TABLE S1. Phosphoproteins of *Chlamydomonas reinhardtii* of known and putative function

No.	**Phosphopeptide sequence**	**Theor. mass [MH+]**	**z**	**Xcorr**	**Gene model (JGI, vs2) / EST / cp**	**Function and/or homologies of depicted proteins to proteins of other organisms including their conserved domains along with their NCBI numbers**

A. Partially or fully characterized proteins from *C. reinhardtii*

1	**FPTPPGTpQK** ***FPTpPPGTpQK***	955,11 1035,09	2 2	2,04 2,10	C_10030	gi|27542567|gb|AAO16494.1| CP29-like protein [Chlamydomonas reinhardtii]; gi|60391855|sp|Q93WD2|CB29_CHLRE chlorophyll a-b binding protein CP29; gi|15430568|dbj|BAB64419.1| light-harvesting chlorophyll-a/b binding protein Lhcb4 [C. reinhardtii]; u.a.: minor chlorophyll a-b binding protein of photosystem II
2	SSpPAPAQAAPQTGAPQPGPPR n	2064,14	3	2,84	C_20130	gi|62860034|ref|NP_001016608.1| hypothetical protein LOC549362 [Xenopus tropicalis], u.a.: novel protein (WD-repeat domain), found in centriole proteome and described as prototcilia-class FABP protein in human centrosome
3	MSILKNAGARAGSTTpSpSLGSpVTVPASGLDTR n ***PLGEMEVPSpSpIAARGMIVTSAPSpYTpSYpK n***	3247,31 3050,33	3 3	2,51 2,92	C_20170	gi|23128981|ref|ZP_00110817.1| COG2319: FOG: WD40 repeat [Nostoc punctiforme PCC 73102], located in flagella

4	**RLTGKHETpSSpMSDFSWGVANR n**	2429,57	3	3,24	C_20337	gi|1353876|gb|AAB01817.1| glutamine synthetase [Chlamydomonas reinhardtii]; u.a.: GS1, cytosolic glutamine synthetase, CO2-responsive gene, located in the flagella, identified as thioredoxin target in *C. reinhardtii*
5	**ASCAGTpACVNSFGDEQLAVDMVADKLLFEALK n**	3398,77	3	5,00	C_30202	gi|515618|emb|CAA52439.1| sedoheptulose-bisphosphatase [Chlamydomonas reinhardtii], identified as thioredoxin target in *C. reinhardtii*
6	***LLAGVAGSAATALETpAVIGSAYGMPVCECR***	2865,36	3	2,90	C_30272	gi|66775516|gb|AAY56333.1| hydroxyproline-rich glycoprotein GAS30 precursor [Chlamydomonas reinhardtii]
7	VISLLSESEVGTYVQPPTpDTpLATpLFK	3050,13	3	3,26	C_50072	gi|23128003|ref|ZP_00109860.1| COG2453: predicted protein-tyrosine phosphatase [Nostoc punctiforme PCC73102]; KOG: protein tyrosine phosphatase (CDC14), located in flagella
8	***LASSpGSVPNSpPVR n***	1235,41	2	2,09	C_50129	gi|12620209|gb|AAG60619.1| adenylate cyclase [Cryptococcus neoformans var. grubii]; gnl|CDD|37 smart00044, CYCc, adenylyl- / guanylyl cyclase, catalytic domain, located in flagella
9	***PAGTpLTpLGVTpLGRSNSMTAPCSGASTPR***	2945,01	3	2,94	C_60100	gi|23479871|gb|EAA16587.1| R27-2 protein [Plasmodium yoelii yoelii]; gnl|CDD|10914 COG1196, Smc, chromosome segregation ATPases, located in flagella
10	LVSGVSpLKELHSVATSENLKGEG	2435,61	3	2,90	C_80065	gi|54649966|dbj|BAD67134.1| Lhc-like protein Lhl1 [Chlamydomonas reinhardtii]

11	***CGAGTpNSpLYGLRGQQLSpWQSpNIATGPTAAYpYTY TpISpGFDK n***	4431,59	3	3,11	C_90101	gi|21039486|gb|AAM33652.1| mastigoneme-like protein [Chlamydomonas reinhardtii]; KOG: fibrillins and related proteins containing Ca2+-binding EGF-like domains, located in flagella
12	ASpGGRGGSpGSDVEEAGAGGDEQQGSpQSpKR n	3042,62	3	2,90	C_110095	No significant similarity found; u.a.: coiled coil protein, located in flagella
13	AAWKAPPLKATpSGTLYpK	1964,09	2	2,35	C_120103	gi|24030434|gb|AAN41372.1| dihydroxy-acid dehydratase [Arabidopsis thaliana]; CDD|25654 pfam00920, ILVD_EDD, dehydratase family, identified as thioredoxin target in C. reinhardtii
14	QELESLRSSpSpPAPASSAPAPAR n	2370,35	3	4,08	C_150094	gi|15011441|gb|AAK77552.1| LCI5 [Chlamydomonas reinhardtii]; u.a.: Lci5, low CO2 inducible
15	DYpKERLVSpSpEGTQTpVFMPQSpGYTIR	3294,11	3	2,61	C_150121	gi|50906913|ref|XP_464945.1| putative PKG-Ib [Oryza sativa (japonica cultivar-group)]; gnl|CDD|17776 cd00180, S_TKc, serine/threonine protein kinases, catalytic domain; gnl|CDD|16536 cd00143, PP2Cc, serine/threonine phosphatases, family 2C, catalytic domain; gnl|CDD|14778 cd00038, CAP_ED, effector domain of the CAP family of transcription factors, located in flagella
16	**TVLPANWRDSpLDEDEPAKPAAGR**	2491,72	3	4,41	C_150160	gi|34398358|gb|AAO22241.1| 41 kDa ribosome-associated protein precursor [Chlamydomonas reinhardtii]; u.a.: chloroplast RNA-binding protein, chloroplast ribosome-associated RAP41 stem-loop-binding protein, found in chloroplast 70 S ribosome proteome

17	***VDSpSpSpLAATpLDNLAQLAQGVTDWQAR***	3051,88	3	2,60	C_180152	gi|14334122|gb|AAK60544.1| hydroxyproline rich glycoprotein Vsp6 [Chlamydomonas reinhardtii]; c.d.: Kringle domain
18	AAVADATGAASpSAAADTpR **TSpSpSGGTAGAALTAPSAPR n**	1737,60 1722,75	3 2	2,52 2,65	C_200025	No significant similarity found; c.d: coiled coil protein, found in centriole proteome
19	ELQELVEMEVRELLSFYpK	2336,58	3	2,99	C_200083	gi|39936346|ref|NP_948622.1| elongation factor Tu [Rhodopseudomonas palustris CGA009]; u.a.: EEF1, putative mitochondrial translation factor Tu; gnl|CDD|9925 COG0050, TufB, GTPases - translation elongation factors, identified as thioredoxin target in C. reinhardtii
20	***NETAPATpGDAGLDGVAVDELPAALR***	2406,61	2	2,16	C_200196	gi|70879596|gb|EAN92756.1| hypothetical protein, conserved [Trypanosoma cruzi]; u.a.: coiled coil protein with homology to a putative transcript CG15792-PC, isoform C [Drosophila melanogaster], a hypothetical protein CE2713 [Corynebacterium efficiens YS-314] and to ciliary rootlet coiled-coil, rootletin NP_055490.2 [Homo sapiens], found in centriole proteome
21	DFDVGRTVSASVQIINRSYpK n	2336,48	3	3,08	C_270111	gi|62650163|ref|XP_575971.1| similar to hypothetical protein A530045M11 [Rattus norvegicus]; u.a.: FAP74, located in flagella

