TABLE S2. Novel proteins of *Chlamydomonas reinhardtii* that are phosphorylated of yet unknown function

No.	**Phosphopeptide sequence**	**Theor. mass [MH+]**	**z**	**Xcorr**	**Gene model (JGI, vs2) / EST**
1	***STpLAGLMASAGSpGTpESpGGRRVTpSpPGSAAGSR n***	2926,03	3	3,17	C_10128
2	***ATALTpGGLEDSLR***	1286,43	2	2,17	C_10259
3	HSpHTpPSpANTAPPRPAAAVLPDTLLPSVTSpIR n	3496,50	3	2,67	C_10312
4	QAAGGTpPVGR	993,98	2	2,27	C_20189
5	GSYpDPLGAALLVMRGAGANPFYSDSpRQR n	3131,26	3	2,59	C_20338
6	GVGGLLGVSpKRQVEILMK	1965,29	2	2,17	C_30141
7	MYPNATpFVFNK	1412,53	2	2,25	C_30198
8	***EAHSpGTpTpSpASpQTpLPLADTpADLR***	2313,33	3	2,82	C_40005
9	ASpGTpGGGLHLTLSRMTLVSpANLTAVRVR n	3080,24	3	2,71	C_40099
10	**KGTpGFSFFGTpGK n**	1296,37	2	3,51	C_50124
	TGSpGFSFFGTGK n	1175,29	2	2,99	
	AGSpGFNFFGTpGK n	1252,27	2	2,92	
	AGSGFNFFGTpGK n	1172,29	2	3,49	
	KAAGFFGTpGR	994,15	2	3,78	
11	WDLLPEEVAAQMSpTRSpANVK n	2406,49	2	2,27	C_60045
12	QTpSpQCSpTpPTPSQLAAAAPYpGGGSpGAR n	2945,52	3	2,70	C_70008
13	***PSpATpSpTpSpGQDGSpAPQPTpSpSAPK***	2112,08	3	3,48	C_70009
14	VAISpAAAAAAAANAASGAQAGVNGDTpRMVVK	2946,08	3	2,82	C_100181
15	GAAAAISpSpKR	994,04	2	2,04	C_110045
16	***LASpSpQQASTpPLQK n***	1501,47	2	2,27	C_110173
17	**PQGRGAGSGGGDPLTpR**	1563,55	2	2,18	C_120170
18	***QPAAPGTpGSpSpSSpGRCAAAGQQQQR n***	2328,41	3	3,19	C_120219
19	***TpAAENSAAVTAAAEAEAEEARRR***	2328,46	3	2,74	C_130160
20	**YGYGSpDDEYIATPYK n**	1724,82	2	4,32	C_130182
21	PFANDTpSPSpRDFVAAALLGSpGGGSpGGGGGRGGGGGR	3498,26	3	3,10	C_140054
22	***YSGGGGEPAAWRGTPEPMTpAAAWAKASpGPR***	3051,25	3	3,14	C_140167
23	PDGASpAQSAVLTAAFPPQAEHRREVLSR n	3043,24	3	3,13	C_150041
24	**RYFDSpADYNLQK n**	1502,63	2	3,79	C_150106

25	***LFSALSGAFSpQRNVDLAGK n***	1964,23	2	2,42	C_150135
26	HTpADEAAGSWQHASpWDALRGSpERGSR n	3079,88	3	2,54	C_160128
27	***SLGGRKVWVPDSpNSpFDGPTpTATpSpMSpEK n***	2846,10	3	3,11	C_180171
28	IIYEHALNIKAYYpLQAQHLRAAGSLR n	3094,46	3	3,27	C_190171
29	SpSQSPGGKKQQQELGPSAAQVAPPR n	2614,75	3	3,47	C_200012
30	**ALGGTGAAYpNALDSpAAMLQR**	2112,14	3	4,25	C_200072
31	***DYpAAMAKDNATpKTEQLYTTK***	2326,48	2	2,19	C_210065
32	***EPSPAVNTSVNATGGTpAAAVPGLSR***	2405,50	2	2,45	C_210132
33	***VAIAMVLERLTTpVEEVAKALAAYTpVAR***	3050,39	3	2,93	C_240085
34	***EASGKEAAPAATSpGAAGAKDGK***	1928,07	3	2,59	C_270119
35	FLKLAEAFPETpR	1502,63	2	2,43	C_280034
36	***PRSSGTpGTGTGGAATpDRSHSpR n***	1963,07	2	2,40	C_290127
