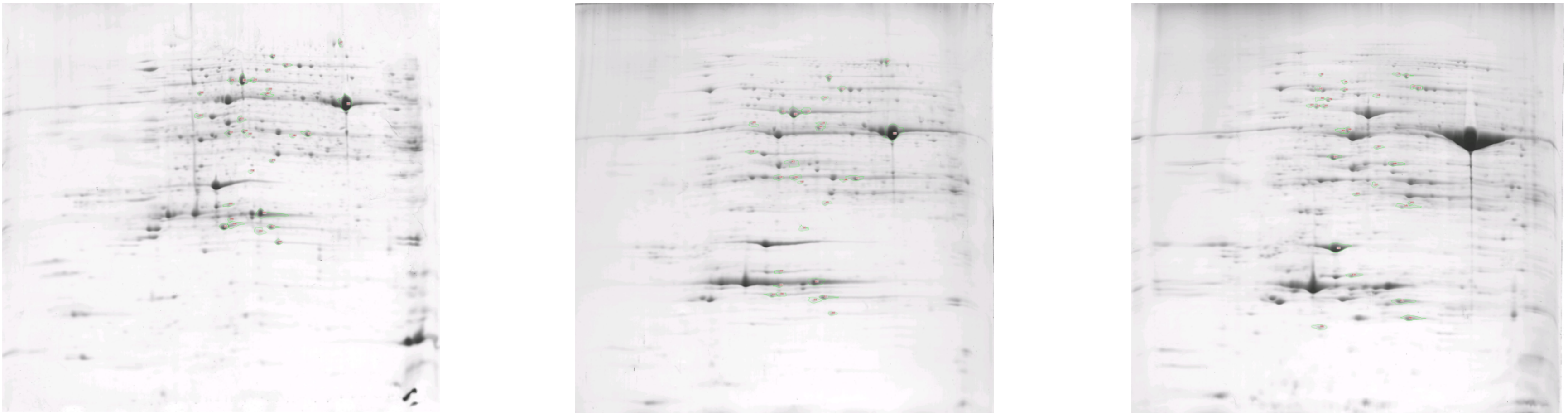
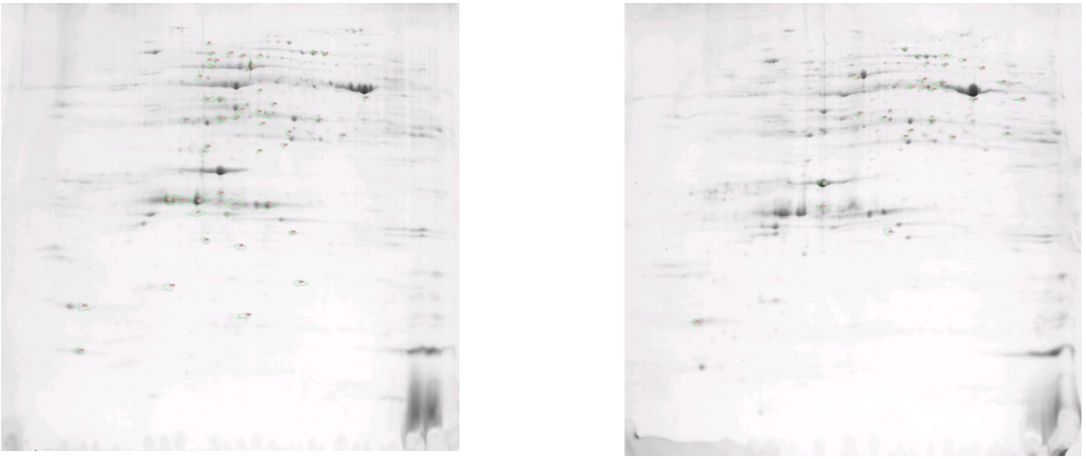
Supplementary Materials



Control HRW SNP



HRW+NaN_3 HRW+Tungstate

Figure S1. 2-DE gel images showed to employe protein spot densitometric analysis.

Table S1. The sequences of all unique peptides matched to each identified differential protein.

