stimulate bacteriolysis; does not affect binding to Complement C3 beta chain (UniProt)
VAR 002004, CA121405, RCV000011935, rs132630261, 414, Y>D, PFD; type III; significantly decreases Complement C3 beta chain binding (UniProt), Properdin deficiency, type III (ClinVar)

>sp|P08603|CFAH_HUMAN Complement factor H OS=Homo sapiens OX=9606 GN=CFH PE=1 SV=4
MRLLAKIICLMLWAICVAEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLG
NVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQL
LGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNS
GYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMG
YEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYP
ATRGNTAKCTSTGWIPAPRCTLKPCDYPDIKHGGLYHENMRRPYFPVAVGKYYSYYCDEH
FETPSGSYWDHIHCTQDGWSPAVPCLRKCYFPYLENGYNQNYGRKFVQGKSIDVACHPGY
ALPKAQTTVTCMENGWSPTPRCIRVKTCSKSSIDIENGFISESQYTYALKEKAKYQCKLG
YVTADGETSGSITCGKDGWSAQPTCIKSCDIPVFMNARTKNDFTWFKLNDTLDYECHDGY
ESNTGSTTGSIVCGYNGWSDLPICYERECELPKIDVHLVPDRKKDQYKVGEVLKFSCKPG
FTIVGPNSVQCYHFGLSPDLPICKEQVQSCGPPPELLNGNVKEKTKEEYGHSEVVEYYCN
PRFLMKGPNKIQCVDGEWTTLPVCIVEESTCGDIPELEHGWAQLSSPPYYYGDSVEFNCS
ESFTMIGHRSITCIHGVWTQLPQCVAIDKLKKCKSSNLIILEEHLKNKKEFDHNSNIRYR
CRGKEGWIHTVCINGRWDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYRDGEKVSVLCQ
ENYLIQEGEEITCKDGRWQSIPLCVEKIPCSQPPQIEHGTINSSRSSQESYAHGTKLSYT
CEGGFRISEENETTCYMGKWSSPPQCEGLPCKSPPEISHGVVAHMSDSYQYGEEVTYKCF
EGFGIDGPAIAKCLGEKWSHPPSCIKTDCLSLPSFENAIPMGEKKDVYKAGEQVTYTCAT
YYKMDGASNVTCINSRWTGRPTCRDTSCVNPPTVQNAYIVSRQMSKYPSGERVRYQCRSP
YEMFGDEEVMCLNGNWTEPPQCKDSTGKCGPPPPIDNGDITSFPLSVYAPASSVEYQCQN
LYQLEGNKRITCRNGQWSEPPKCLHPCVISREIMENYNIALRWTAKQKLYSRTGESVEFV
CKRGYRLSSRSHTLRTTCWDGKLEYPTCAKR

CA1305197, RCV001100290, RCV001100291, RCV001100292, RCV001100293, RCV001856363, rs142937931, 303, R>W, Basal laminar drusen (ClinVar), Variant assessed as Somatic; 0.0 impact. (NCI-TCGA), CFH-Related Dense Deposit

Disease/Membranoproliferative Glomerulonephritis Type II (ClinVar), Age related macular degeneration 4 (ClinVar), Hemolytic uremic syndrome, atypical, susceptibility to, 1 (ClinVar)
VAR 031980, CA1305282, RCV001304040, RCV001332256, rs201671665, 400, Q>K, Hemolytic uremic syndrome atypical 1 (AHUS1) (UniProt), Factor H deficiency (ClinVar)
VAR 001979, RCV000018015, RCV000018016, rs1061170, 402, Y>H, associated with ARMD4 (UniProt), Basal laminar drusen (ClinVar), Age related macular degeneration 4 (ClinVar)
CA1305626, RCV001097067, RCV001097068, RCV001097069, RCV001097070, rs772553879, 760, I>L, Basal laminar drusen (ClinVar), CFH-Related Dense Deposit Disease/Membranoproliferative Glomerulonephritis Type II (ClinVar), Hemolytic uremic syndrome, atypical, susceptibility to, 1 (ClinVar), Age related macular degeneration 4 (ClinVar)
CA1305665, RCV001098818, RCV001098819, RCV001098820, RCV001098821, rs752302466, 808, I>M, Basal laminar drusen (ClinVar), CFH-Related Dense Deposit Disease/Membranoproliferative Glomerulonephritis Type II (ClinVar), Hemolytic uremic syndrome, atypical, susceptibility to, 1 (ClinVar), Age related macular degeneration 4 (ClinVar)
VAR 025870, 978, W>C, Hemolytic uremic syndrome atypical 1 (AHUS1) (UniProt)
CA1305781, RCV001097264, RCV001097265, RCV001100998, RCV001100999, rs149938052, 982, P>S, Basal laminar drusen (ClinVar), CFH-Related Dense Deposit Disease/Membranoproliferative Glomerulonephritis Type II (ClinVar), Hemolytic uremic syndrome, atypical, susceptibility to, 1 (ClinVar), Age related macular degeneration 4 (ClinVar)
CA10588915, RCV000256395, rs886039869, 984, C>R, Hemolytic uremic syndrome, atypical, susceptibility to, 1 (ClinVar)
VAR 025872, 1043, C>R, Hemolytic uremic syndrome atypical 1 (AHUS1) (UniProt)
CA1305867, COSM146717, RCV000266613, RCV000324131, RCV000359462, RCV000362490, RCV001701841, rs55679475, 1058, Y>H, Basal laminar drusen (ClinVar), CFH-Related Dense Deposit Disease/Membranoproliferative Glomerulonephritis Type II (ClinVar), stomach (Cosmic), Hemolytic uremic syndrome, atypical, susceptibility to, 1 (ClinVar), Age related macular degeneration 4 (ClinVar)
CA1305869, COSM146718, RCV000296097, RCV000330790, RCV000334829, RCV000388133, RCV001701937, rs55771831, 1060, V>L, Basal laminar drusen (ClinVar), CFH-Related Dense Deposit Disease/Membranoproliferative Glomerulonephritis Type II (ClinVar), stomach (Cosmic), Age related macular degeneration 4 (ClinVar), Hemolytic uremic syndrome, atypical, susceptibility to, 1 (ClinVar)
VAR 025878, 1163, C>W, Hemolytic uremic syndrome atypical 1 (AHUS1) (UniProt)
VAR 063650, 1169, I>L, Hemolytic uremic syndrome atypical 1 (AHUS1) (UniProt)
VAR 019407, CA257503, RCV000018014, rs121913055, 1189, L>R, Hemolytic uremic syndrome atypical 1 (AHUS1) (UniProt), Hemolytic uremic syndrome, atypical, susceptibility to, 1