22	***PGTSGAGAGGGGGKPASpPQRGGSSpGGLAASpSATpTPR n***	3052,17	3	3,34	C_290071	gi|68353830|ref|XP_690098.1| similar to cold autoinflammatory syndrome 1 protein (cryopyrin) (NACHT-, LRR- and PYD-containing protein 3) (PYRIN-containing APAF1-like protein 1) (Angiotensin/vasopressin receptor AII/AVP-like) [Danio rerio]; c.d.: leucine-rich repeats (LRRs), ribonuclease inhibitor (RI)-like subfamily, located in flagella
23	RLSpDDEEDEVELR	1685,62	2	3,81	C_320111	gi|40714511|dbj|BAD06919.1| light-harvesting chlorophyll-a/b protein of photosystem I (Type III) [Chlamydomonas reinhardtii]
24	***IIEVLSASpEGNILEDETpAINVISpSSpK***	2759,00	3	2,66	C_360006	gi|27529748|dbj|BAA76788.2| KIAA0944 protein [Homo sapiens]; u.a.: DHC6, dynein heavy chain 6 (putative flagellar inner arm dynein heavy chain), located in flagella
25	IDVDYpRLVPPGSpAFGTpRFSFEPPAGR n ***VLTpCHIPHLDASpCEPFAR*** ***YpAVTPARGIHFGPVTpYNTASpK n***	3093,12 2072,31 2491,47	3 2 3	3,03 3,16 2,62	C_410060	gi|57087161|ref|XP_536793.1| similar to hydrocephalus-inducing protein [Canis familiaris]; u.a.: similar to mouse hydrocephaly protein hydin HY3, located in flagella
26	VSpPVPPGTpQLPIEMSpINGVPAVAACPQK n	3042,25	3	3,03	C_420012	gi|29135339|ref|NP_619615.2| polycystic kidney and hepatic disease 1-like 1 [Mus musculus]; u.a.: PKHD1-1, similar to the polycystic kidney and hepatic disease gene product fibrocystin, located in flagella
27	LTVDASVRQSSpAR n	1470,51	2	2,17	C_550085	No significant similarity found; u.a.: FAP1, located in flagella

28	WMTYSpMQEK n	1284,38	2	2,51	C_570035	gi|50057451|emb|CAH03435.1| hypothetical transmembrane protein [Paramecium tetraurelia]; u.a.: FAP113, located in flagella
29	LAGAERTpINVQDERIALLQSR	2434,63	3	3,20	C_590094	No significant similarity found; u.a.: located in flagella
30	***TpATpYpQSpIITLTpQALALWKR n***	2383,49	3	3,44	C_590099	gi|68371158|ref|XP_695404.1| similar to SI:PACKTRZ.2 (novel protein similar to human polycystic kidney disease 2-like 1 (PKD2L1)), partial [Danio rerio]; u.a.: PKD2, weakly similar to polycystin-2 KOG: Ca2+-modulated nonselective cation channel polycystin, located in flagella
31	CIRCHTpEAGIVEMTPALRGKLLDEVTpN **LDDEFMDYpEIDEYpK**	3131,43 1985,89	3 2	2,93 2,07	C_700061	gi|67475672|ref|XP_653525.1| plasma membrane calcium-transporting ATPase, putative [Entamoeba histolytica HM-1:IMSS], u.a.: related to plant potential calcium-transporting ATPase 9, plasma membrane-type Ca(2+)-ATPase isoform; located in flagella
32	**VLVHIEEQSPDIGQGVHGMGTpK**	2314,62	3	6,24	C_750005	gi|10441431|gb|AAG17036.1| S-adenosylmethionine synthetase [Pinus contorta]; u.a.: located in flagella, identified as thioredoxin target in *C. reinhardtii*
33	***TpAGPPPGTAPAHPPPGGSpYHLVTpDGSR***	2737,77	3	2,73	C_750038	gi|71755035|ref|XP_828432.1| hypothetical protein Tb11.02.0990 [Trypanosoma brucei]; u.a.: FAP75, flagellar associated P-loop containing protein, located in flagella

34	***PFSpAGPSpGPGAGAGGAGGTpRSR***	2112,92	3	3,21	C_760066	No significant similarity found; u.a.: located in flagella
35	APDPCSLDSpWLRSALPEAAPPAASpSSER	3043,10	3	2,77	C_850039	No significant similarity found; u.a.: located in flagella
36	***RSpSpISpTpATpAAINTPADLISSpPPVTPSFR n***	2947,14	3	2,68	C_870044	No significant similarity found; u.a.: located in flagella
37	***GLGLGGSpVNGGSpAASpAAAAAAAAATpSpVTpTDAASpMTpR n***	3314,23	3	3,49	C_910056	gi|29827935|ref|NP_822569.1| putative ABC transporter solute-binding protein [Streptomyces avermitilis MA-4680]; located in flagella
38	LPGAQSpGGVENLKPLFKLYpGGK	2434,61	3	3,36	C_970003	gi|50750584|ref|XP_422048.1| similar to tubulin alpha-5 chain - chicken [Gallus gallus]; u.a.: located in flagella (FAP248)
39	**VAVAPAAPARSpASpVR**	1485,63	2	2,36	C_1120028	gi|16974385|gb|AAL31118.1| AT5g19940/F28I16_90 [Arabidopsis thaliana]; gnl|CDD|16052 pfam04755 PAP_fibrillin; u.a.: located in flagella, found in centriole proteome as "unknown"
40	ELSQAQVVVAQATKECNELLEVISpTpNTpVDVETK ***FYFISDDELLSpILGTSpDPTSpVQEHMLK*** IEAEVLSVVSSQIKNIQEALKNDLTpR n ***SpKGAIQKQVMNK***	3830,94 3033,45 2979,27 1412,58	3 3 3 2	2,51 2,85 3,15 2,30	C_1150005	gi|7441384|pir||T08164 dynein alpha heavy chain [Chlamydomonas reinhardtii]; u.a.: DHC1, flagellar inner arm dynein 1 heavy chain alpha, located in flagella
41	***FDLNTpLASpTpKEKEAKK***	1966,03	2	3,12	C_1340006	gi|18164|emb|CAA32061.1| OEE3 precursor protein [Chlamydomonas reinhardtii]; u.a.: oxygen evolving enhancer protein 3 (PsbQ), located in flagella

42	**LAANTAAALGGANPEQTLAKISpSpKR n**	2516,75	3	3,55	C_1350034	gi|11967769|emb|CAC19368.1| putative plasma membrane hydrogen ATPase [Chlamydomonas reinhardtii]; u.a.: PMH1; gi:11967769; gnl|CDD|10347 COG0474, MgtA, cation transport ATPase [Inorganic ion transport and metabolism]
43	FVGTGYpFDLVSTVITQGTSpSpTNALK n	2847,84	3	3,42	C_1460023	gi|619932|gb|AAB61446.1| isocitrate lyase; u.a.: located in flagella; identified as thioredoxin target in *C. reinhardtii*
44	**LGADSpGALEFVPK**	1286,47	2	4,51	C_1580045	gi|130264|sp|P18068|PLAS_CHLRE plastocyanin, chloroplast precursor (PC6-2); gnl|CDD|15127 pfam00127, copper binding proteins, plastocyanin/azurin family; u.a.: located in flagella
45	***PTpAGSpIIALGDAKSVKVGGTpHVHAHTpYpTR n***	3052,27	3	3,86	C_1600004	gi|50660327|gb|AAT80888.1| chloroplast chaperonin 21 [Vitis vinifera], identified as thioredoxin target in *C. reinhardtii*
46	FNAETTANKTITFSSpLTTPGIFQMSIEGAVEK n	3515,83	3	2,81	C_1710010	gi|2494209|sp|Q39575|DYHG_CHLRE dynein gamma chain, flagellar outer arm; u.a.: ODA2, located in flagella
47	***LTDELETpQKLNLR*** TIMENEQMSIELSYpQSRQTEKLLNK n	1653,75 3095,39	2 3	2,30 2,69	C_2350009	No significant similarity found; u.a.: FAP157, located in flagella
48	SpLLHTpLPTpNLNYpNLK TpLDGKILFLTKSpEGTLIFTADPNFNK	2061,93 3045,26	2 3	2,07 2,63	Chloroplast Genome	putative_rpoC2; gi[41179047] RNA polymerase beta' subunit [Chlamydomonas reinhardtii]