Spot No.	Protein name	Species	Pep. Count	Start Seq.	End Seq.	Sequences of unique peptides
201	ATP synthase CF1 alpha subunit (chloroplast)	*Lilium superbum*	21	166	172	ELIIGDR
				17	22	IEQYNR
				273	279	QMSLLLR
				406	413	ATQNQLAR
				120	128	GEISASESR
				6	14	ADEISNIIR
				15	22	ERIEQYNR
				481	491	TLTEQAEALLK
				129	140	LIESPAPGIISR
				108	119	VINALAKPIDGR
				177	188	TAVATDTILNQK
				256	266	HTLIIYDDLSK
				95	107	IAQIPVSEAYLGR
				255	266	RHTLIIYDDLSK
				468	480	NKPQFQEIISSTK
				285	297	EAYPGDVFYLHSR
				26	41	IVNTGTVLQVGDGIAR
				26	41	IVNTGTVLQVGDGIAR
				142	162	SVYEPLQTGLIAIDAMIPIGR
				385	405	LELAQFAELEAFAQFASD LDK
				141	162	RSVYEPLQTGLIAIDAMIPI
259	ATP synthase alpha subunit, partial (mitochondrion)	*Erythronium dens-canis*	10	110	119	AVDSLVPIGR
				87	97	VEVKAPGIIER
				134	145	TAIAIDTILNQK
				248	260	EAFPGDVFYLHSR
				49	64	TGSIVDVPAGKALLGR
				215	229	DNGMHALIIYDDLSK
				151	166	DVNPLYCVYVAIGQKR
				134	150	TAIAIDTILNQKQMNSR
				99	119	SVHEPMQTGLKAVDSLVPIG
				146	165	QMNSRDVNPLYCVYVAIGQK
202	ATP synthase CF1 alpha subunit (chloroplast)	*Lilium superbum*	22	166	172	ELIIGDR
				17	22	IEQYNR
				273	279	QMSLLLR
				406	413	ATQNQLAR
				120	128	GEISASESR
				6	14	ADEISNIIR
				15	22	ERIEQYNR
				481	491	TLTEQAEALLK
				129	140	LIESPAPGIISR
				108	119	VINALAKPIDGR
				177	188	TAVATDTILNQK
				256	266	HTLIIYDDLSK
				129	141	LIESPAPGIISRR
				95	107	IAQIPVSEAYLGR
				273	284	QMSLLLRRPPGR
				255	266	RHTLIIYDDLSK
				468	480	NKPQFQEIISSTK
				285	297	EAYPGDVFYLHSR
				26	41	IVNTGTVLQVGDGIAR
				26	41	IVNTGTVLQVGDGIARGR
				142	162	SVYEPLQTGLIAIDAMIPIGR
				141	162	RSVYEPLQTGLIAIDAMIPIGR
908	Photosystem II oxygen evolving complex protein 2 precursor	*Fritillaria agrestis*	5	117	126	EVEFPGQVLR
				234	244	LYICKAQAGDK
				27	42	LVPTIKPSQLICRAQK
				92	111	TNTDFLPYTGDGFNLLIPAK
				2	26	ASSACFLLHHAPSTPATTSRTPSHR
284	ATP synthase CF1 beta subunit, partial (plastid)	Lilium superbum	15	192	205	AHGGVSVFGGVGER
				487	498	AMNLEGESNLKK
				278	291	FVQAGSEVSALLGR
				249	261	VGLTALTMAEYFR
				232	246	VALVYGQMNEPPGAR
				3	18	INPTTSGLGVSTLEEK
				2	18	RINPTTSGLGVSTLEEK

				110	127	IFNVLGEPVDNLGPVDTR
				128	145	TTSPIHRSAPAFIQLDTK
				360	378	GIYPAVDPLDSTSTMLQPR
				88	109	GMEVIDTGTPLSVPVGGATLGR
				292	312	MPSAVGYQPTLSTEMGS LQER
				53	73	DTVGPQINVTCEVQQLLGNNR
				179	205	TVLIMELINNIAKAHGGVS
294	Ribulose-1,5-bisphosphate carboxulase/oxygenase large subunit, partial (chloroplast)	*Heloniopsis kawanoi*	29	301	307	NHGMHFR
				183	189	AVYECLR
				301	307	NHGMHFR
				291	298	AMHAVIDR
				28	36	DTDILAAFR
				417	426	VALEACVQAR
				299	307	QKNHGMHFR
				281	290	DNGLLLHIHR
				435	445	EGNEIIREASK
				213	222	FLFCAEALYK
				335	345	EMTLGFVDLLR
				301	311	NHGMHFRVLAK
				17	27	LTYYTPDYETK
				130	141	LEDLRIPTSYSK
				197	208	DDENVNSQPFMR
				142	154	TFQGPPHGIQVER
				160	172	YGRPLLGCTIKPK
				211	222	DRFLFCAEALYK