(ClinVar), Hemolytic uremic syndrome, atypical, susceptibility to, 1 (ahus1) (Ensembl)
VAR_019408, CA341428, rs460897, 1191, S>L, Hemolytic uremic syndrome atypical 1 (AHUS1) (UniProt), Hemolytic uremic syndrome, atypical, susceptibility to, 1 (ahus1) (Ensembl)
VAR_025882, CA1305983, RCV000788876, rs761877050, 1194, G>D, Hemolytic uremic syndrome atypical 1 (AHUS1) (UniProt)
VAR_025885, CA128563, rs121913059, 1210, R>C, Complement factor H deficiency (CFHD) and Macular degeneration, age-related, 4 (ARMD4); rare penetrant mutation that confers high risk of age-related macular degeneration (UniProt), Hemolytic uremic syndrome, atypical, susceptibility to, 1 (ahus1) (Ensembl)
CA1305996, COSM901548, RCV000276556, rs121913051, 1215, R>*, CFH-Related Disorders (ClinVar), Variant assessed as Somatic; 0.0 impact. (NCI-TCGA), endometrium (Cosmic), Hemolytic uremic syndrome, atypical, susceptibility to, 1 (ahus1) (Ensembl)
VAR_025886, CA257490, RCV000018008, RCV001328244, rs121913051, 1215, R>G, Hemolytic uremic syndrome atypical 1 (AHUS1) (UniProt), Atypical hemolytic-uremic syndrome (ClinVar), Hemolytic uremic syndrome, atypical, susceptibility to, 1 (ClinVar), Hemolytic uremic syndrome, atypical, susceptibility to, 1 (ahus1) (Ensembl)
VAR_025887, 1215, R>Q, Complement factor H deficiency (CFHD) (UniProt)

>sp|P08603-2|CFAH_HUMAN Isoform 2 of Complement factor H OS=Homo sapiens OX=9606 GN=CFH
MRLLAKIICLMLWAICVAEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLG
NVIMVCRKGEWVALNPLRKCQK**RPCGHPGDT**PFGTFTLTGGNVFEYGVKAVYTCNEGYQL
LGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNS
GYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMG
YEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQC**RNGFYP**
ATRGNTAKCTSTGWI**PAPRCTLKP**CDY**PDIKHGGLY**HEN**MRRPYFPVAVGKYYSYY**CDEH
FETPSG**SYWDHIHCT**QDGWS**PAVPCLRKCYFPYL**ENG**YNQNYGRKF**VQGKSIDVACHPGY
ALPKAQTTVTCMENGWSPTPRCIRVSFTL

CA1305197, RCV001100290, RCV001100291, RCV001100292, RCV001100293, RCV001856363, rs142937931, 303, R>W, Basal laminar drusen (ClinVar), Variant assessed as Somatic; 0.0 impact. (NCI-TCGA), CFH-Related Dense Deposit Disease/Membranoproliferative Glomerulonephritis Type II (ClinVar), Age related macular degeneration 4 (ClinVar), Hemolytic uremic syndrome, atypical, susceptibility to, 1 (ClinVar) [By similarity]
VAR_031980, CA1305282, RCV001304040, RCV001332256, rs201671665, 400, Q>K, Hemolytic uremic syndrome atypical 1 (AHUS1) (UniProt), Factor H deficiency (ClinVar) [By similarity]
VAR_001979, RCV000018015, RCV000018016, rs1061170, 402, Y>H, associated with ARMD4 (UniProt), Basal laminar drusen (ClinVar), Age related macular degeneration 4 (ClinVar) [By similarity]

>sp|P15529|MCP_HUMAN Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46 PE=1 SV=3

MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVLPPSSTKPPALSHS
VSTSSTTKSPASSASG**PRPTYKPPV**SNYPGYPKPEEGILDSLDVWVIAVIVIAIVVGVAV
ICVVPYRYLQRRKKKGTYLTDETHREVKFTSL

CA1371561, COSM1295809, RCV001099808, rs761000846, 82, R>Q, urinary_tract (Cosmic), Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar), Variant assessed as Somatic; 9.285e-05 impact. (NCI-TCGA)
VAR_022263, CA1371821, RCV001096379, RCV001521407, rs41317833, 324, P>L, Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar)

>sp|P15529-2|MCP_HUMAN Isoform B of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVLPPSSTKPPALSHS
VSTSSTTKSPASSASGPRPTYKPPVSNYPGYPKPEEGILDSLDVWVIAVIVIAIVVGVAV
ICVVPYRYLQRRKKKGKADGGAEYATYQTKSTTPAEQRG