B: Proteins that show significant homology to proteins of other organisms or contain conserved domains

49	VRVQLFGSpILRQEVAWFDDADHSSGK	3042,25	3	3,08	C_10157	gi|27368855|emb|CAD59585.1| MDR-like (multi drug resistance) ABC transporter [Oryza sativa (japonica cultivar-group)]
50	NGTTTAGNSpSpQVTDGAAVALMMTRAEATR n	3044,12	3	3,07	C_10176	gi|393707|emb|CAA47926.1| 3-ketoacyl-CoA thiolase; acetyl-CoA acyltransferase [Cucumis sativus]; gnl|CDD|27979 cd00751, thiolase
51	WTpYEACIFKHAVQR	1833,00	2	2,41	C_10342	gi|49257646|gb|AAH74301.1| gene info MGC84105 protein [Xenopus laevis]; KOG: protein kinase C substrate, 80 KD protein, heavy chain
52	**KAAGGHNVGYESpDDSpNAGQGLPDGAGGEVGGEVVESAK n**	3649,66	3	6,98	C_10354	gi|23198376|gb|AAN15715.1| RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]; gnl|CDD|25351 smart00715, LA, domain in the RNA binding Lupus La protein
53	ATpADQVLSpSPWLGR n PENFMLSpAPTpQQQKVEAEAASpAAAGGDGGLALGIGAR	1661,63 3825,89	2 3	2,08 2,52	C_20233	gi|4510380|gb|AAD21468.1| putative calcium-dependent protein kinase [Arabidopsis thaliana]; gnl|CDD|17776 cd00180, S_TKc, serine/threonine protein kinases, catalytic domain
54	QVEFYpFSDANLPTpDKK	2063,04	2	2,74	C_20239	gi|57899257|dbj|BAD87502.1| putative RNA-binding protein homolog [Oryza sativa (japonica cultivar-group)]

55	DIALTpGAYpVAMLNAICSTSQSLLADSPR n	3043,25	3	3,15	C_20259	gi|1183864|emb|CAA63061.1| squamosa [gene involved in determination of floral meristem] - promoter binding protein 2 [Antirrhinum majus]; u.a.: SBP domain containing
56	LGPLAAEAEQLRSpQVAILEARVGTpLTR n	3024,25	3	3,14	C_20381	gi|53761781|ref|ZP_00350820.1| COG1463: ABC-type transport system involved in resistance to organic solvents, periplasmic component [Ralstonia eutropha JMP134]
57	AASTQAFSKVGASpNDDGLDGGGGEEAEAETR PLQVTpGAVLELPSpAGEGGSAHSVFAPASPPTpRR	3079,00 3498,57	3 3	2,54 3,05	C_30102	gi|29824376|gb|AAP04148.1| unknown protein [Arabidopsis thaliana]; c.d.: RNA-binding region RNP-1 (RNA recognition motif)
58	***MAADGGSpTpSTpTpHTpLSpANQELRLECPSpGK***	3032,06	3	2,91	C_30169	gi|50906345|ref|XP_464661.1| putative ATP/GTP-binding protein [Oryza sativa (japonica cultivar-group)]; u.a.: similar to mRNA cleavage and polyadenylation factor complex II subunit CLP1 [Homo sapiens]
59	GAAAGSTpSpSpAGGQAPLPAPLVPLSSpR n ***LTpLLLGPPSCGKSSFMRALTGR***	2641,50 2386,76	3 2	2,92 2,10	C_40065	gi|41052472|dbj|BAD07483.1| PDR-type (pleiotropic drug resistance) ABC (ATP binding cassette) transporter 1 [Nicotiana tabacum]; gnl|CDD|10851 COG1131, CcmA, ABC-type multidrug transport system, ATPase component
60	HAVWYLDDSpVICQRRLDEHVSpHVR n	3095,23	3	2,97	C_40179	gi|4235644|gb|AAD13304.1| polyprotein [Lycopersicon esculentum]; gnl|CDD|25582 pfam00665, rve, integrase core domain; gnl|CDD|14766 cd00024, CHROMO, chromatin organization modifier

61	**PVSpDRAAAVLVGLFEDSTGVVRVLLTQR**	3050,40	3	2,89	C_50125	gi|50945105|ref|XP_482080.1| putative phosphohydrolase [Oryza sativa (japonica cultivar-group)]
62	VKPFPLNNTLLRQLCASpALVAR	2505,91	3	2,79	C_50131	gi|67480485|ref|XP_655592.1| protein kinase, putative [Entamoeba histolytica HM-1:IMSS]
63	***GVVETYpHVTSYEMSATDVVSpQDWALGSpGVVEK n***	3489,74	3	2,71	C_70067	gi|30680365|ref|NP_566313.2| membrane protein, putative [Arabidopsis thaliana]; gnl|CDD|24323 smart00665, B561, cytochrome b-561 / ferric reductase transmembrane domain; gnl|CDD|15053 smart00664, DoH, possible catecholamine-binding domain
64	GRGLSpYpDGENGPALSpSpPPSpQPSPDVR n	3041,69	3	2,69	C_70174	gi|68383231|ref|XP_683663.1| similar to natriuretic peptide receptor-A [Danio rerio]; c.d.: adenylyl- / guanylyl cyclase, catalytic domain
65	***LTpSpGAAARPVLTpVLLLLAAGALMASGSQR***	3050,29	3	2,99	C_80024	gi|18419973|ref|NP_568378.1| outer membrane OMP85 family protein [Arabidopsis thaliana]; u.a.: hypothetical conserved protein similar to OEP80 (At5g19620) and related proteins from plants and cyanobacteria; annotation refers to N-terminal exons only; conserved ATP/GTP-binding site motif A (P-loop); gnl|CDD|25688 pfam01103, Bac_surface_Ag, Surface antigen
66	NFVTTLVTpQMEKSGRGGR	2062,23	3	2,52	C_80107	gi|20259956|gb|AAM13325.1| putative protein [Arabidopsis thaliana]; KOG: predicted membrane protein

67	SpGAMFAKDDLDWKWYpNK	2236,28	3	2,66	C_80131	gi|67539162|ref|XP_663355.1| hypothetical protein AN5751.2 [Aspergillus nidulans FGSC A4]; gnl|CDD|10116 COG0241, HisB, histidinol phosphatase and related phosphatases
68	**KYpVAELFPLLTQLIRADYAPADVHR**	2981,33	3	2,86	C_80228	gi|15217579|ref|NP_171698.1| guanine nucleotide exchange family protein [Arabidopsis thaliana]; gnl|CDD|14836 cd00171, Sec7 domain
69	***GSLDRAGGGAGGAGSpGAGGMYAGEVSR***	2406,43	2	2,25	C_90133	gi|50898810|ref|XP_450193.1| putative serine/threonine-protein kinase ctr1 [Oryza sativa (japonica cultivar-group)]; gnl|CDD|17776 cd00180, S_TKc, serine/threonine protein kinases, catalytic domain
70	**FFDSpADWAMNK** ***RVSpHLDPLDK***	1314,47 1162,34	2 3	3,79 3,41	C_90179	gi|22136292|gb|AAM91224.1| unknown protein [Arabidopsis thaliana]; KOG: regulator of ATP-sensitive K+ channels alpha-endosulfine/ARPP-19 and related cAMP-regulated phosphoproteins
71	**ALVRDVSpKATpSpGSpGLLAGVGSpTTEVVR**	3031,87	3	2,82	C_100060	gi|45508602|ref|ZP_00160940.1| COG0702: predicted nucleoside-diphosphate-sugar epimerases [Anabaena variabilis ATCC 29413]
72	***LGSpGSpHGMRSpGPARALAIAAGIFGFGESK***	2946,14	3	2,72	C_100098	gi|29609969|dbj|BAC74017.1| putative ABC transporter solute-binding protein [Streptomyces avermitilis MA-4680]
73	***DARVLYVSATpGATpESENLCYMER***	2641,83	3	3,80	C_100154	gi|54645696|gb|EAL34434.1| GA17476-PA [Drosophila pseudoobscura]; KOG: nuclear helicase MOP-3/SNO (DEAD-box superfamily)