				446	458	WSPELAAACEVWK
				142	156	TFQGPPHGIQVERDK
				446	460	WSPELAAACEVWKEI
				232	247	GHYLNATAGTCEEMIK
				330	345	LEGEREMTLGFVDLLR
				232	248	GHYLNATAGTCEEMIKR
				335	351	EMTLGFVDLLRDDFIEK
				190	208	GGLDFTKDDENVNSQPFMR
				17	36	LTYYTPDYETKDTDILAAFR
				254	280	ELGVPIVMHDYLTGGFTANTSLSHYCR
				37	74	VTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR
180	ATP synthase CF1 alpha subunit (chloroplast)	*Lilium superbum*	21	166	172	ELIIGDR
				17	22	IEQYNR
				273	279	QMSLLLR
				406	413	ATQNQLAR
				120	128	GEISASESR
				6	14	ADEISNIIR
				15	22	ERIEQYNR
				481	491	TLTEQAEALLK
				129	140	LIESPAPGIISR
				108	119	VINALAKPIDGR
				177	188	TAVATDTILNQK
				256	266	HTLIIYDDLSK
				95	107	IAQIPVSEAYLGR
				255	266	RHTLIIYDDLSK
				468	480	NKPQFQEIISSTK
				285	297	EAYPGDVFYLHSR
				26	41	IVNTGTVLQVGDGIAR
				26	41	IVNTGTVLQVGDGIAR
				142	162	SVYEPLQTGLIAIDAMIPIGR
				385	405	LELAQFAELEAFAQFASD LDK
				141	162	RSVYEPLQTGLIAIDAMIPI
896	Carbonic anhydrase	*Musa acuminata subsp.*	4	37	46	FLVFACADSR
				1	13	MDPVERLTSGFER
				94	109	VEYIVVIGHSRCGGIK
				47	64	VCPSVVLSFQPGEAFIVR
716	PDZ domain-containing protein	*Cynara cardunculus var.*	6	152	157	TMYTIR
				160	169	IGPLLMRMQK
				288	297	SEEFEPLMKK
				199	209	VREIQMQNYLR
				298	312	YDESFINENALNAIK
				297	312	KYDESFINENALNAIK

913	Chlorophyll a-b binding protein, chloroplastic	*Musa acuminata subsp.*	3	184 171 107	191 183 123	QYFLGLEK RFQDWANPGSMGK YAMLGAVGAIAPEIFGK
431	Actin	*Lilium davidii var. Davidii*	15	21 42 199 31 362 87 180 241 194 218 71 98 294 293 150	30 52 208 41 374 97 193 256 208 233 86 115 314 314 179	AGFAGDDAPR HTGVMVGMGQK GYMFTTTAER AVFPSIVGRPR AEFDESGPAIVHR IWHHTFYNELR LDLAGRDLTDSLMK NYELPDGQVITIGAER ILTERGYMFTTTAER LAYVALDYEQELETAK YPIEHGIVSNWDDMEK VAPEEHPVLLTEAPLNPK DLYGNIVLSGGSTMFPGIADR KDLYGNIVLSGGSTMFPGIADR TTGIVLDSGDGVSHTVPIYEGYALPHAILR
511	Glutamine synthetase	*Tulipa pulchella*	5	296 279 333 141 53	305 291 353 165 79	HETADINTFK EHISAYGEGNERR RPASNMDPYVVTSMIAETTLL WPIGWPIGGYPGPQGPYYCSAGADK WNYDGSSTGQAPGEDSEVILYPQAIFK
479	Actin	*Lilium regale*	16	21 42 199 31 362 87 180 199 241 218 71 98 2 294 293 150	30 52 208 41 374 97 193 212 256 233 86 115 20 314 314 179	AGFAGDDAPR HTGVMVGMGQK GYMFTTTAER AVFPSIVGRPR AEFDESGPAIVHR IWHHTFYNELR LDLAGRDLTDSLMK GYMFTTTAEREIVR NYELPDGQVITIGAER LAYVALDYEQELETAK YPIEHGIVSNWDDMEK VAPEEHPVLLTEAPLNPK ADAEDIQPLVCDNGTGMVK DLYGNIVLSGGSTMFPGIADR KDLYGNIVLSGGSTMFPGIADR TTGIVLDSGDGVSHTVPIYEGYALPHAILR
492	Monodehydroascorbate reductase	*Lilium longiflorum*	14	305 53 311 77 422 40 8 63 166 287 202 249 413 184	310 62 319 85 433 52 22 76 183 304 218 269 433 201	LYNEIR AYLFPQGAAR RVEHVDHAR LLPEWYTEK QLITEGLNFASK EAVAPYERPALSK YIIIGGGVSAGYAAR LPGFHVCVGSGGER AVIVGGGYIGLELGATLK TSITDVYAVGDVATFPLK LFTAEIAAFYEGYYANK VLDADIVVVGVGGRPLTTLFK LQPAVADPKQLITEGLNFASK INNLDVTMVYPEPWCMPR
