

TABLE S1. Functional categorization of flagellar phosphoproteins

Protein-ID		AA / MW	Phosphopeptide along with the number of the first amino acid within its protein	z	Xcorr	Function and/or homologies of depicted proteins determined by NCBI BLASTp
Vs2	Vs3					
Structural proteins of the flagella						
157798	189083	749 AA / 83.4 kD	345-TISGADTpPEEVLAYWEGLK -> TISpGADTPEEVLAYWEGLK -> TpISGADTPEEVLAYWEGLK 694-ILGYTGSpDVEEEEEPESEEEETEEEEANKDDGVVDR -> ILGYTGSpDVEEEEEPESEEEETpEEEEANKDDGVVDR -> ILGYpTGSDVEEEEEPESEEEETEEEEANKDDGVVDR -> ILGYTpGSDVEEEEEPESEEEETEEEEANKDDGVVDR -> ILGYTpGSDVEEEEEPESEEEETpEEEEANKDDGVVDR -> ILGYpTGSDVEEEEEPESEEEETpEEEEANKDDGVVDR -> ILGYTGSDVEEEEEPESEEEETpEEEEANKDDGVVDR	2 2 2 3 3 3 3 3 3 3	4.76 4.34 4.21 6.05 5.78 5.54 5.49 5.19 5.16 4.60	ref XP_001691579.1 , gb EDP04687.1  outer dynein arm-docking complex subunit 1 (ODA3; ODA-DC1) [Chlamydomonas reinhardtii], 0.0
171763	132719	552 AA / 62.2 kD	9- <b>GGGSpAGSpMGKGTpLGAGDTLGHK</b> -> <b>GGGSpAGSMGKGTpLGAGDTLGHK</b> -> <b>GGGSAGSpMGKGTpLGAGDTLGHK</b>	3 3 3	5.47 4.43 3.73	ref XP_001701436.1 , gb EDO97433.1  flagellar outer dynein arm-docking complex protein 2 (ODA1; ODA-DC2) [Chlamydomonas reinhardtii], 0.0
157215	158948 <sup>a</sup>	1057 AA / 111.2 kD <sup>b</sup>	129-AGWYSpNADSGTHTpPKSEADYpDYEGEKK -> AGWYSNADSpGTHTpPKSEADYDYEGEKK -> AGWYSNADSGTpHTpPKSEADYDYEGEKK -> AGWYSpNADSGTHTpPKSpEADYDYEGEKK -> AGWYSNADSpGTHTpPKSpEADYDYEGEKK -> AGWYSNADSGTpHTpPKSpEADYDYEGEKK -> AGWYSNADSpGTpHTPKSEADYDYEGEKK -> AGWYSNADSpGTpHTPKSEADYDYEGEKK -> AGWYSNADSGTHTpPKSEADYDYEGEKK -> AGWYSNADSpGTHTPKSEADYDYEGEKK -> AGWYSNADSGTpHTPKSEADYDYEGEKK -> AGWYSpNADSGTHTPKSpEADYDYEGEKK	3 3 3 3 3 3 3 3 3 3 3 3	5.26 5.13 5.10 5.02 4.88 4.86 4.85 4.59 4.53 4.33 4.00	ref XP_001696921.1 , gb AAU93505.1 , gb EDP00613.1  flagellar axonemal inner dynein arm I1 intermediate chain IC138 (BOP5) [Chlamydomonas reinhardtii], 4e- 37