37	***VQQALLETpAKQLEDATpADKHALLER***	2757,13	3	2,62	C_300047
38	SpPGAVLLASPRSPGAPGLLFPDTpGGSpPPHR	3150,22	3	2,82	C_320075
39	***MAAVSKCQSpEGVRPDAVSpAATpSpR***	2642,53	3	3,12	C_350081
40	**IDFSAISpGR**	948,07	2	2,73	C_360092
41	TpSpSpGACGTASpCACACGTpCGTCSpCVWSpCGELR n	3497,21	3	2,80	C_370107
42	SpLTAAVGRIATQPNVYVPRDK	2337,56	3	2,67	C_390020
43	**NFKEYFEFEGSpTAKVGK n**	1964,18	2	2,56	C_390083
44	PRPAGYPGVQRVSpSpTNGNITLLTpTDLK n	3097,16	3	3,90	C_420066
45	VAVGVCQMLPPLLASRGYpTGSQALAAALTR n	3096,56	3	2,79	C_430098
46	***VRGTADAGVAAAGTADAAGGARSpR***	2112,27	3	3,81	C_440055
47	***KPSpARMSpQAVYK***	1330,62	2	2,46	C_450080
48	***FFTpTLPALTQLPNTpSpTpAASpHTR n***	2384,63	3	3,11	C_480027
	FDGYpIVTpQPMYETpRRAQYSNITR n	3051,07	3	2,64	
49	***QQVSLLTpALLQEQQRR***	1894,18	2	2,51	C_520072
50	***PVLAEIPDPRQYVEAALARVGASSpPTR***	2945,22	3	3,43	C_560107
51	VPFPGAHTLPGATPPSpPQHTpGGPKPSTRQA n	3150,29	3	3,00	C_580029
52	***ATpASpSpVLPLAAALGTpVGVALISpTVLGLLLK***	2927,39	3	3,87	C_580033
53	***AAAAADAASpGAGGTKSPKPPQR***	1963,16	2	2,10	C_600033
54	CTpLRSGAGAGGLAAGLGLAFAAAAGEAAPAAVTPR n	3149,47	3	2,83	C_600081
55	***KAVSpPQSpPPSpPNQESAMNAR n***	2239,26	3	5,14	C_620036
	KAVSPQSpPPSpPNQESAMNAR n	2159,28	3	5,59	
56	LTpTpTpLVDRAGSPDELTRLTAIHWLR n	3077,17	3	3,22	C_650063

57	RLSpSpEAGYALQR n	1511,45	2	3,78	C_670063
58	HDVVTpAVSSCTpYVTVTpATpCK n	2406,30	2	2,47	C_740004
59	***GSpGSpGHGGGNGTpAANVAGASpWVRR***	2406,22	2	2,40	C_740055
60	QTSpRASpVDDEVLPTDEIAK n	2235,18	3	4,53	C_800072
	QTpSpRASpVDDEVLPTDEIAK n	2119,20	2	4,44	
61	STpSARSpLDVHTAEPVAAAAAGAR n	2370,35	3	4,30	C_820009
	AGSpSSpGRLSRTpASpIQR n	1562,78	2	2,05	
62	PPAVPPSLSpPRSTGPPHTpQHQR n	2505,57	3	2,98	C_890013
63	***LVDDLLGRATSpGTSSpASGATHTpSpHSHR n***	2944,81	3	4,19	C_920015
64	***RSpGAASpVTVVLPGGGSpGGPGHSpR***	2384,17	3	2,64	C_920038
65	***TATSpRDSSPDTSpAR n***	1514,45	2	2,65	C_1050045
66	***RMLMPLVPASGDGWSRLSpR n***	2112,53	3	3,64	C_1080010
67	**PPASpGTpWQSpAAGEQAQPASLLQLQLR**	2946,94	3	2,89	C_1100026
68	***EITpLDRLYTAVGAVCYDGAISGITGSpR n***	2865,12	3	2,86	C_1180012
69	**VPMSPVGSpDDEVPSpDAEGDVPVVGIRPSGGAFR n**	3359,58	3	4,07	C_1200006
70	**ASSGTAASpSTpSpGGGGAGTGPGVSGVVRAAYRR**	3050,92	3	3,10	C_1200033
71	**PGAYpVSEAEAGPEASHVSPPPAK**	2329,40	3	3,34	C_1210024
72	**GAGLSpPVGSpIGSPGGLK n**	1516,63	2	3,78	C_1220012
73	***SpSAGGGEEAQAAGAATpSpRGLRHTpPTpGDAGSGTR n***	3051,11	3	3,03	C_1280007