220	ATP synthase CF1 alpha subunit (chloroplast)	*Lilium superbum*	19	166 17 406 6 15 481 129 108 177 256 191	172 22 413 14 22 491 140 119 188 266 202	ELIIGDR IEQYNR ATQNQLAR ADEISNIIR ERIEQYNR TLTEQAEALLK LIESPAPGIISR VINALAKPIDGR TAVATDTILNQK HTLIIYDDLSK NVICVYVAIGQK

				95 468 189 285 26 142 385 141	107 480 202 297 41 162 405 162	IAQIPVSEAYLGR NKPQFQEIISSTK GKNVICVYVAIGQK EAYPGDVFYLHSR IVNTGTVLQVGDGIAR SVYEPLQTGLIAIDAMIPIGR LELAQFAELEAFAQFASDLDK RSVYEPLQTGLIAIDAMIPIGR
988	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast)	*Gagea wilczekii*	12	13 284 115 2 182 127 196 300 217 431 266 22	21 292 126 12 193 139 207 314 232 446 283 59	DTDILAAFR QKNHGIHFR LEDLRIPASYSK LTYYTPDYETK DDENVNSQPFMR TFQGPPHGIQVER DRFLFCAEAIYK MSGGDHIHSGTVVGK GHYLNATAGTCEEMMK WSPELAAACEVWKEIK DNGLLLHIHRAMHAVIDR VTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR
1060	Pathogenesis-related protein 10	*Lilium regale*	7	67 19 53 77 53 31 69	76 30 66 92 68 52 92	ERLDFVDHEK AAILDWHTLGPK QLNFTSVMPFSYVK FECQSTIIEGGHLGTR QLNFTSVMPFSYVKER LVPEIISSGTGESGDGGAGSVR LDFVDHEKFECQSTIIEGGHLGTR
136	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast)	*Trillium camschatcense*	9	1 8 279 122 191 212 212 315 295	7 16 287 134 202 227 228 331 314	TPDYTPK DTDILAAFR QKNHGIHFR TFQGPPHGIQVER DRFLFCAEALYK GHYLNATAGTCEEMMK GHYLNATAGTCEEMMKR EMTLGFVDLLRDDVVLK MSGGDHIHSGTVVGKLEGER
985	ATP synthase beta subunit, partial (chloroplast)	*Fritillaria acmopetala*	16	203 187 273 374 244 227 1 257 105 355 203 83 287 48 350 452	212 200 286 385 256 241 17 272 122 373 220 104 307 68 373 483	EGNDLYMEMK AHGGVSVFGGVGER FVQAGSEVSALLGR IVGEEHYEIAQR VGLTALTMAEYFR VALVYGQMNEPPGAR TTSGLGVSTLEEKNLGR DVNEQDVLLFIDNIFR IFNVLGEPVDNLGPVDTR GIYPAVDPLDSTSTMLQPR EGNDLYMEMKESGVINEK GMEVIDTGTPLSVPVGGATLGR MPSAVGYQPTLSTEMGSLQER DTVGPQINVTCEVQQLLGNNR GLAAKGIYPAVDPLDSTSTMLQPR GFQLILSGELDSLPEQAFYLVGNIDEATAKAM
142	ATP synthase CF1 alpha subunit (chloroplast)	*Ripogonum album*	10	6 129 129 95 468 285 26 1 142 468	14 140 141 107 480 297 41 14 162 491	ADEISNIIR LIESPAPGIISR LIESPAPGIISRR IAQIPVSEAYLGR NKPQFQEIISSTK EAYPGDVFYLHSR IVNTGTVLQVGDGIAR MVTLRADEISNIIR SVYEPLQTGLIAIDSMIPIGR NKPQFQEIISSTKTFTEQAEALLK
415	Glutamine synthetase	*Erythranthe guttata*	7	295 278 276 18	304 289 289 33	HETADINTFK EHIAAYGEGNER HKEHIAAYGEGNER IIAEYVWIGGSGMDLR

				332	355	RPASNMDPYIVTSMIAETTILGKQ
				84	111	GNNILVMCDAYTPAGVPIPGNNRHNAAK
				52	78	WNYDGSSTGQAPGEDSEVILYPQAIFK
405	6-phosphogluconate dehydrogenase, decarboxylating	*Citrus sinensis*	13	26	34	GFPISVYNR
				353	361	SIEKGWDLK
				292	300	FLSGLKEER
				445	454	LPANLVQAQR
				455	464	DYFGAHTYER
				339	350	ICSYAQGMNLIR
				465	477	VDMSGSFHTEWFK
				339	352	ICSYAQGMNLIRAK
				79	96	AGSPVDQTIKTLSVYMEK
				97	113	GDCIIDGGNEWYENTER
				209	227	SVGKLSNEELQQVFSEWNK
				269	291	WTVQQAADLSVAAPTIESSLDAR
				416	441	VVCLAINSGISTPGMSSSLAYFDTYR
444	Elongation factor tu	*Vigna angularis var. Angularis*	14	323	333	VGETVDLVGLR