74	SpASpGDAGSpRMAVVTpFAKGGK	2218,05	2	2,14	C_110077	gi|4689034|emb|CAB41419.1| chloroplast ribosome recycling factor protein [Spinacia oleracea]; gnl|CDD|24166 cd00520, RRF, ribosome recycling factor (RRF)
75	***TSpENRITVTEPLTAASpVAARQK n***	2406,59	2	2,26	C_110167	gi|17104663|gb|AAL34220.1| unknown protein [Arabidopsis thaliana]; gnl|CDD|10501 COG0631, PTC1, serine/threonine protein phosphatase
76	PSpQIWAYpNVTSGDVLWKMNAREGYMSPDNDGDNR	4049,16	3	2,86	C_110171	gi|76257967|ref|ZP_00765624.1| protein kinase: pyrrolo-quinoline quinone [Chloroflexus aurantiacus]; gnl|CDD|5324 cd00216, PQQ_DH, dehydrogenases with pyrrolo-quinoline quinone (PQQ) as cofactor, like ethanol, methanol, and membrane bound glucose dehydrogenases. The alignment model contains an 8-bladed beta-propeller
77	DLDWTNVPFPQYpYpSR	2062,02	3	2,77	C_110176	gi|42572713|ref|NP_974452.1| exostosin family protein [Arabidopsis thaliana]
78	***ASMSpFTpAGTpSGSpGLAGPHGPSpPLSNSSAGR n***	3049,86	3	3,25	C_110227	gi|3122300|sp|Q00771|KCC1_EMENI calcium/calmodulin-dependent protein kinase (CMPK); gnl|CDD|24220 smart00219, TyrKc, tyrosine kinase, catalytic domain
79	MLEEAAGRVSpDERLYDK n	2063,17	2	2,93	C_120100	gi|8778961|gb|AAD49766.2| contains similarity to HARP gene [Homo sapiens]; gnl|CDD|7500 pfam00176, SNF2_N, SNF2 family N-terminal domain; KOG: chromatin remodeling protein HARP/SMARCAL1, DEAD-box superfamily

80	***TpTSpQGFGSNTpASpGDEPGDALTpAVTpAILNTR***	2944,09	3	3,03	C_130052	gi|72114805|ref|XP_784044.1| similar to cyclin-dependent kinase-like 2 [Strongylocentrotus purpuratus]; KOG: mitogen-activated protein kinase; gnl|CDD|17776 cd00180, S_TKc, serine/threonine protein kinases, catalytic domain; gnl|CDD|5392 cd00192, TyrKc, tyrosine kinase, catalytic domain
81	QNTYGVDVTQGSpTQDQSR n	2065,00	3	3,03	C_130173	gi|72008408|ref|XP_782686.1| similar to deleted in malignant brain tumors 1 isoform c precursor [Strongylocentrotus purpuratus]; gnl|CDD|178 smart00202, SR, scavenger receptor Cys-rich
82	**EGEGATPQPGDTpVEVHWAGFTKGYQGK n**	2928,01	3	3,50	C_140146	gi|51968578|dbj|BAD42981.1| unknown protein [Arabidopsis thaliana]; u.a.: FKB16-8, FKBP-type peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8), probably targeted to the chloroplast lumen
83	***SpSpSSpGGATpANTpTpTpSK n***	1329,34	2	2,14	C_150118	gi|55238385|gb|EAA11047.2| gene info ENSANGP00000017775 [Anopheles gambiae str. PEST]; gnl|CDD|456 smart00504, Ubox, modified RING finger domain, without the full complement of Zn2+-binding ligands, probable involvement in E2-dependent ubiquitination
84	SpKIPIICICNDK	1427,65	2	2,45	C_160032	gi|30314655|dbj|BAC76085.1| replication factor C 110 kDa subunit [Oryza sativa (japonica cultivar-group)]; c.d.: HolB, ATPase involved in DNA replication or repair, replication factor C large subunit

85	QKDWSKVESpELNELEQK	2171,24	3	2,84	C_160132	gi|62467587|gb|AAX83943.1| Sgt1b [Capsicum annuum]; gnl|CDD|14219 COG5091, SGT1, suppressor of G2 allele of skp1 and related proteins
86	***QGGAMGGAGVVVASpGPPGSVSPASpSLSR***	2405,71	3	2,84	C_170061	gi|39584866|emb|CAE64290.1| hypothetical protein CBG08960 [Caenorhabditis briggsae]; gnl|CDD|25296 smart00220, S_TKc, serine/threonine protein kinases, catalytic domain
87	VYMVFDYpAGSSpVQSpVMERAGGGLGGAATK	3150,22	3	2,68	C_180026	gi|72114805|ref|XP_784044.1| similar to cyclin-dependent kinase-like 2 [Strongylocentrotus purpuratus]; gnl|CDD|17776 cd00180, S_TKc, serine/threonine protein kinases, catalytic domain
88	RQYPGTHNAVQEPEHAPSpNGGYETSR n	2963,97	3	2,79	C_190078	gi|55637361|ref|XP_522248.1| similar to hypothetical protein BC016153 [Pan troglodytes]; gnl|CDD|17533 pfam04819, DUF716, family of unknown function
89	LRDQLDDESpSpYVEDDAASGHPGALLSR n **RWPEDGINTpEDMVWLAEEANKR**	3078,00 2642,90	3 3	3,39 8,04	C_190173	gi|75756302|gb|ABA27197.1| morn repeat protein 1 [Bigelowiella natans]
90	***FSpPDSQMLAVASpR***	1373,59	2	2,42	C_200004	gi|21593320|gb|AAM65269.1| unknown [Arabidopsis thaliana]; WD-40 repeat containing protein
91	VDNASpLTGESEACER	1661,63	2	2,44	C_200014	gi|12408294|ref|NP_074039.1| Na+/K+ -ATPase alpha 4 subunit [Rattus norvegicus]; u.a.: related to mammalian sodium/potassium-transporting ATPase alpha-1 chain precursor (sodium pump 1) (Na+/K+ ATPase 1); gnl|CDD|15125 pfam00122, E1-E2_ATPase

92	***PHTpSGGGGSpSpGNSpGGTGAAQQQLLR n***	2407,32	2	2,35	C_200111	gi|66856833|ref|ZP_00400894.1| parallel beta-helix repeat [Anaeromyxobacter dehalogenans 2CP-C]
93	***VAQSpRFLNNRLVEVVAFMENIAVK***	2829,21	3	2,52	C_210046	gi|56202035|dbj|BAD73564.1| putative kinase-like protein splice variant 1 [Oryza sativa (japonica cultivar-group)]; gnl|CDD|17776 cd00180, S_TKc, serine/threonine protein kinases
94	MNSGPDTpAGRTpLHQCQQLEEAR	2603,62	3	2,74	C_210167	gi|57087513|ref|XP_546906.1| similar to tyrosylprotein sulfotransferase 1 [Canis familiaris]; gnl|CDD|25886 K+ channel tetramerisation domain; gnl|CDD|25886 and gnl|CDD|24221 smart00225, BTB, Broad-Complex, Tramtrack and Bric a brac, domain in Broad-Complex
95	***AGLTpPTVHSpASpGK***	1172,37	2	2,05	C_220028	gi|27125515|emb|CAD27718.1| putative vacuolar ATPase subunit 100 kDa subunit [Mesembryanthemum crystallinum]
96	***LAAAAASGAGSGAGTpLQAYpIGGIPTAATASpAARFEER***	3648,66	3	3,61	C_220079	gi|54633411|gb|AAV35813.1| kinase domain containing protein [Oryza sativa (japonica cultivar-group)]; gnl|CDD|17776 cd00180, S_TKc, serine/threonine protein kinases, catalytic domain
97	SSRMGSSpGGGGGGGGADEDGSpSAR	2216,98	2	2,12	C_220126	gi|50912113|ref|XP_467464.1| putative NAD(P)-dependent cholesterol dehydrogenase [Oryza sativa (japonica cultivar-group)]; gnl|CDD|16885 pfam01073, 3Beta_HSD, 3-beta hydroxysteroid dehydrogenase/isomerase family