74	GLVELDLRPSHGSpVCDEALGAVASTpSSpL n	3025,02	3	3,14	C_1290028
75	IFSKGDGGAATpTYEEALNATpRVVDQLR n	3044,11	3	2,87	C_1480031
76	***SpAASCGISpMAPVQLSAAAAAAAAAAGGVTpGAAVR***	2946,28	3	2,78	C_1510026
77	FFGGDSpGEWDEVQLER	1951,92	2	4,04	C_1660033
78	***SpPTpQAAASpILPAGAASALVSpPSpASKQSR***	2927,84	3	3,39	C_1740014
79	AMAGLISADRSSSpGSAYTLACAPGTGAVAAALR n	3149,44	3	2,64	C_1850001
80	SpRSpLLQLVPLSQSLTpEDDQSpLRR n	2962,87	3	2,77	C_1860007
81	**RGMRLAQEAATpAAATpASpVDLTATAEAR**	2944,94	3	2,98	C_1880014
82	FISGPYpFDVIPSQYEHVTpTSR n	2604,64	3	3,13	C_1970020
83	TpSTYpGLVRNLLEGPAGPDDTpEWPQGK n	3042,97	3	2,96	C_1990015
84	***VAATASpALTpGSpSpSpPR***	1286,50	2	2,10	C_2220010
85	***NVIVVAVADDASpCPLAVR***	1893,09	2	2,39	C_2230006
86	LLVSpPQPLGELLSIELTpCQQPGILSpTR n	3147,36	3	2,78	C_2370008
87	**GGRGGGSGSGSpGSpSAAAVVGPGGAAEGIR n**	2406,43	2	2,26	C_2420007
88	FVSpDATVPSpAKITESQVSRAGVVGSGPAGGR n	3149,25	3	2,74	C_2670002

89	TPVLVGSpPPAPTpCDLRGAAPPPGTHTCIR n	3043,30	3	3,28	C_2700008
90	***GLGGADGGGAMAAGPQLPAGLHSpSpSpSATpRSpSAADR n***	3050,35	3	3,68	C_2940001
91	GSAVNSpEADGAEGK	1372,27	2	2,17	C_3850003
92	SpDPNLDGPTGKATpLAAMSR	2063,07	3	2,78	C_4820001
93	TASASLCSpAEKVTIKVSFHR n	2216,44	2	2,13	C_5060003
94	HPHQATPQSHASpHATPSLSpHSpQSQSR	3042,86	3	2,52	C_5540001
95	DILSCIDLIGCHYpQRSVR	2172,41	3	3,04	C_6070001
96	***TpPETPNWPTpPSpLLPSTPPQLSpASAASLR n***	2944,23	3	2,89	C_10520001
97	LGAVNVSVRSVRAGGGSAVPSLSpQR n	2505,71	3	2,92	C_10920001
98	FETKPSpLVVIFESLINSYDGNSDISpGR n	3149,24	3	2,74	C_18720001
99	PSTVSRGARGAGGGGGAAPGSpR	1963,99	2	2,24	C_19430001
100	***SpHSAGAASpLAAATpASAINQSR n***	1987,05	2	2,19	C_21830001
101	***AQQLLVVSpAVTSFELSR n***	1831,12	2	2,15	C_23720001
102	***GASLSGVYANGDGAGTSAAAGGGGRLGASpAGTSpR n***	2944,98	3	3,09	C_32510001
103	MLSALGLPDLSSASpAIFRSNAPQPRITR n	3051,41	3	3,04	AV387966; 179.3.1.91
104	LLSpAKLCFTPISFKREYPDAPDGTVI n	2963,33	3	2,67	AV391807
105	LDCRLGLQSpLAGNLSQLPWAQPQGPPPR	3094,43	3	3,56	AV396325; 8.52.1.51
106	PPQFRRSLPHLPTpPGHPFLSpHPPSMR	3148,43	3	2,99	AV396603, 80.32.1.5
107	DAGSpCIFLCIRAGACLDNSPK n	2235,49	3	2,98	AV619068 ; 128.29.1.51
108	**VVEPEVVSpEEEPPSpPK**	1813,89	3	3,98	AV619529; 20021010.665.1, 90.6.2.11
109	PKVYpSpECLQSRLVLALVSSpASpSAGTR n	3044,05	3	4,15	AV626527; 38.88.1.51
	PKVYpSECLQSRLVLALVSpSASpSAGTR n	2964,07	3	3,47	
110	HAVSpELFSPSYpTLESpYPTpEADSpL n	2944,61	3	2,70	AV627521
111	GASpLAGKPRHTPR	1428,52	2	2,32	AV631541 ; 187.9.1.5,