				472	483	TVGAGVIQSIIE
				121	131	YDEIDAAPEER
				120	131	KYDEIDAAPEER
				199	211	QVGVPNMVVFLNK
				319	333	GTIRVGETVDLVGLR
				349	364	ILDEALAGDNVGLLLR
				150	164	HYAHVDCPGHADYVK
				134	149	GITINTATVEYETENR
				83	99	KKPHVNIGTIGHVDHGK
				44	60	LTTLSSSFLQPSTVLRR
				100	119	TTLTAALTMALASLGNSA
				212	229	QDQVDDEELLQLVELEVR
				165	191	NMITGAAQMDGAILVVSGADGPMPQTK
868	Chlorophyll a-b binding protein, chloroplastic	*Kalanchoe fedtschenkoi*	7	98	105	ELEVIHSR
				127	134	FGEAVWFK
				96	105	NRELEVIHSR
				106	122	WAMLGALGCVFPELLSR
				38	56	TGAKPKPVSSGSPWYGPDR
				239	267	GPLENLADHLADPVNNNAWAYATNFVPGK
				59	95	YLGPFSGEAPSYLTGEFPGDYGWDTAGLSADPETFAK
517	Glutamine synthetase	*Lolium perenne*	10	279	290	EHIAAYGEGNER
				259	272	KDGGFEVIVAAVEK
				277	290	HKEHIAAYGEGNER
				19	34	IIAEYIWIGGSGMDLR
				1	18	MALLTDLLNLDLSGSTEK
				292	311	LTGKHETADIHTFSWGVANR
				296	316	HETADIHTFSWGVANRGASIR
				85	106	GNNILVMCDCYTPAGEPIPTNK
				85	107	GNNILVMCDCYTPAGEPIPTNKR
				53	79	WNYDGSSTGQAPGEDSEVILYPQAIFK
866	Chlorophyll a-b binding protein, chloroplastic	*Carya cathayensis*	5	98	105	ELEVIHSR
				127	134	FGEAVWFK
				38	56	TAGRPKPVSSGSPWYGPDR
				218	238	NGRLAMFSMFGFFVQAIVTGK
				239	267	GPLENLADHLADPVNNNAWAYATNFVPGK
880	Beta carbonic anhydrase 3	*Arabidopsis thaliana*	6	82	91	FLVFACADSR
				110	120	NIANMVPPYDK
				155	167	GLMAIEDNTAPTK
				77	91	SQTPKFLVFACADSR
				187	203	QDCKDLSFEDQCTNCEK
				232	250	GAHYDFVKGTFDLWELDFK
864	Chlorophyll a-b binding protein,	*Kalanchoe fedtschenkoi*	10	127	134	FGEAVWFK
				96	105	NRELEVIHSR

	chloroplastic			123	134	NGVKFGEAVWFK
				106	122	WAMLGALGCVFPELLSR
				106	122	WAMLGALGCVFPELLSR
				38	56	TGAKPKPVSSGSPWYGPDR
				221	238	LAMFSMFGFFVQAIVTGK
				239	267	GPLENLADHLADPVNNNAWAYATNFVPGK
				178	212	VAGGPLGEVVDPLYPGGSFDPLGLADDPEAFAELK
				59	95	YLGPFSGEAPSYLTGEFPGDYGWDTAGLSADPETFAK
860	Carbonic anhydrase	*Zea mays*	10	474	482	KPELFGPLK
				27	39	LRPPGSGSSGTPR
				530	545	YTGIGSAIEYAVCALK
				311	326	AFTVRNIAAMVPGYDK
				528	545	TKYTGIGSAIEYAVCALK
				21	39	AVLLLRLRPPGSGSSGTPR
				392	408	KEHASVPFDDQCSILEK
				8	26	ATTSSIVPACHPRAVLLLR
				593	609	KEHASVPFDDQWSILEK
				165	185	DGAPDNFTFVEDWVRIGSPAK
542	Ribulose bisphosphate carboxylase/oxygenase activase	*Medicago truncatula*	15	354	360	VYDDEVR
				305	311	FYWAPTR
				174	183	SFQCELVFAK
				56	66	VSAKIDYNEEK
				305	314	FYWAPTRDDR
				361	373	NWISGIGVESIGK
				312	323	DDRVGVCQGIFR
				361	374	NWISGIGVESIGKR
				418	433	YLSEAALGDANDDAIK
				224	238	MCCLFINDLDAGAGR
				1	17	MATSVTIVGAINMAQLK
				335	351	IVDTFPGQSIDFFGALR
				222	238	GKMCCLFINDLDAGAGR
				280	298	VPIIVTGNDFSTLYAPLIR
				184	206	MGISPIMMSAGELESGNAGEPAK
1037	Type II peroxiredoxin	*Medicago truncatula*	10	214	222	STLVSNMHR
				185	195	YALLAEDGVVK
				40	52	FNSKPLRFSSSPK
				47	62	FSSSPKISATISVGDK
				10	25	LLSSSTTTSLLSPKTK
				214	228	STLVSNMHRQVMQTK
				164	181	AIGVELDLSDKPVGLGVR