CA1371561, COSM1295809, RCV001099808, rs761000846, 82, R>Q, urinary_tract (Cosmic), Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar), Variant assessed as Somatic; 9.285e-05 impact. (NCI-TCGA) [By similarity]

>sp|P15529-11|MCP_HUMAN Isoform C of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVSTSSTTKSPASSAS
G**PRPTYKPPV**SNYPGYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKKK
GTYLTDETHREVKFTSL

CA1371561, COSM1295809, RCV001099808, rs761000846, 82, R>Q, urinary_tract (Cosmic), Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar), Variant assessed as Somatic; 9.285e-05 impact. (NCI-TCGA) [By similarity]
VAR_022263, CA1371821, RCV001096379, RCV001521407, rs41317833, 309, P>L, Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar) [By similarity]

>sp|P15529-3|MCP_HUMAN Isoform D of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVSTSSTTKSPASSAS

GPRPTYKPPVSNYPGYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKKK
GKADGGAEYATYQTKSTTPAEQRG

CA1371561, COSM1295809, RCV001099808, rs761000846, 82, R>Q, urinary_tract (Cosmic), Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar), Variant assessed as Somatic; 9.285e-05 impact. (NCI-TCGA) [By similarity]
VAR_022263, CA1371821, RCV001096379, RCV001521407, rs41317833, 309, P>L, Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar) [By similarity]

>sp|P15529-12|MCP_HUMAN Isoform E of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIGKPKPYYEIGERV
DYKCKKGYFYIPPLATHTICDRNHTWLPVSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GFGKKFYYKATVMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKGPRPTYKPPVSNYPG
YPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKKKGTYLTDETHREVKFT
SL

CA1371561, COSM1295809, RCV001099808, rs761000846, 82, R>Q, urinary_tract (Cosmic), Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar), Variant assessed as Somatic; 9.285e-05 impact. (NCI-TCGA) [By similarity]
VAR_022263, CA1371821, RCV001096379, RCV001521407, rs41317833, 294, P>L, Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar) [By similarity]

>sp|P15529-4|MCP_HUMAN Isoform F of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIGKPKPYYEIGERV
DYKCKKGYFYIPPLATHTICDRNHTWLPVSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GFGKKFYYKATVMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKGPRPTYKPPVSNYPG
YPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKKKGKADGGAEYATYQTK
STTPAEQRG

CA1371561, COSM1295809, RCV001099808, rs761000846, 82, R>Q, urinary_tract (Cosmic), Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar), Variant assessed as Somatic; 9.285e-05 impact. (NCI-TCGA) [By similarity]
VAR_022263, CA1371821, RCV001096379, RCV001521407, rs41317833, 294, P>L, Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar) [By similarity]

>sp|P15529-13|MCP_HUMAN Isoform G of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIGKPKPYYEIGERV
DYKCKKGYFYIPPLATHTICDRNHTWLPVSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GFGKKFYYKATVMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVLPPSSTKPPALSHS
VSTSSTTKSPASSASGYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKK
KGTYLTDETHREVKFTSL

CA1371561, COSM1295809, RCV001099808, rs761000846, 82, R>Q, urinary_tract (Cosmic), Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar), Variant assessed as Somatic; 9.285e-05 impact. (NCI-TCGA) [By similarity]

>sp|P15529-5|MCP_HUMAN Isoform H of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKATV**MFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVLPPSSTKPPALSHS
VSTSSTTKSPASSASGYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKK
KGKADGGAEYATYQTKSTTPAEQRG

CA1371561, COSM1295809, RCV001099808, rs761000846, 82, R>Q, urinary_tract (Cosmic), Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar), Variant assessed as Somatic; 9.285e-05 impact. (NCI-TCGA) [By similarity]

>sp|P15529-14|MCP_HUMAN Isoform I of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVSTSSTTKSPASSAS
GYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKKKGTYLTDETHREVKF
TSL

CA1371561, COSM1295809, RCV001099808, rs761000846, 82, R>Q, urinary_tract (Cosmic), Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar), Variant assessed as Somatic; 9.285e-05 impact. (NCI-TCGA) [By similarity]

>sp|P15529-6|MCP_HUMAN Isoform J of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVSTSSTTKSPASSAS
GYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKKKGKADGGAEYATYQT
KSTTPAEQRG

CA1371561, COSM1295809, RCV001099808, rs761000846, 82, R>Q, urinary_tract (Cosmic), Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar), Variant assessed as Somatic; 9.285e-05 impact. (NCI-TCGA) [By similarity]

>sp|P15529-15|MCP_HUMAN Isoform K of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSG**KPPICEKVL**CTPPPKIKNGKHTFSEVEV

FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKATV**MFECDKGFYLDGSDTIVCDSNSTWDPPVPK**CLKGYPKPE**EGILDSLDV
WVIAVIVIAIVVGVAVICVVPYRYLQRRKKKGTYLTDETHREVKFTSL

CA1371561, COSM1295809, RCV001099808, rs761000846, 82, R>Q, urinary_tract (Cosmic), Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar), Variant assessed as Somatic; 9.285e-05 impact. (NCI-TCGA) [By similarity]
CA10609582, RCV000342161, rs886045838, 288, P>A, Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar)

>sp|P15529-7|MCP_HUMAN Isoform L of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSG**KPPICEKVL**CTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKATV**MFECDKGFYLDGSDTIVCDSNSTWDPPVPK**CLKGYPKPE**EGILDSLDV
WVIAVIVIAIVVGVAVICVVPYRYLQRRKKKGKADGGAEYATYQTKSTTPAEQRG

CA1371561, COSM1295809, RCV001099808, rs761000846, 82, R>Q, urinary_tract (Cosmic), Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar), Variant assessed as Somatic; 9.285e-05 impact. (NCI-TCGA) [By similarity]
CA10609582, RCV000342161, rs886045838, 288, P>A, Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar)