98	SIACVGGLLRSLGHLQVLSYpTpESpLAFR n	3132,31	3	2,77	C_230037	gi|3894383|gb|AAC78591.1| disease resistance protein [Lycopersicon esculentum]; gnl|CDD|5333 cd00116, LRR_RI, leucine-rich repeats (LRRs), ribonuclease inhibitor (RI)-like subfamily
99	***SpLFEDMDPFIEQLVAR***	1893,17	2	2,14	C_230155	gi|51703984|gb|AAH81318.1| MGC89395 protein [Xenopus tropicalis]; CAP10, putative lipopolysaccharide-modifying enzyme
100	RTpSpTpGSKVFGCLKGALDGGLDIPHNEK n	3042,10	3	2,52	C_240141	gi|2599104|gb|AAB84056.1| 60S ribosomal protein [Dunaliella salina]; u.a.: RPL5, cytosolic 80S ribosomal protein L5, cytosolic 60S large ribosomal subunit protein L5
101	AGVVSpASpRLLSLPDELQEK	2173,24	3	3,14	C_250134	gi|50754691|ref|XP_414473.1| similar to sodium bicarbonate cotransporter [Gallus gallus]; gnl|CDD|14848 cd00204, ANK, ankyrin repeats
102	**KGSpAQIFGFFGK**	1269,49	2	4,37	C_270042	gi|21616072|emb|CAC87810.2| Tic62 protein [Pisum sativum]; u.a: TIC62, part of the inner membrane domain of the system for translocating proteins into plastids; gnl|CDD|10325 COG0451 WcaG, nucleoside-diphosphate-sugar epimerases [cell envelope biogenesis, outer membrane / carbohydrate transport and metabolism]

103	WGVVTIGATPWVGNYNVPLSpGVDMATpAR	3093,29	3	3,00	C_270169	gi|34898040|ref|NP_910366.1| OSJNBa0038F22.18 cDNA; similar to formiminotransferase-cyclodeaminase/ formiminotetrahydrofolate cyclodeaminase [Oryza sativa (japonica cultivar-group)]; gnl|CDD|12966 COG3643, COG3643, glutamate formiminotransferase
104	***LPSpPPPSPGATAATpAGADAGRGGTpAAATpGAGAS RGR n***	3131,31	3	3,38	C_280158	gi|7630021|emb|CAB88363.1| pasticcino 1 [Arabidopsis thaliana]; u.a.: FKB9, multidomain protein with FKBP-type peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (rotamase), three TPR-repeats, a calmodulin-binding motif, a nuclear localization signal; possibly a fibrinoin C-terminal domain
105	PYAASVYpSpDLGSpELSQR n	2083,91	2	2,20	C_300048	gi|23479871|gb|EAA16587.1| predicted R27-2 protein, unknown function [Plasmodium yoelii yoelii]; gnl|CDD|16998 pfam01576, myosin_tail_1; gnl|CDD|10914 COG1196, Smc, chromosome segregation ATPases; gnl|CDD|10293 COG0419, SbcC, ATPase involved in DNA repair
106	YGDSAAYpDDVVAAASpVPAPGPSpSpSpAAAAR n	3095,74	3	2,93	C_300116	gi|68365730|ref|XP_688712.1| similar to testis expressed gene 9 [Danio rerio]
107	**FTPTSpPKPPAGAAAGGPSGFGAVHPYGSpSDR n**	3005,16	3	4,04	C_320047	gi|11094252|dbj|BAB17667.1| PEX14 [Arabidopsis thaliana]; gnl|CDD|15992 pfam04695, Pex14_N, peroxisomal membrane anchor protein (Pex14p) conserved region

108	DLFLGLSpGAVGGTLPSpAALFFATpEAAAR	2965,03	3	2,98	C_330077	gi|50931181|ref|XP_475118.1| putative mitochondrial carrier protein [Oryza sativa (japonica cultivar-group)]
109	***MLSpYpIFSpPAGSpKTIVLSpPTpIEAGILR n***	3050,21	3	2,92	C_330094	gi|11991504|emb|CAC19663.1| adenylate cyclase [Blumeria graminis]; gnl|CDD|37 smart00044, CYCc, adenylyl- / guanylyl cyclase, catalytic domain
110	***KYVITpVQLFAPGGGSpR***	1853,93	2	2,47	C_340071	gi|66855787|ref|ZP_00399859.1| peptidase S8 and S53, subtilisin, kexin, sedolisin: Nepovirus coat protein, N-terminal [Anaeromyxobacter dehalogenans 2CP-C]; gnl|CDD|25387 pfam00082, peptidase_S8, subtilase family
111	***TpSpHAALRLAPPSpPAPPPATSRGAR***	2326,70	2	2,15	C_350048	gi|62858575|ref|NP_001016356.1| hypothetical protein LOC549110 [Xenopus tropicalis]; gnl|CDD|14848 cd00204, ANK, ankyrin repeats
112	***PTFSSpGAGGALGGLDGAAPAAER***	2111,15	3	2,99	C_350061	gi|45935119|gb|AAS79577.1| putative PHD (plant homeo domain) zinc finger protein [Ipomoea trifida]
113	RSPLTAGTSpSGDGDAGGRAGGGPDPSNLLSpR n	3044,97	3	2,86	C_350083	gi|57900392|dbj|BAD87602.1| transcriptional regulator family protein-like [Oryza sativa (japonica cultivar-group)]
114	***AGAATAAPSpTpGR***	995,11	2	2,19	C_350089	gi|50933765|ref|XP_476410.1| tetratricopeptide repeat(TPR)-containing protein-like [Oryza sativa (japonica cultivar-group)]; u.a.: protein with similarity to Arabidopsis At4g37460 and rice BAC80093; predicted chloroplast targeting

115	TpMGGELPTLTDPWVREDLTpSpQYHR n	3044,03	3	2,93	C_360017	gi|21038943|emb|CAD31740.4| chitinase [Tenebrio molitor]; u.a.: putative lectin/glycoside hydrolase, extracellular; gnl|CDD|24313 smart00636, Glyco_18 domain
116	SpSpSpGATpSpSLVMPSTAAAVMGATDSSSALRAWR n	3515,35	3	3,23	C_370035	gi|42572713|ref|NP_974452.1| exostosin family protein [Arabidopsis thaliana]
117	ISpIDRLAMVGYpPTAAAVTLSFAEVGACR	3044,33	3	3,22	C_370058	gi|24583871|ref|NP_723736.1| CG31759-PB, isoform B; gene product from transcript [Drosophila melanogaster]; it encodes a product with putative transcription regulator activity putatively involved in nucleobase, nucleoside, nucleotide and nucleic acid metabolism [FlyBase Info]; gnl|CDD|14361 COG5239, CCR4, mRNA deadenylase, exonuclease subunit and related nucleases
118	**RQRSpPSpPAAAVPSAGGAAGR n**	1927,03	3	4,14	C_370142	KOG: splicing factor RNPS1, SR protein superfamily
119	***TSpVPGSpVAAPATpLDSpPGLASpGGSpPIATpPFTR n***	3052,13	3	2,94	C_380133	gi|62739190|ref|NP_067390.3| calcium channel alpha13.2 subunit [Mus musculus]
120	***FLSGAVALLGTpASpLLVGAVTpVGPSPVMAKPR*** ***FLSGAVALLGTpASpLLVGAVTVGPSPVMAKPR***	2927,59 2945,59	3 3	3,58 3,73	C_390058	gi|2198677|gb|AAB61311.1| htrA-like protein [Haematococcus pluvialis]; u.a.: DEGP1, serine protease, trypsin family, DegP type (HtrA), most similar to At3g27925
121	***LAAYHLMAGQVLETQRLLSpLDWR***	2766,11	2	2,16	C_390071	gi|22652299|gb|AAN03676.1| putative nucleoporin PRECOZ [Arabidopsis thaliana]; u.a.: similar to NUP98; KOG: nuclear pore complex, Nup98 component