				123	139	GIDTIACISVNDAFVMK
304	ATP synthase CF1 beta subunit, partial (plastid)	*Lilium superbum*	28	146	154	LSIFETGIK
				155	163	VVDLLAPYR
				135	145	SAPAFIQLDTK
				76	87	AVAMSATDGLMR
				192	205	AHGGVSVFGGVGER
				487	498	AMNLEGESNLKK
				278	291	FVQAGSEVSALLGR
				379	390	IVGEEHYEIAQR
				179	191	TVLIMELINNIAK
				206	217	TREGNDLYMEMK
				74	87	VRAVAMSATDGLMR
				232	246	VALVYGQMNEPPGAR
				23	39	IAQIIGPVLDVVFPPGK
				232	248	VALVYGQMNEPPGARMR
				1	18	MRINPTTSGLGVSTLEEK
				262	277	DVNEQDVLLFIDNIFR
				110	127	IFNVLGEPVDNLGPVDTR
				360	378	GIYPAVDPLDSTSTMLQPR
				88	109	GMEVIDTGTPLSVPVGGATLGR
				400	418	ELQDIIAILGLDELSEEDR
				53	73	DTVGPQINVTCEVQQLLGNNR
				292	312	MPSAVGYQPTLSTEMGS
				398	418	YKELQDIIAILGLDELSEEDR
				51	73	GRDTVGPQINVTCEVQQLLGNNR
				53	75	DTVGPQINVTCEVQQLLGNNRVR

				400	423	ELQDIIAILGLDELSEEDRLTVAR
				457	486	GFQLILSGELDGLPEQAFYLVGNIDEATAK
				318	354	EGSITSIQAVYVPADDLTDPAPAATFAHLDATTVLSR
964	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast)	*Cardiocrinum giganteum var.*	12	13	21	DTDILAAFR
				444	451	EIKFEFEP
				198	207	FLFCAEAIYK
				420	430	EGNEIIREACK
				2	12	LTYYTPDYETK
				164	174	NYGRAVYECLR
				127	139	TFQGPPHGIQVER
				300	314	MSGGDHIHSGTVVGK
				1	12	KLTYYTPDYETK
				217	232	GHYLNATAGTCEEMIK
				427	443	EACKWSPELAAACEVWK
				22	59	VTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR
299	ATP synthase CF1 beta subunit, partial (plastid)	*Lilium superbum*	21	146	154	LSIFETGIK
				146	145	SAPAFIQLDTK
				146	205	AHGGVSVFGGVGER
				146	498	AMNLEGESNLKK
				146	291	FVQAGSEVSALLGR
				146	390	IVGEEHYEIAQR
				146	261	VGLTALTMAEYFR
				146	52	MPNIYNALVVKGR
				146	246	VALVYGQMNEPPGAR
				146	18	INPTTSGLGVSTLEEK
				146	248	VALVYGQMNEPPGARMR
				146	277	DVNEQDVLLFIDNIFR
				146	127	IFNVLGEPVDNLGPVDTR
				146	378	GIYPAVDPLDSTSTMLQPR
				146	109	GMEVIDTGTPLSVPVGGATLGR
				146	418	ELQDIIAILGLDELSEEDR
				146	312	MPSAVGYQPTLSTEMGSLQER
				146	73	DTVGPQINVTCEVQQLLGNNR
				146	418	YKELQDIIAILGLDELSEEDR
				146	73	GRDTVGPQINVTCEVQQLLGNNR
				146	354	EGSITSIQAVYVPADDLTDPAPAATFAHLDATTVLSR
130	70 kda heat shock protein	*Sandersonia aurantiaca*	3	234	244	NALENYAYNMR
				20	36	MDKSTVHDVVLVGGSTR
				119	141	EQVFSTYSDNQPGVLIQVYEGER
633	NADP-dependent alkenal double bond reductase P2	*Morus notabilis*	7	222	231	FGFDEAFNYK
				97	108	TLQPITGYGVAK
				2	12	AEVINKQVLLR
				46	56	NLYLSCDPYMR
				8	20	QVLLRDYVSGSAK
				46	56	NLYLSCDPYMR
				46	58	NLYLSCDPYMRGR
				41	56	GVLVKNLYLSCDPYMR
90	Elongation factor G, mitochondrial	*Medicago truncatula*	17	265	276	AIVWGGEELGAK
				554	566	VEANVGAPQVNYR
				513	524	LAQEDPSFHFSR
				725	737	VSHKTLSPCAYIK
				582	595	QSGGQGQFADITVR
				31	42	FMGTCFRPVQSR
				413	429	VYSGKLTAGSYVLNSNK
				551	566	EYKVEANVGAPQVNYR
				142	158	GITITSAATTTFWDNHR
				330	348	GSIAATFVPVMCGSAFKNK
				159	176	INIIDTPGHVDFTLEVER
				506	524	MAAGLVKLAQEDPSFHFSR