>sp|P15529-8|MCP_HUMAN Isoform M of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVSTSSTTKSPASSAS
G**PRPTYKPPV**SNYPGYPKPEEGILDSLDVWVIAVIVIAIGKQMVELNMPLTRLNQPLQQS
REAE

CA1371561, COSM1295809, RCV001099808, rs761000846, 82, R>Q, urinary_tract (Cosmic), Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar), Variant assessed as Somatic; 9.285e-05 impact. (NCI-TCGA) [By similarity]
VAR_022263, CA1371821, RCV001096379, RCV001521407, rs41317833, 309, P>L, Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar)

>sp|P15529-9|MCP_HUMAN Isoform N of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCKKGYFYIPPLATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSG**KPPICEKVL**CTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKATV**MFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKG**PRPTYKPPV**SNYPG
YPKPEEGILDSLDVWVIAVIVIAIGKQMVELNMPLTRLNQPLQQSREAE

CA1371561, COSM1295809, RCV001099808, rs761000846, 82, R>Q, urinary_tract (Cosmic), Atypical hemolytic-uremic syndrome

with MCP/CD46 anomaly (ClinVar), Variant assessed as Somatic; 9.285e-05 impact. (NCI-TCGA) [By similarity]
VAR_022263, CA1371821, RCV001096379, RCV001521407, rs41317833, 294, P>L, Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar)

>sp|P15529-10|MCP_HUMAN Isoform 2 of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVLPPSSTKP**PALSHS**
TTKSPASSASGPRPTYKPPVSNYPGYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVP
YRYLQRRKKKGTYLTDETHREVKFTSL

CA1371561, COSM1295809, RCV001099808, rs761000846, 82, R>Q, urinary_tract (Cosmic), Atypical hemolytic-uremic syndrome with MCP/CD46 anomaly (ClinVar), Variant assessed as Somatic; 9.285e-05 impact. (NCI-TCGA) [By similarity]

>sp|P17927|CR1_HUMAN Complement receptor type 1 OS=Homo sapiens OX=9606 GN=CR1 PE=1 SV=3 [Isoform F/CR1-A/CR1*1)
MGASSPRSPEPVGPPAPGLPFCCGGSLLAVVVLLALPVAWGQCNAPEWLPFARPTNLTDE
FEFPIGTYLNYECRPGYSGRPFSIICLKNSVWTGAKDRCRRKSCRNPPDPVNGMVHVIKG
IQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTITNGDFIST
NRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTP
PNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPP
PDVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDD
FMGQLLNGRVLFPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIF
CPSPPVIPNGRHTGKPLEVFPFGKTVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNGVW
SSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYEC**RPEYYGRPF**SITCLDNL
VWSSPKDVCKRKSCKTPPDPVNGMVHVITDIQVGSRINYSCTTGH**RLIGHSSAE**CILS**GN**
AAHWSTKPPICQRIPCGLPPTIANGDFISTN**RENFHYGSV**VTYRCNPGSGGRKVFELVGE
PSIYCTSNDDQVGIWSG**PAPQCIIPN**KCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGF
VMKGPRRVKCQALNKWEPELPS**CSRVCQPPP**DVLHAERTQRDKDNFSPGQEVFYSCEPGY
DLRGAASMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF
QLKGSSASYCVLAGMESLWNSSVPVC**EQIFCPSPP**VIPNGRHTGKPLEVFPFGKAVNYTC
DPHPDRGTSFDLIGESTIRCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNA
SDFPIGTSLKYEC**RPEYYGRPF**SITCLDNLVWSS**PKDVCKRKS**CKTPPDPVNGMVHVITD
IQVGSRINYSCTTGH**RLIGHSSAE**CILS**GNTAHWSTK**PPICQRIPCGLPPTIANGDFIST
N**RENFHYGSV**VTYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSG**PAPQCIIPN**KCTP
PNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS**CSRVCQPP**
PEILHGE**HTPSHQDNF**SPGQEVFYSCEPGYDLRGAASLHCTPQGDWSP**EAPRCAVKS**CDD
FL**GQLPHGRVL**FPLNLQLGAKVSFVCDEGFRLKGSSVSHCVLVGMRSLWNNSVPVCEHIF
CPNPPAILNGRHTGTPSGDIPYGKEISYTCDPHPDRGMTFNLIGESTIRCTSDPHGNGVW
SSPAPRCELS**VRAGHCKTP**EQFPFASPTIPINDFEFPVGTSLNYECRPGYFGKMFSISCL
ENLVWSSVEDNCRRKSCGPPPEPFNGMVHINTDTQFGSTVNYSCNEGFRLIGSPSTTCLV
SGNNVTWDKKAPICEIISCEPPPTISNGDFYSNN**RTSFHNGTV**VTYQCHTGPDGEQLFEL
VGERSIYCTSKDDQVGVWSSPPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIIRFRCQ
PGFVMVGSHTVQCQTNGRWG**PKLPHCSRV**CQPPPEILHGE**HTLSHQDNF**SPGQEVFYSCE
PSYDLRGAASLHCTPQGDWSPEAPRCTVKSCDDFL**GQLPHGRVL**LPLNLQLGAKVSFVCD
EGFRLKG**RSASHCVLA**GMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPFGDIPYGKEIS
YACDTHPDRGMTFNLIGESSIRCTSDPQGNGVWSSPAPRCELSVP**AACPHPPKI**QNGHYI
GGHVSLYLPGMTISYICDPGYLLVGKGFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISK
ELEM**KKVYHYGDYVTLK**CEDGYTLEGSPWSQCQADDRWDPPLAKC**TSRTHD**ALIVGTLSG