122	***RAAFTpLSSpGKSLLLPALPGALPCQVVR***	2927,29	3	2,82	C_410119	gi|39996937|ref|NP_952888.1| ATP-dependent helicase HrpB [Geobacter sulfurreducens PCA]; gnl|CDD|11354 COG1643, HrpA, HrpA-like helicases
123	**NLVTpDSpEDLEEKPGER**	1893,90	2	3,76	C_460094	gi|633607|emb|CAA58720.1| chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]; u.a.: similar to Toc75, component of the translocating aparatus of the plastid outer membrane; c. d.: 1. gnl|CDD|25688 pfam01103, Bac_surface_Ag, Surface antigen. 2. gnl|CDD|13913 COG4775, COG4775, outer membrane protein/protective antigen OMA87. 3. gnl|CDD|12184 COG2831, FhaC, hemolysin activation/secretion protein
124	**TKVGDWVGVHYpVGKLENGEEFDNSITR**	3131,30	3	2,98	C_480037	gi|58386685|ref|XP_314956.2| ENSANGP00000019325 [Anopheles gambiae str. PEST]; u.a.: FKB15-2 FKBP-type peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)
125	**RAAGGGGGAGGGGVSpVSAAEVMALER n**	2325,44	2	2,41	C_480048	gi|30696564|ref|NP_851194.1| SWAP (Suppressor-of-White-APricot)/surp domain-containing protein [Arabidopsis thaliana]; gnl|CDD|9014 smart00648, SWAP, Suppressor-of-White-APricot splicing regulator; domain present in regulators which are responsible for pre-mRNA splicing processes
126	QPSAIIPSpATpR	1301,26	3	2,81	C_490004	gi|6850844|emb|CAB71083.1| 3-methyl-2-oxobutanoate hydroxy-methyl-transferase-like protein [Arabidopsis thaliana]; gnl|CDD|3056 pfam02548, pantoate_transf, ketopantoate hydroxymethyltransferase

127	SpIPPPAPPVQQQQSpQGSRGQGAQSpQK	2927,85	3	2,55	C_490062	gi|30692943|ref|NP_190373.2| ubiquitin carboxyl-terminal hydrolase family protein [Arabidopsis thaliana]
128	**ALGFCSpIPAGRLISCTPPDLLVPSpVAER n**	2946,39	3	3,66	C_580061	gi|62733652|gb|AAX95768.1| putative ribosomal-protein S6 kinase homolog protein [Lycopersicon esculentum]; gnl|CDD|17776 cd00180, S_TKc, serine/threonin protein kinases, catalytic domain
129	***LAKTSpLSTVLESpNATpFSpR n***	1854,16	2	2,12	C_580076	gi|6016708|gb|AAF01534.1| putative protein kinase [Arabidopsis thaliana]; gnl|CDD|5392 cd00192, TyrKc, tyrosine kinase, catalytic domain
130	**FSQVASpAGSpLAGLGLGR n**	1653,77	2	4,48	C_600010	gi|77553679|gb|ABA96475.1| pyruvate kinase, barrel domain [Oryza sativa (japonica cultivar-group)]; u.a.: PYK2, putative pyruvate kinase, EC 2.7.1.40
131	IAILAEKFAPSpMQWYMDVVLQLLER	3046,53	3	3,04	C_630070	gi|20466205|gb|AAM20420.1| alpha-adaptin [Arabidopsis thaliana]; gnl|CDD|25788 pfam01602, adaptin N terminal region
132	***TpVLSpIVFTpSpGLTDAARNTLLQSLTpGYSpDLSCMTGAVAAKLR***	4433,83	3	3,44	C_630085	gi|46581099|ref|YP_011907.1| hypothetical protein DVU2695 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]; gnl|CDD|22634 smart00702, P4Hc, prolyl 4-hydroxylase alpha subunit
133	***RMGSpDAAALLPDVLLVHGTpADK***	2313,57	3	2,93	C_660079	gi|53792603|dbj|BAD53618.1| carboxylesterase-like [Oryza sativa (japonica cultivar-group); gnl|CDD|16555 cd00312, esterases and lipases

134	CGQLAALVLLTHLLQLCSGLPLAPGLVTpR ***CGQLAALVLLTpHLLQLCSpGLPLAPGLVTR n***	3052,63 3034,63	3 3	3,01 2,95	C_670006	gi|67941863|ref|ZP_00533852.1| ribonucleoside-diphosphate reductase alpha chain [Chlorobium phaeobacteroides BS1]; gnl|CDD|11120 COG1405, SUA7, transcription initiation factor TFIIIB, Brf1 subunit/transcription initiation factor TFIIB
135	YGAPVDVWSpAGCTLAELATpGRPLFPGR	2966,15	3	2,99	C_710045	gi|74026340|ref|XP_829736.1| mitogen activated protein kinase [Trypanosoma brucei]; gnl|CDD|17776 cd00180, S_TKc, serine/threonine protein kinases, catalytic domain
136	***DYpELEGTAVTCSDDTTIKIWDLSpK***	2766,93	2	2,18	C_720047	gi|75907778|ref|YP_322074.1| WD-40 repeat [Anabaena variabilis ATCC 29413]
137	DYCIKVWDTRTPQSpVGEFGTpLDSASGR n	3150,21	3	3,62	C_740064	gi|68126596|emb|CAJ03967.1| G-protein (beta)-like protein; beta transducin-like protein; guanine nucleotide-binding protein beta subunit-like protein [Leishmania major]; gnl|CDD|5398 cd00200, WD40 domain
138	***YTpPNLDPGRVSpTDPTpLLSPVPEPCPPGER n***	3052,46	3	3,11	C_750015	gi|67926838|ref|ZP_00520033.1| protein of unknown function DUF11 [Solibacter usitatus Ellin6076]; c.d.: FTP, eel-fucolectin tachylectin-4 pentaxrin-1 domain
139	***IGKSSGIISpATpSSpIQNVLFFTpRECLR n*** ***IGKSSGIISpATpSpSpIQNVLFFTpRECLR n***	3051,21 3033,21	3 3	2,71 2,74	C_800030	gi|77164348|ref|YP_342873.1| alpha amylase, catalytic region [Nitrosococcus oceani ATCC 19707]; Interpro Desc.: ATP/GTP-binding site motif A (P-loop)