				627	646	GLEECMSNGVLAGFPVVDVR
				690	709	VEVVTPEEHLGDVIGDLNSR
				122	141	IGEVHEGTATMDWMEQEQER
				525	547	DEEINQTVIEGMGELHLEIIVDR
671	Cysteine synthase	*Populus*	11	293	304	LIVVVFPSFGER

		trichocarpa		159	170	VHYETTGPEIWK
				50	63	DRIGYSMIADAEAK
				265	282	EGLLVGISSGAAAAAAVK
				96	109	LIITMPASMSNERR
				35	49	IAAKLEGMEPCSSVK
				114	129	AFGAELVLTNPAKGMK
				93	108	GYKLIITMPASMSNER
				159	175	VHYETTGPEIWKGSGGK
				242	259	IVDEVVQISSDEAIETAK
				142	158	TPNAYILQQFENPSNPK
839	Putative L-ascorbate peroxidase 2, cytosolic-like	*Solanum chacoense*	9	31	38	NCAPIILR
				39	50	LAWHSAGTYDVK
				39	52	LAWHSAGTYDVKTK
				209	222	ALLEDPVFRPLVEK
				192	208	ELLSGEKEGLLQLPSDK
				68	85	HGANNGLDIAVRLLEPIK
				223	240	YAADEDAFFADYAEAHLK
				172	191	SGFEGAWTNNPLIFDNSYFK
				143	166	EVFGHMGLSDKDIVALSGGHTLGR
618	Trypsin-like serine protease	Medicago truncatula	10	325	333	VTRPILGIK
				419	428	EKIPVILEPK
				106	116	KLQTDELATVR
				158	169	DGHIVTNYHVIR
				188	201	VVGFDQDKDVAVLR
				209	225	LRPIPVGVSADLLVGQK
				207	225	DKLRPIPVGVSADLLVGQK
				226	248	VYAIGNPFGLDHTLTTGVISGLR
				135	157	QDAFTLDVLEVPQGSGSGFVWDK
				135	169	QDAFTLDVLEVPQGSGSGFVWDKDGHIVTNYHVIR
182	Ftsh-like protein pftf	*Nicotiana tabacum*	24	340	350	GTGIGGGNDER
				660	668	ETMTGDEFR
				101	109	FLEYLDKDR
				609	618	MMARNSMSEK
				338	350	QRGTGIGGGNDER
				241	251	QDFMEVVEFLK
				379	391	ADILDSALLRPGR
				241	251	QDFMEVVEFLK
				471	484	IVAGMEGTVMTDGK
				419	431	FDSDVSLEVIAMR
				457	470	TAIASKEIDDSIDR
				522	537	GLTWFIPADDPTLISK
				1	17	MATSSVCIAGNSLSTHR
				197	217	SPGGMGGPGGPGNPLAFGQSK
				1	18	MATSSVCIAGNSLSTHRR
				321	337	ENAPCIVFVDEIDAVGR
				630	646	LSDSAYEIALTHIRNNR
				319	337	AKENAPCIVFVDEIDAVGR
				432	453	TPGFSGADLANLLNEAAILAGR
				220	240	FQMEPNTGVTFDDVAGVDEAK
				113	134	VDLFENGTIAIVEAISPELGNR
				487	511	SLVAYHEVGHAICGTLTPGHDAVQK
				283	311	AIAGEAGVPFFSISGSEFVEMFVGVGASR
				351	378	EQTLNQLLTEMDGFEGNTGIIVVAATNR
				580	608	QMVVTFGMSELGPWSLMDSSAQSGDVIMR
307	ATP synthase alpha subunit, partial (mitochondrion)	*Lilium lancifolium*	13	133	139	ELIIGDR
				87	94	GALSDHER
				361	367	LELAQYR
				120	129	AVDSLVPIGR
				75	86	VVDALGVPIDGR
				109	119	SVHEPMQTGLK
				144	155	TAIAIDTILNQK
				168	178	LYCVYVAIGQK
				329	342	GIRPAINVGLSVSR
				261	273	EAFPGDVFYLHSR
				228	242	DNGMHALIIYDDLSK

				9	28	VYGLNEIQAGEMVEFASGVK
				368	389	EVAAFAQFGSDLDAATQALLNR
313	Atpb (chloroplast)	*Lilium distichum*	17	393	399	QTSQRYK
				135	145	SAPAFIQLDTK
				208	217	EGNDLYMEMK
				192	205	AHGGVSVFGGVGER
				278	291	FVQAGSEVSALLGR
				379	390	IVGEEHYEIAQR
				249	261	VGLTALTMAEYFR
				232	246	VALVYGQMNEPPGAR
				3	18	INPTTSGLGVSALEEK
				1	18	MRINPTTSGLGVSALEEK
				262	277	DVNEQDVLLFIDNIFR
				110	127	IFNVLGEPVDNLGPVDTR
				360	378	GIYPAVDPLDSTSTMLQPR
				208	225	EGNDLYMEMKESGVINEK
				88	109	GMEVIDTGTPLSVPVGGATLGR
				292	312	MPSAVGYQPTLSTEMGSLQER
				53	73	DTVGPQINVTCEVQQLLGNNR