TIFFILLIIFLSWIILKHRKGNNAHENPKEVAIHLHSQGGSSVHPRTLQTNEENSRVLP

VAR_013819, CA1370009, RCV000018595, rs2274567, 1208, H>R, Malaria, severe, resistance to (ClinVar)

>tr|E9PDY4|E9PDY4_HUMAN Complement receptor type 1 OS=Homo sapiens OX=9606 GN=CR1 PE=1 SV=1 [Isoform S/CR1-B/CR1*2)
MGASSPRSPEPVGPPAPGLPFCCGGSLLAVVVLLALPVAWGQCNAPEWLPFARPTNLTDE
FEFPIGTYLNYECRPGYSGRPFSIICLKNSVWTGAKDRCRRKSCRNPPDPVNGMVHVIKG
IQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTITNGDFIST
NRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTP
PNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPP
PDVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDD
FMGQLLNGRVLFPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIF
CPSPPVIPNGRHTGKPLEVFPFGKTVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNGVW
SSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYEC**RPEYYGRPF**SITCLDNL
VWSSPKDVCKRKSCKTPPDPVNGMVHVITDIQVGSRINYSCTTGH**RLIGHSSAE**CILS**GN**
AAHWSTKPPICQRIPCGLPPTIANGDFISTN**RENFHYGSV**VTYRCNPGSGGRKVFELVGE
PSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGF
VMKGPRRVKCQALNKWEPELPS**CSRVCQPPP**DVLHAERTQRDKDNFSPGQEVFYSCEPGY
DLRGAASMRCTPQGDWSP**AAPTCEVKS**CDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF
QLKGSSASYCVLAGMESLWNSSVPVC**EQIFCPSPP**VIPNGRHTGKPLEVFPFGKTVNYTC
DPHPDRGTSFDLIGESTIRCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNA
SDFPIGTSLKYEC**RPEYYGRPF**SITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVHVITD
IQVGSRINYSCTTGH**RLIGHSSAE**CILS**GNAAHWSTKPPICQRIPCGLPP**TIANGDFIST
N**RENFHYGSV**VTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTP
PNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS**CSRVCQPP**
PDVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDD
FMGQLLNGRVLFPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIF
CPSPPVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNGVW
SS**PAPRCGILGHCQAPD**HFLFAKLKTQTNASDFPIGTSLKYEC**RPEYYGRPF**SITCLDNL
VWSSPKDVCKRKSCKTPPDPVNGMVHVITDIQVGSRINYSCTTGH**RLIGHSSAE**CILS**GN**
TAHWSTKPPICQRIPCGLPPTIANGDFISTN**RENFHYGSV**VTYRCNLGSRGRKVFELVGE
PSIYCTSNDDQVGIWSG**PAPQCIIPN**KCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGF
VMKGPRRVKCQALNKWEP**ELPSCSRVCQPPP**EILHGE**HTPSHQDNF**SPGQEVFYSCEPGY
DLRGAASLHCTPQGDWSPEAPRCAVKSCDDFL**GQLPHGRVL**FPLNLQLGAKVSFVCDEGF
RLKGSSVSHCVLVGMRSLWNNSVPVCEHIFCPNPPAILNGRHTGTPSGDIPYGKEISYTC
DPHPDRGMTFNLIGESTIRCTSDPHGNGVWSSPAPRCELS**VRAGHCKTP**EQFPFASPTIP
INDFEFPVGTSLNYECRPGYFGKMFSISCLENLVWSSVEDNCRRKSCGPPPEPFNGMVHI
NTDTQFGSTVNYSCNEGFRLIGSPSTTCLVSGNNVTWDK**KAPICEIIS**CEPPPTISNGDF
YSNN**RTSFHNGTV**VTYQCHTGPDGEQLFELVGERSIYCTSKDDQVGVWSSPPPRCISTNK
CTAPEVENAIRVPGNRSFFTLTEIIRFRCQPGFVMVGSHTVQCQTNGRWG**PKLPHCSRVC**
QPPPEILHGE**HTLSHQDNF**SPGQEVFYSCEPSYDLRGAASLHCTPQGDWSP**EAPRCTVKS**
CDDFL**GQLPHGRVL**LPLNLQLGAKVSFVCDEGFRLKGRSASHCVLAGMKALWNSSVPVCE
QIFCPNPPAILNGRHTGTPFGDIPYGKEISYACDTHPDRGMTFNLIGESSIRCTSDPQGN
GVWSSPAPRCELSVP**AACPHPPKI**QNGHYIGGHVSLYLPGMTISYICDPGYLLVGKGFIF
CTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEM**KKVYHYGDYVTLK**CEDGYTLEGSPWS
QCQADDRWDPPLAKC**TSRTHD**ALIVGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKE
VAIHLHSQGGSSVHPRTLQTNEENSRVLP

VAR_013819, CA1370009, RCV000018595, rs2274567, 1658, H>R, Malaria, severe, resistance to (ClinVar)[By similarity]

>sp|Q02985|FHR3_HUMAN Complement factor H-related protein 3 OS=Homo sapiens OX=9606 GN=CFHR3 PE=1 SV=2
MLLLINVILTLWVSCANGQVKPCDF**PDIKHGGLF**HEN**MRRPYFPVAVGKYYSYY**CDEHFE