112	LLVRPPAPAPTTPSpACLDAR n	2127,39	2	2,45	AV635896; 79.47.1.0,
113	ASpAPKTpLAHSpRLTPYpK	2061,94	2	2,55	AV640199; 93.24.1.5
114	YpILLSDDCFANMTTLPIAINQNTpTI n	2947,16	3	2,87	AV640777; 435.2.1.5
115	SpWIECSVSpEEIASWLQCHYFKACTL	3095,31	3	2,72	AV641655; 42.28.1.5
116	CRQSARTpVAGMLPRTVAVLTAAALTPLL	2962,47	2	2,10	AV643276, 60.45.1.5
117	YpLAATINRAADSpAAGSpLAGKSQK n	2505,45	3	2,73	1030009D08.y1, 163.5.1.0
118	SPPPPPSpPAATpATAATSSpPPPTpSpAMPPTPR n	2945,13	3	3,17	1030118A09.y1; 30.16.2.51
119	***TpSpVEFELHTpDTpVVLKRLEFTpHLNK***	2866,22	3	3,56	106.29.1.5
120	KLPALSpNTpAPPEPQAESpPTSRLHLGAK n	3052,11	3	2,57	1115015F03.x1

121	SLSMWVGYRGLSpKGLTpASYAAALSAFR	3025,26	3	3,04	144.3.1.0, 20021010.2585.1, 1031080H11.y1
122	QKRHATTpLPLQK	1501,65	2	2,44	20021010.1082.1, 20021010.1240.1, 131.2.2.11
123	***NLVTpPHTpHVVKTpSpR***	1811,76	2	2,34	20021010.3311.1
124	***QCLGNNASpETpSpSQLVR***	1653,85	2	2,61	20021010.5201.1
125	RGLSpLSpLTAASpSpAGSpRGAR	2218,92	3	2,77	20021010.5711.2, 133.10.2.51, 1112112E07.y1
126	***KLNFTpTpKTpTYINNK n***	1828,89	2	2,08	20021010.6005.2
127	***LTGGWAVRLTpVGAGGAPQLPRTQVATpTpGSR n***	2926,38	3	2,51	20021010.713.1
128	VPTpDRLPSpSSPDYpGDLHMR	2384,29	3	2,69	20021010.7141.1, 894066C01.x1
129	APVHNPPRETpSLAANTLLSAHAR n	2504,68	2	2,03	20021010.7912.2
130	LTpPTpGSpTpSVACTpSTTVTPFHASpLNVR n	3129,84	2	2,35	20021010.9158.1,
131	***RTMTpCIAEPVTTSAQVAPSpAATpASpASpAPR***	3052,15	3	2,61	20021010.9406.1
132	***VRMTpASTpSTpSTPPATAAPAAGSGPKP n***	2359,69	3	2,83	220.7.1.5
133	***GATpGRNALGSSNTpTQSTpHEPTpRTSpLHVR n***	2946,10	3	3,20	224.5.1.5
134	GYSpVNSVLVHLEADPRSATGSSEQSTDR	3044,09	3	3,06	2815.1.1.5, 894005F08.y1, AV640439
135	***GLSADPSpCPSpASpGAAGHGSpAVATpSSASPTpVTpPITGEK***	3398,53	3	3,78	29.72.1.5
136	QTpSpKNPTpNTpVPQTKMNTGSpQAAPHR	3095,85	3	2,77	49.25.8.32
137	AVLMEATTNYATTPVVETpQLLKSpAACR	3043,29	3	2,72	67.38.1.5
138	***AVDSPPGPLDSpIATKTpIEDLDTDYCDDFVCTSSPAVEQTVR n***	4435,71	3	4,51	96.45.1.51
139	***LGTpNRNPHKSEPPAPSpNATpAPK n***	2329,49	3	2,63	963009B02.y9
140	***PTETpPEPRSAETpKTpPK***	1813,91	3	2,64	963009D06.x9
141	YINIITSYHILYpYpK	1965,07	2	2,91	963032D06.x1
142	***SpSpTpGLVPRMTpPVAVRSpTpLALQSTpMR***	2927,06	3	3,57	98.2.5.51
	SpSpTpGLVPRMTPVAVRSpTpLALQSTpMR	2847,08	3	3,46	

Theor. mass, theoretical mass of the peptide ion [MH+]; z, charge; 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.