140	AHTpSTpTpGESSpVDLVSpYVEFQRNYR n	3147,81	3	2,66	C_800032	488 AS, for 241: gi|66818687|ref| XP_643003.1| hypothetical protein DDB0202917 [Dictyostelium discoideum]; gnl|CDD|5369 cd00130, PAS domain
141	***FSpSpLWAIDGSpASpAQDLQVTpSpGYFSSGR n*** ***FSSpLWAIDGSpASpAQDLQVTpSGYpFSSGR n***	2926,98 2944,98	3 3	2,60 2,93	C_800038	gi|7489849|pir||T10518 fruit bromelain (EC 3.4.22.33) FB1035 precursor - pineapple (fragment) gi|2463588|dbj|BAA22546.1| FB1035 precursor [Ananas comosus]; u.a.: N-terminal papaine-type Cys protease domain; gnl|CDD|28332 cd02248, peptidase C1A subfamily
142	**NRGGFYLDLTAGAAAQAADNTpWSpQQR**	2943,91	3	2,76	C_850041	gi|50920439|ref|XP_470580.1| putative membrane protein [Oryza sativa (japonica cultivar-group)]; gnl|CDD|24323 smart00665, B561, cytochrome b-561 / ferric reductase transmembrane domain
143	GTFLGGDSpSpPALTWLESpKIAAVTDIPR n	3044,09	3	3,15	C_860022	gi|40809925|dbj|BAD07294.1| prolyl 4-hydroxylase [Nicotiana tabacum]; KOG: prolyl 4-hydroxylase alpha subunit
144	PTATTPNALVDSLLVGQSpNTTpAK n	2460,51	3	2,62	C_870040	gi|9651031|dbj|BAB03528.1| fucolectin-6 [Anguilla japonica]; gnl|CDD|15031 smart00607, FTP, eel-fucolectin tachylectin-4 pentaxrin-1 domain
145	AGAIFTpIGAVGR	1213,31	2	2,03	C_900005	gi|55644247|ref|XP_511104.1| predicted golgi apparatus protein 1 [Pan troglodytes]; gnl|CDD|1394 pfam00839, Cys_rich_FGFR, cysteine rich repeat

146	LPATpLYQLHSpTALVLRAALQRPLTR	2964,29	3	2,67	C_910024	gi|68478074|ref|XP_716906.1| adenylate cyclase [Candida albicans SC5314]; c.d.: adenylyl- /guanylyl cyclase, catalytic domain
147	GGGGGSGEGSDDGALSpPTpSpSpSVPARDQGRR n	3095,72	3	2,69	C_910028	1610 AS, for 50: gi|18390446|ref|NP_563719.1| ubiquitin-specific protease 2 (UBP2) [Arabidopsis thaliana]; gnl|CDD|28362 cd02257, peptidase_C19, peptidase C19 contains ubiquitinyl hydrolases
148	ITDAQALLRSpEFVEGDIITVTLR	2641,90	3	3,29	C_910060	gi|54035749|sp|O87444|CLPB_PLEBO chaperone clpB; gnl|CDD|10413 COG0542, ClpA, ATPases with chaperone activity, ATP-binding subunit; KOG: chaperone HSP104 and related ATP-dependent Clp proteases
149	***MTpDSpGTpFVPVCVPTpCTpENSpCPAGK***	2925,68	3	2,53	C_920010	gi|62647053|ref|XP_578230.1| similar to neurogenic locus notch homolog protein 1 precursor (Notch 1) (Motch A) (mT14) (p300) [Rattus norvegicus]
150	***TYpDLILMDIHMPEMDGLEASpKR n***	2641,98	3	3,77	C_930062	gi|75907252|ref|YP_321548.1| multi-sensor hybrid histidine kinase [Anabaena variabilis ATCC29413]; u.a.: HKR2, putative histidine kinase response regulator, PAC motif
151	***SpHLSIDDTGAAPGAAGALLLVYQLRR n***	2649,02	2	2,29	C_940010	gi|27524348|emb|CAC81748.1| adenylate cyclase [Aspergillus fumigatus]; gnl|CDD|37 smart00044, CYCc, adenylyl- / guanylyl cyclase, catalytic domain

152	FITADTpECDTpLANVLANAPK n	2268,32	2	2,29	C_980022	gi|18765766|dbj|BAB85219.1| matrix metalloproteinase [Volvox carteri f. nagariensis];u.a.: matrix metalloproteinase, MMP, with atypical QExxH site showing copper preference, gnl|CDD|23772 pfam05548, peptidase_M11, gametolysin peptidase M11
153	***TpQPTASPLRSRWSR***	1723,81	2	2,32	C_980037	c.d.: RNA-binding region RNP-1 (RNA recognition motif)
154	AGVERSFVQFVLEPLYpK	2063,28	2	3,10	C_990022	gi|51090357|dbj|BAD35618.1| putative elongation factor 2 [Oryza sativa (japonica cultivar-group)]; u.a.: EFG3 like elongation factor 2 (EF-2), EF-Tu/also similar to U5 snRNP-specific protein, 116 kDa gnl|CDD|10353 COG0480, FusA, translation elongation factors (GTPases)
155	VQGDEGGKAATpAGTGPAGSpSSpSpGSGLMLR n	2927,72	3	2,57	C_1000002	gi|67469291|ref|XP_650626.1| protein kinase, putative [Entamoeba histolytica HM-1:IMSS]; gnl|CDD|17776 cd00180, S_TKc, serine/threonine protein kinases
156	**KTpLSYAVAELTpKDAEK**	1927,96	3	2,92	C_1000008	gi|50258251|gb|EAL20943.1| hypothetical protein CNBE0100 [Cryptococcus neoformans var. neoformans B-3501A]; gnl|CDD|11942 COG2236, COG2236, predicted phosphoribosyltransferases
157	ILWAFKLNPFEKLNLHFDATpPEEIK	3095,48	3	2,68	C_1090047	gi|13374867|emb|CAC34501.1| putative protein [Arabidopsis thaliana]; gnl|CDD|24391 pfam00226, DnaJ domain

158	PVSDEEAAALAAAAGDTRPWSpSPR n	2506,56	3	2,76	C_1100034	gi|26333531|dbj|BAC30483.1| unnamed protein product [Mus musculus]; gnl|CDD|24291 smart00487, DEXDc, DEAD-like helicases superfamily
159	SSSNFDTGSVGSGTPRGGNQVRHVFTpGPR	3043,11	3	3,10	C_1250032	gi|7547107|gb|AAF63779.1| unknown protein [Arabidopsis thaliana]; gnl|CDD|28418 cd01994, Alpha_ANH_like_IV, this is a subfamily of adenine nucleotide alpha hydrolases superfamily
160	GSpSTGQLPLRPTPVEVPSVPSLQPPSLTR	3079,39	3	2,67	C_1260006	gi|66815923|ref|XP_641978.1| tyrosine kinase-like protein [Dictyostelium discoideum]; KOG: tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs; gnl|CDD|17776 cd00180, S_TKc, serine/threonine protein kinases, catalytic domain
161	***AAVGAGTpVAGGLGAVGSpAGGVGSGLGGSpAADVSpSpP***	2946,88	3	2,98	C_1260011	gi|20466448|gb|AAM20541.1| putative vacuolar proton-ATPase subunit [Arabidopsis thaliana]; gnl|CDD|23219 pfam01496, V_ATPase_I, V-type ATPase 116kDa subunit family
162	***MSpSpIFGSITVETPKYTVLKTLGTSGAELR n***	3052,57	3	2,75	C_1270009	gi|30687330|ref|NP_565876.2| SOUL heme-binding family protein [Arabidopsis thaliana]
163	RLSpSpTSMSGTPTTPARPTSpGER n	2518,43	3	2,96	C_1290019	gi|47220696|emb|CAG11765.1| unnamed protein product [Tetraodon nigroviridis]; gnl|CDD|3835 smart00153, VHP, villin headpiece domain
164	**KESVAEKSpFYEVAR n** SLSpSpIDAATAHEDLPDTEALLAGTFGAYYSGSGSK n	1625,82 3664,67	3 3	4,64 4,38	C_1310007	u.a.: hypothetical protein, has limited similarity to the haploid specific alanine rich acidic protein, chromosome X in mouse