TPSGSYWDYIHCTQNGWSPAVPC**LRKCYFPYL**ENG**YNQNYGRKF**VQGNSTEVACHPGYGL
PKAQTTVTCTEKGWS**PTPRCIRVR**TCSKSDIEIENGFISESSSIYILNKEIQYKCKPGYA
TADGNSSGSITCLQNGWSAQPICINSSEKCGPPPPISNGDTTSFLLKVYVPQSRVEYQCQ
PYYELQGSNYVTCSNGEWS**EPPRCIHPCIITE**ENMNKNNIKLKGR**SDRKYYAKTG**DTIEF
MCKLGYNANTSILS**FQAVCREGI**VEYPRCE

CA1306293, RCV000626208, rs745503234, 268, C>F, Age related macular degeneration 1 (ClinVar)

>sp|Q02985-2|FHR3_HUMAN Isoform 2 of Complement factor H-related protein 3 OS=Homo sapiens OX=9606 GN=CFHR3
MLLLINVILTLWVSCANGQVKPCDF**PDIKHGGLF**HEN**MRRPYFPVAVGKYYSYY**CDEHFE
TPSGSYWDYIHCTQNGWSPAVPC**LRKCYFPYL**ENG**YNQNYGRKF**VQGNSTEVACHPGYGL
PKAQTTVTCTEKGWSPTPRCIRVNSSEKCGPPPPISNGDTTSFLLKVYVPQSRVEYQCQP
YYELQGSNYVTCSNGEWS**EPPRCIHPCII**TEENMNKNNIKLKGR**SDRKYYAKTG**DTIEFM
CKLGYNANTSILS**FQAVCREGI**VEYPRCE

CA1306293, RCV000626208, rs745503234, 207, C>F, Age related macular degeneration 1 (ClinVar)

>sp|Q9BXR6|FHR5_HUMAN Complement factor H-related protein 5 OS=Homo sapiens OX=9606 GN=CFHR5 PE=1 SV=1
MLLLFSVILISWVSTVGGEGTLCD**FPKIHHGFLY**DEEDYNPFSQVPTGEVFYYSCEYNFV
SPSKSFWTRITCTEEGWSPTPKCLRMCSFPF**VKNGHSESS**GLIHLEGDTVQIICNTGYSL
QNNEKNISCVERGWS**TPPICSFTKGECHVPIL**EANVDAQPKKESYKVGDVLKFSCRKNLI
RVGSDSVQCYQFGWSPNFPTCKGQVRSCGPPPQLSNGEVKEIRKEEYGHNEVVEYDCNPN
FIINGPKKIQCVDGEWTTLPTCVEQVKTCGYIPELEYGYVQPSVPPYQHGVSVEVNCRNE
YAMIGNNMITCINGIWTELPM**CVATHQLKR**CKIAGVNIKTLLKLSG**KEFNHNSRI**RYRCS
DIFRYRHSVCINGKWNPEVDCTEKREQFCPPPPQIPNAQNMTTTVNYQDGEKVAVLCKEN
YLLPEAKEIVCKDGRWQ**SLPRCVEST**AYCGPPPSINNGDTTSFPLSVYPPGSTVTYRCQS
FYKLQGSVTVTCRNKQWSEPPRCLDPCVVSEENMNKNNIQLKWRNDGKLYAKTGDAVEFQ
CKFPHKAMISSPPFRAICQEGKFEYPICE

RCV001097650, rs1653577983, 26, P>S, CFH-Related Dense Deposit Disease/Membranoproliferative Glomerulonephritis Type II (ClinVar)
CA1307751, RCV001101405, RCV001819805, RCV002069699, rs181511327, 144, K>N, CFH-Related Dense Deposit Disease/Membranoproliferative Glomerulonephritis Type II (ClinVar)

Defects in CFHR5 have been found in patients with atypical hemolytic uremic syndrome and may contribute to the disease. Atypical hemolytic uremic syndrome is a complex genetic disease characterized by microangiopathic hemolytic anemia, thrombocytopenia, renal failure and absence of episodes of enterocolitis and diarrhea. In contrast to typical hemolytic uremic syndrome, atypical forms have a poorer prognosis, with higher death rates and frequent progression to end-stage renal disease. Susceptibility to the development of atypical hemolytic uremic syndrome can be conferred by mutations in various components of or regulatory factors in the complement cascade system. Other genes may play a role in modifying the phenotype.

10 unique entries/genes

28 sequences

Species with detected PTMs (PhosphoSitePlus)