580	Glyceraldehyde-3-phosphate dehydrogenase, partial	*Lilium regale*	12	114	125	EGAGKHIQAGAK
				261	271	TFAEEVNAAFR
				260	271	KTFAEEVNAAFR
				209	223	AAALNIVPTSTGAAK
				56	68	YDSTLGIFGADVK
				332	344	VVDLADIVANNWK
				182	195	GTMTTTHSYTGDQR
				33	48	DSPLEIIAINDTGGVK
				32	48	KDSPLEIIAINDTGGVK
				243	259	VPTPNVSVVDLVVQVSK
				318	331	VIAWYDNEWGYSQR
				280	295	GILSVCDEPLVSVDFR
349	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast)	*Cardiocrinum giganteumvar. Yunnanense*	19	168	174	AVYECLR
				13	21	DTDILAAFR
				402	411	VALEACVQAR
				284	292	QKNHGMHFR
				266	275	DNGLLLHIHR
				420	430	EGNEIIREACK
				320	330	EMTLGFVDLLR
				2	12	LTYYTPDYETK
				182	193	DDENVNSQPFMR
				127	139	TFQGPPHGIQVER
				145	157	YGRPLLGCTIKPK
				431	443	WSPELAAACEVWK
				431	446	WSPELAAACEVWKEIK
				217	233	GHYLNATAGTCEEMIKR
				427	443	EACKWSPELAAACEVWK
				320	336	EMTLGFVDLLRDDFIEK
				175	193	GGLDFTKDDENVNSQPFMR
				239	265	ELGVPIVMHDYLTGGFTANTSLSHYCR
				22	59	VTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR
489	Monodehydroascorbate reductase	*Lilium longiflorum*	18	305	310	LYNEIR
				53	62	AYLFPQGAAR
				311	319	RVEHVDHAR
				77	85	LLPEWYTEK
				27	39	QGLAPGELAIISK
				86	97	GIELLLSTEIVK
				422	433	QLITEGLNFASK
				40	52	EAVAPYERPALSK
				8	22	YIIIGGGVSAGYAAR
				63	76	LPGFHVCVGSGGER
				391	405	VVGAFLESGSPDENK
				166	183	AVIVGGGYIGLELGATLK
				225	243	GTVAVGFDSDANGDVTAVK
				287	304	TSITDVYAVGDVATFPLK
				202	218	LFTAEIAAFYEGYYANK
				249	269	VLDADIVVVGVGGRPLTTLFK
				184	201	INNLDVTMVYPEPWCMPR

				413	433	LQPAVADPKQLITEGLNF
752	Photosystem II oxygen evolving complex protein 1 precursor	*Fritillaria agrestis*	16	235	242	GSSFLDPK
				206	213	VPFLFTVK
				89	97	LTFDEIQSK
				320	329	IQGIWYAQLE
				88	97	RLTFDEIQSK
				235	242	GSSFLDPK
				262	273	GDEEELVKENIK
				245	261	GGSAGYDNAVALPAGGR
				243	261	GRGGSAGYDNAVALPAGGR
				189	205	DGIDYAAVTVQLPGGER
				33	53	AFGFDNSTAGRLTCSINSDLR
				214	234	QLVATGKPESFSGSYLVPSYR
				164	184	LTYTLDEIEGPFEVAPDGTVK
				245	269	GGSAGYDNAVALPAGGRGDEEELVK
				289	313	SKPETGEVIGVFESIQPSDTDLGSK
				189	213	DGIDYAAVTVQLPGGERVPFLFTVK
263	Dihydrolipoyl dehydrogenase	*Salvia miltiorrhiza*	6	417	427	VGKFPLLANSR
				495	507	EAAMATYDKPIHI
				482	494	TCHAHPTMSEALK
				92	104	ALLHSSHMYHEAK
				76	91	GALGGTCLNVGCIPSK
				290	314	LTIEPAAGGEQTTLEADVVLVSAGR
192	Malic enzyme	*Phaseolus angularis*	9	135	143	GLAFTEGER
				606	616	GLAFTEGER
				252	263	GLAFTEGER
				180	189	GLAFTEGER
				480	494	AIKPTVLIGSSGVGK
				630	643	AYDLGLASHLPRPK
				648	662	YAESCMYSPGYRSYR
				480	498	AIKPTVLIGSSGVGKTFTK
				2	20	SHSSGCDVSKTLGLCICER
604	604	Fructose-bis phosphate aldolase	9	240	246	TFEVAQK
				204	211	EAAWGLAR
				174	183	TAAYYQQGAR
				349	358	TWGGRPENVK
				282	293	ATPEQVADYTLK
				84	96	LASIGLENTEANR
				69	82	GILAMDESNATCGK
				83	96	RLASIGLENTEANR
				151	173	GLVPLAGSNDESWCQGLDGLASR