165	**QKFVYpVLNRDAAANLTISpSPLEAHK**	2947,13	3	2,72	C_1340045	gi|7019655|emb|CAB75756.1| Gene info spliceosomal-like protein [Arabidopsis thaliana]; KOG: splicing factor 3b, subunit 3; gnl|CDD|26038 pfam03178, CPSF_A, CPSF A subunit region
166	LLLQFSpYpPVNLLMLK VSVTLTVEGGASSpPLQLSDGGGVGGASTMTK	1953,21 2945,14	2 3	2,22 2,63	C_1360021	gi|66806589|ref|XP_637017.1| hypothetical protein DDB0219267 [Dictyostelium discoideum]; gnl|CDD|12045 COG2373, COG2373, large extracellular alpha-helical protein
167	VDLVTDTpASDVVLHWGVSPIGSR	2504,68	2	2,37	C_1470018	gi|20384925|gb|AAM18228.1| R1 [Citrus reticulata]; gnl|CDD|9298 pfam01326, PPDK_N, pyruvate phosphate dikinase, PEP/pyruvate binding domain
168	***PPATPPTpGPGAGGLAGVR***	1653,76	2	2,36	C_1620002	gi|15668711|ref|NP_247510.1| hypothetical protein MJ0531 [Methanocaldococcus jannaschii DSM2661]; gnl|CDD|10459 COG0589, UspA, universal stress protein UspA and related nucleotide binding proteins
169	***MYpKEVKYpDDEITLR n***	1964,02	2	2,76	C_1650015	gi|34897012|ref|NP_909852.1| putative thiamin biosynthesis protein [Oryza sativa]; gnl|CDD|2489 pfam01964, ThiC, ThiC family
170	MTpSRSRGPAAVAAVVGK	1738,93	3	2,56	C_1690026	gi|50929653|ref|XP_474354.1| gene info OSJNBa0064G10.19 [Oryza sativa (japonica cultivar-group)]; U.a.: EFG4 GTP binding elongation factor-like protein; conserved domain; gnl|CDD|14378 COG5256, TEF1, translation elongation factor EF-1alpha (GTPase)

171	YTpIEEVLGAGSNAVAYR n	1893,97	2	2,66	C_1800013	gi|23125436|ref|ZP_00107369.1| COG0515: serine/threonine protein kinase [Nostoc punctiforme PCC 73102]; gnl|CDD|17776 cd00180, S_TKc, serine/threonine protein kinases, catalytic domain
172	GAAYpSAVQSpASpASPAGSPSR	2062,85	2	2,75	C_1950015	gi|3488|emb|CAA27175.1| unnamed protein product [Saccharomyces cerevisiae]; gnl|CDD|37 smart00044, CYCc, adenylyl- /guanylyl cyclase [synthesis of cAMP], catalytic domain
173	***TpCLRASEELAPFLQPAKR***	2111,35	3	3,52	C_1960007	gi|50508194|dbj|BAD31511.1| exocyst complex component Sec8-like [Oryza sativa (japonica cultivar-group)]; gnl|CDD|9607 pfam04048, Sec8_exocyst, Sec8 exocyst complex component specific domain
174	VLETpLHDASQQSpAAVAASAGAPAPSpGPSpYNTSLGGTSVR n	4047,91	3	3,43	C_2530002	gi|42563356|ref|NP_178082.2| protein kinase family protein [Arabidopsis thaliana]; gnl|CDD|17776 cd00180, S_TKc, serine/threonine protein kinases, catalytic domain
175	***KLAASpGEKPEPVR***	1364,59	3	2,97	C_3470003	gi|31126745|gb|AAP44665.1| putative 40S ribosomal protein S15 [Oryza sativa (japonica cultivar-group)]; u.a.: RPS15, cytosolic 80S ribosomal protein S15; cytosolic 40S small ribosomal subunit protein S15

176	PVSSGAAVQLALPASpLKNIHHTFHVSMVR	3149,56	3	3,00	C_3540003	gi|28558781|gb|AAO45752.1| pol protein is encoded by a resistance gene cluster (coding reverse transcriptase, RNAse H and integrase) [Cucumis melo]; gnl|CDD|25582 pfam00665, rve, integrase core domain
177	AASpAPTAGAGASSAGGPSpSpAAAAK n	2127,93	2	2,46	C_3630002	gi|16331146|ref|NP_441874.1| serine/threonine protein kinase [Synechocysis sp. PCC 6803]
178	***EINKSpPYAKQALELSR***	1830,09	2	2,51	C_3630003	gi|6714430|gb|AAF26118.1| putative 26S proteosome regulatory subunit [Arabidopsis thaliana]; KOG: AAA+-type ATPase
179	***YPKISpTpPSpLQK n***	1502,42	2	2,36	C_3670002	gi|57104060|ref|XP_534343.1| similar to Rpl23a protein [Canis familiaris]; u.a.: RPL23a, 60S ribosomal protein L23a
180	TTpLVFNIPLAEVVTDYpFDQLKSRSK n	3046,25	3	2,80	C_6660001	gi|50252173|dbj|BAD28168.1| putative LepA protein [Oryza sativa (japonica cultivar-group)]; u.a.: EFG9 putative C-terminal of elongation factor G; gnl|CDD|26534 pfam06421, LepA_C, GTP-binding protein LepA C-terminus
181	***LSpNVAVDAVFDSpVSIATpTpFKADLLK***	2945,92	3	3,02	C_7720002	gi|22298033|ref|NP_681280.1| ABC transporter subunit [Thermosynechococcus elongatus BP-1]; u.a.: related to SufB, which is involved in FeS cluster biogenesis in plastids
182	**LRDEQKTpLSDSLPPILQYpALGQVAK**	2945,15	3	3,51	C_10310002	gi|10174798|dbj|BAB05898.1| ATP-dependent proteinase [Bacillus halodurans C-125]; gnl|CDD|5390 cd00189, TPR, tetratricopeptide repeat domain

183	**QICNHPALYpLKETEPK**	1965,16	2	2,97	C_24980001	gi|52140319|ref|YP_086511.1| SNF2 family helicase [Bacillus cereus E33L]; gnl|CDD|10424 COG0553, HepA, superfamily II DNA/RNA helicases, SNF2 family
184	**RAVTpWVNEVR**	1212,40	2	3,15	AV393403	gi|7270530|emb|CAB81487.1| putative protein [Arabidopsis thaliana]; gnl|CDD|5392 cd00192, TyrKc, tyrosine kinase, catalytic domain; gnl|CDD|17776 cd00180, S_TKc, serine/threonine protein kinases, catalytic domain
185	SpKGILAIKGSDDK	1412,51	2	2,61	1030070A09.y1	gi|35211095|dbj|BAC88475.1| glr0534 [Gloeobacter violaceus PCC 7421]; gnl|CDD|24627 pfam02492, cobW, cobalamin synthesis protein/P47K
186	***PYpWRCYFPCTpQAIIYVVDSpTpDTER***	3052,25	3	2,83	91.39.1.0	gi|3182922|sp|Q96361|ARF1_BRARP ADP-ribosylation factor 1 gi|1654142|gb|AAB17725.1| small GTP-binding protein ARF; gnl|CDD|5377 cd00154, RAB, Rab subfamily of small GTPases

Theor. mass, theoretical mass of the peptide ion [MH+]; z, charge; cp, chloroplast genome; u.a., user annotation notes, which can be found on the JGI web site under the gene model number; c.d. conserved domain; Tp, phosphorylated Thr or Methyldehydroalanine; Sp, phosphorylated Ser or Dehydroalanine; Yp, phosphorylated Tyr; n, the exact phosphorylation site(s) within the peptide cannot be specified with certainty;**bold writing**, the phosphopeptide was identified by MS/MS and in addition by MS/MS/MS spectra;***bold and in parallel italics writing***, the peptide was solely identified by MS/MS/MS spectra.