>sp|P01024|CO3_HUMAN Complement C3 OS=Homo sapiens OX=9606 GN=C3 PE=1 SV=2
MGPTSGPSLLLLLLTHLPLALGSPMYSIITPNILRLESEETMVLEAHDAQGDVPVTVTVH
DFPGKKLVLSSEKTVLTPATNHMGNVTFTIPANREFKSEKGRNKFVTVQATFGTQVVEKV
VLVSLQSGYLFIQTDKTIYTPGSTVLYRIFTVNHKLLPVGRTVMVNIENPEGIPVKQDSL
SSQNQLGVLPLSWDIPELVNMGQWKIRAYYENSPQQVFSTEFEVKEYVLPSFEVIVEPTE
KFYYIYNEKGLEVTITARFLYGKKVEGTAFVIFGIQDGEQRISLPESLKRIPIEDGSGEV
VLSRKVLLDGVQNPRAEDLVGKSLYVSATVILHSGSDMVQAERSGIPIVTSPYQIHFTKT
PKYFKPGMPFDLMVFVTNPDGSPAYRVPVAVQGEDTVQSLTQGDGVAKLSINTHPSQKPL
SITVRTKKQELSEAEQATRTMQALPYSTVGNSNNYLHLSVLRTELRPGETLNVNFLLRMD
RAHEAKIRYYTYLIMNKGRLLKAGRQVREPGQDLVVLPLSITTDFIPSFRLVAYYTLIGA
SGQREVVADSVWVDVKDSCVGSLVVKSGQSEDRQPVPGQQMTLKIEGDHGARVVLVAVDK
GVFVLNKKNKLTQSKIWDVVEKADIGCTPGSGKDYAGVFSDAGLTFTSSSGQQTAQRAEL
QCPQPAARRRRSVQLTEKRMDKVGKYPKELRKCCEDGMRENPMRFSCQRRTRFISLGEAC
KKVFLDCCNYITELRRQHARASHLGLARSNLDEDIIAEENIVSRSEFPESWLWNVEDLKE
PPKNGISTKLMNIFLKDSITTWEILAVSMSDKKGICVADPFEVTVMQDFFIDLRLPYSVV
RNEQVEIRAVLYNYRQNQELKVRVELLHNPAFCSLATTKRRHQQTVTIPPKSSLSVPYVI
VPLKTGLQEVEVKAAVYHHFISDGVRKSLKVVPEGIRMNKTVAVRTLDPERLGREGVQKE
DIPPADLSDQVPDTESETRILLQGTPVAQMTEDAVDAERLKHLIVTPSGCGEQNMIGMTP
TVIAVHYLDETEQWEKFGLEKRQGALELIKKGYTQQLAFRQPSSAFAAFVKRAPSTWLTA
YVVKVFSLAVNLIAIDSQVLCGAVKWLILEKQKPDGVFQEDAPVIHQEMIGGLRNNNEKD
MALTAFVLISLQEAKDICEEQVNSLPGSITKAGDFLEANYMNLQRSYTVAIAGYALAQMG
RLKGPLLNKFLTTAKDKNRWEDPGKQLYNVEATSYALLALLQLKDFDFVPPVVRWLNEQR
YYGGGYGSTQATFMVFQALAQYQKDAPDHQELNLDVSLQLPSRSSKITHRIHWESASLLR
SEETKENEGFTVTAEGKGQGTLSVVTMYHAKAKDQLTCNKFDLKVTIKPAPETEKRPQDA
KNTMILEICTRYRGDQDATMSILDISMMTGFAPDTDDLKQLANGVDRYISKYELDKAFSD
RNTLIIYLDKVSHSEDDCLAFKVHQYFNVELIQPGAVKVYAYYNLEESCTRFYHPEKEDG
KLNKLCRDELCRCAEENCFIQKSDDKVTLEERLDKACEPGVDYVYKTRLVKVQLSNDFDE
YIMAIEQTIKSGSDEVQVGQQRTFISPIKCREALKLEEKKHYLMWGLSSDFWGEKPNLSY
IIGKDTWVEHWPEEDECQDEENQKQCQDLGAFTESMVVFGCPN

From PhosphositePlus (Minimum 5 references)
S297, Phosphorylation
S672, Phosphorylation

>sp|P08603|CFAH_HUMAN Complement factor H OS=Homo sapiens OX=9606 GN=CFH PE=1 SV=4
MRLLAKIICLMLWAICVAEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLG
NVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQL
LGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNS
GYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMG
YEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYP
ATRGNTAKCTSTGWIPAPRCTLKPCDYPDIKHGGLYHENMRRPYFPVAVGKYYSYYCDEH
FETPSGSYWDHIHCTQDGWSPAVPCLRKCYFPYLENGYNQNYGRKFVQGKSIDVACHPGY
ALPKAQTTVTCMENGWSPTPRCIRVKTCSKSSIDIENGFISESQYTYALKEKAKYQCKLG
YVTADGETSGSITCGKDGWSAQPTCIKSCDIPVFMNARTKNDFTWFKLNDTLDYECHDGY
ESNTGSTTGSIVCGYNGWSDLPICYERECELPKIDVHLVPDRKKDQYKVGEVLKFSCKPG
FTIVGPNSVQCYHFGLSPDLPICKEQVQSCGPPPELLNGNVKEKTKEEYGHSEVVEYYCN
PRFLMKGPNKIQCVDGEWTTLPVCIVEESTCGDIPELEHGWAQLSSPPYYYGDSVEFNCS
ESFTMIGHRSITCIHGVWTQLPQCVAIDKLKKCKSSNLIILEEHLKNKKEFDHNSNIRYR
CRGKEGWIHTVCINGRWDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYRDGEKVSVLCQ
ENYLIQEGEEITCKDGRWQSIPLCVEKIPCSQPPQIEHGTINSSRSSQESYAHGTKLSYT
CEGGFRISEENETTCYMGKWSSPPQCEGLPCKSPPEISHGVVAHMSDSYQYGEEVTYKCF

EGFGIDGPAIAKCLG**EKWSHPPSCIKTDCLSLP**SFENAIPMGEKKDVYKAGEQVTYTCAT
YYKMDGASNVTCINSRWT**GRPTCRDTSCVNPP**T**VQNAYIVSR**QMSKYPSGERVRYQCRSP
YEMFGDEEVMCLNGNWTEPPQCKDSTGKCGPPPPIDNGDITSFPLSVYAPASSVEYQCQN
LYQLEGNKRITCRNGQWSEP**PKCLHPCVI**SREIMENYNIALRWTA**KQKLYSR**TGESVEFV
CKRGYRL**SSRSHTLRTTCWDGK**LEYPTCAKR

From PhosphositePlus (Minimum 5 references)
T1193, Phosphorylation

>sp|P15529|MCP_HUMAN Membrane cofactor protein OS=Homo sapiens
OX=9606 GN=CD46 PE=1 SV=3
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVLPPSSTKPPALSHS
VSTSSTTKSPASSASG**PRPTYKPPV**SNYPGYPKPEEGILDSLDVWVIAVIVIAIVVGVAV
ICVVPYRYLQRRKK**K**GT**Y**LTDETHREVKFTSL

From PhosphositePlus (Minimum 5 references)
K375, Ubiquitylation
Y378, Phosphorylation

>sp|P15529-2|MCP_HUMAN Isoform B of Membrane cofactor protein
OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVLPPSSTKPPALSHS
VSTSSTTKSPASSASGPRPTYKPPVSNYPGYPKPEEGILDSLDVWVIAVIVIAIVVGVAV
ICVVPYRYLQRRKK**K**GKADGGAEYATYQTKSTTPAEQRG

From PhosphositePlus (Minimum 5 references)
K375, Ubiquitylation [By similarity]

>sp|P15529-11|MCP_HUMAN Isoform C of Membrane cofactor protein
OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVSTSSTTKSPASSAS
G**PRPTYKPPV**SNYPGYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKK**K**
GT**Y**LTDETHREVKFTSL

From PhosphositePlus (Minimum 5 references)
K360, Ubiquitylation [By similarity]
Y363, Phosphorylation [By similarity]

>sp|P15529-3|MCP_HUMAN Isoform D of Membrane cofactor protein
OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS

GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVSTSSTTKSPASSAS
G**PRPTYKPPV**SNYPGYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKK**K**
GKADGGAEYATYQTKSTTPAEQRG

From PhosphositePlus (Minimum 5 references)
K360, Ubiquitylation [By similarity]

>sp|P15529-12|MCP_HUMAN Isoform E of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSG**KPPICEKVL**CTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKG**PRPTYKPPV**SNYPG
YPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKK**K**GT**Y**LTDETHREVKFT
SL

From PhosphositePlus (Minimum 5 references)
K345, Ubiquitylation [By similarity]
Y348, Phosphorylation [By similarity]

>sp|P15529-4|MCP_HUMAN Isoform F of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSG**KPPICEKVL**CTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKG**PRPTYKPPV**SNYPG
YPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKK**K**GKADGGAEYATYQTK
STTPAEQRG

From PhosphositePlus (Minimum 5 references)
K345, Ubiquitylation [By similarity]

>sp|P15529-13|MCP_HUMAN Isoform G of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVLPPSSTKPPALSHS
VSTSSTTKSPASSASGYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKK
KGT**Y**LTDETHREVKFTSL

From PhosphositePlus (Minimum 5 references)
K361, Ubiquitylation [By similarity]
Y364, Phosphorylation [By similarity]

>sp|P15529-5|MCP_HUMAN Isoform H of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKATV**MFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVLPPSSTKPPALSHS
VSTSSTTKSPASSASGYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKK

KGKADGGAEYATYQTKSTTPAEQRG

From PhosphositePlus (Minimum 5 references)
K361, Ubiquitylation [By similarity]

>sp|P15529-14|MCP_HUMAN Isoform I of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIGKPKPYYEIGERV
DYKCKKGYFYIPPLATHTICDRNHTWLPVSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GFGKKFYYKATVMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVSTSSTTKSPASSAS
GYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKKKGTYLTDETHREVKF
TSL

From PhosphositePlus (Minimum 5 references)
K346, Ubiquitylation [By similarity]
Y349, Phosphorylation [By similarity]

>sp|P15529-6|MCP_HUMAN Isoform J of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIGKPKPYYEIGERV
DYKCKKGYFYIPPLATHTICDRNHTWLPVSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GFGKKFYYKATVMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVSTSSTTKSPASSAS
GYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVPYRYLQRRKKKGKADGGAEYATYQT
KSTTPAEQRG

From PhosphositePlus (Minimum 5 references)
K346, Ubiquitylation [By similarity]

>sp|P15529-15|MCP_HUMAN Isoform K of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIGKPKPYYEIGERV
DYKCKKGYFYIPPLATHTICDRNHTWLPVSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GFGKKFYYKATVMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKGYPKPEEGILDSLDV
WVIAVIVIAIVVGVAVICVVPYRYLQRRKKKGTYLTDETHREVKFTSL

From PhosphositePlus (Minimum 5 references)
K331, Ubiquitylation [By similarity]
Y334, Phosphorylation [By similarity]

>sp|P15529-7|MCP_HUMAN Isoform L of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIGKPKPYYEIGERV
DYKCKKGYFYIPPLATHTICDRNHTWLPVSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GFGKKFYYKATVMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKGYPKPEEGILDSLDV
WVIAVIVIAIVVGVAVICVVPYRYLQRRKKKGKADGGAEYATYQTKSTTPAEQRG

From PhosphositePlus (Minimum 5 references)
K331, Ubiquitylation [By similarity]

>sp|P15529-9|MCP_HUMAN Isoform N of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCKKGYFYIPPLATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSG**KPPICEKVL**CTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKATV**MFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKG**PRPTYKPPV**SNYPG
YPKPEEGILDSLDVWVIAVIVIAIGKQMVELNMPLTRLNQPLQQSREAE

>sp|P15529-10|MCP_HUMAN Isoform 2 of Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46
MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIG**KPKPYYEIG**ERV
DYKCK**KGYFYIPPL**ATHTI**CDRNHTWLP**VSDDACYRETCPYIRDPLNGQAVPANGTYEFG
YQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV
FEYLDAVTYSCDPAPGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS
GF**GKKFYYKAT**VMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLKVLPPSSTKP**PALSHS**
TTKSPASSASGPRPTYKPPVSNYPGYPKPEEGILDSLDVWVIAVIVIAIVVGVAVICVVP
YRYLQRRKK**K**GT**Y**LTDETHREVKFTSL

From PhosphositePlus (Minimum 5 references)
K370, Ubiquitylation [By similarity]
Y373, Phosphorylation [By similarity]

3 unique entries/genes
16 sequences