168881	24358	482 AA / 52.8 kD	419-INLAQRPPSpSVASpFAMSpDMSAPR	3	6.99	ref XP_001697824.1 , gb EDO99707.1  tektin, flagellar protein associated with inner arm dynein [Chlamydomonas reinhardtii], 0.0
			-> INLAQRPPSSpVASpFAMSpDMSAPR	3	6.96	
			-> INLAQRPPSpSVASpFAMSDMSpAPR	3	6.31	
			-> INLAQRPPSSpVASpFAMSDMSpAPR	3	6.29	
			-> <b>INLAQRPPSSpVASpFAMSDMSAPR</b>	3	6.26	
			-> <b>INLAQRPPSpSVASpFAMSDMSAPR</b>	3	6.15	
			-> INLAQRPPSSpVASFAMSpDMSAPR	3	5.78	
			-> INLAQRPPSpSVASFAMSpDMSpAPR	3	5.68	
			-> INLAQRPPSSpVASFAMSpDMSpAPR	3	5.55	
			-> INLAQRPPSpSpVASFAMSpDMSAPR	3	5.51	
			-> <b>INLAQRPPSSpVASpFAMSpDMSpAPR</b>	3	5.50	
			-> INLAQRPPSpSVASFAMSpDMSAPR	3	5.48	
			-> <b>INLAQRPPSpSVASpFAMSpDMSpAPR</b>	3	5.46	
			-> INLAQRPPSpSpVASFAMSDMSAPR	3	4.94	
			-> INLAQRPPSpSpVASpFAMSDMSAPR	3	4.83	
			-> INLAQRPPSpSpVASFAMSDMoSpAPR	3	4.80	
			-> INLAQRPPSpSpVASFAMSpDMSpAPR	3	4.79	
			-> INLAQRPPSSpVASFAMSDMSpAPR	3	4.76	
			-> INLAQRPPSpSpVASpFAMSDMSpAPR	3	4.71	
			-> INLAQRPPSSVASpFAMSpDMSAPR	3	4.69	
			-> INLAQRPPSSVASpFAMSpDMSpAPR	3	4.58	
			-> INLAQRPPSpSVASFAMSDMSpAPR	3	4.50	
			448-IRELEASpLTSpAR	2	3.94	
			-> IRELEASpLTpSAR	2	3.45	
			-> IRELEASLTpSpAR	2	3.18	
			165101	196397	926 AA / 98.5 kD	
-> RRSpSATpGAAANLAAVISGAALNEIK	3	6.53				
-> RRSSpATpGAAANLAAVISGAALNEIK	3	6.41				
-> RRSSpATGAAANLAAVISpGAALNEIK	2	2.92				
-> RRSSATpGAAANLAAVISpGAALNEIK	2	2.87				
728-LMSpMDPQAAWAEWQALCR	2	4.57				

168923	181848 <sup>a</sup>	1769 AA / 182.2 kD	471-AEAEAAAAEEGSpEDSpGPAFKPMMSAAEALK -> AEAEAAAAEEGSpEDSGPAFKPMMSpAAEALK	3 3	6.15 3.99	ref XP_001702469.1 , gb EDP06248.1  flagellar central pair-associated protein [Chlamydomonas reinhardtii] gb AAK38270.1 AF327876_1 PF6 protein [Chlamydomonas reinhardtii], 0.0
165004 <sup>c</sup>	116240 <sup>a</sup>	4891 AA / 523.9 kD	358-DALLDSpYLFTDR -> DALLDSYpLFTDR	2 2	3.87 3.52	ref XP_001689997.1 , gb EDP09735.1  hydin-like protein (similar to mouse hydrocephaly protein hydin HY3) [Chlamydomonas reinhardtii], 0.0
169483	142470	272 AA / 28.8 kD	66-HVASpTNFAPSpGDDEPAPAPSR	2	5.98	gb ABU93234.1  intraflagellar transport protein IFT43 [Chlamydomonas reinhardtii] ref XP_001696653.1 , gb EDP08630.1  predicted protein [Chlamydomonas reinhardtii], 3e-116; annotated in Vs3 as MOT41, protein of unknown function; identified by comparative genomics as being present only in organisms having motile cilia
Enzymes						
167547	181974	1027 AA / 114.8 kD	122-IYEVSpDSpEDEELEDDPSER -> IYpEVSDSpEDEELEDDPSER -> IYpEVSpDSEDEELEDDPSER	2 2 2	4.64 4.35 3.77	ref XP_001701644.1 , gb AAT81143.1  cGMP-dependent protein kinase [Chlamydomonas reinhardtii], 0.0
168935	58843 <sup>a</sup>	585 AA / 63.3 kD	151- <b>SRPPYTpDYpVSTR</b> -> SRPPYpTDYpVSTR -> <b>SRPPYTpDYVSpTR</b> -> <b>SRPPYTDYpVSpTR</b> -> <b>SRPPYpTDYVSpTR</b>	2 2 2 2	3.77 3.27 3.18 2.94 2.73	ref XP_001697865.1 , gb EDO99748.1  mitogen-activated protein kinase 7 [Chlamydomonas reinhardtii], 5e-178

155077 <sup>d</sup>	144070	2058 AA / 206.1 kD	1613- <b>YLPGRPTSpHLTpDYpVATR</b> -> <b>YLPGRPTpSHLTpDYpVATR</b> -> YLPGRPTSpHLTpDYVATpR -> <b>YLPGRPTSpHLTDYpVATpR</b> -> <b>YLPGRPTpSpHLTDYpVATR</b> -> YLPGRPTpSHLTpDYVATpR -> <b>YLPGRPTpSHLTDYpVATpR</b> -> YLPGRPTpSpHLTDYVATpR -> YLPGRPTpSpHLTpDYVATR -> YLPGRPTSHLTpDYpVATpR -> YpLPGRPTSHLTpDYpVATR	2 2 2 2 2 2 2 2 2 2 2	4.47 3.83 3.77 3.44 3.41 3.39 3.27 3.07 3.05 2.96 2.94	ref XP_001703541.1 , gb EDP06223.1  flagellar associated protein [Chlamydomonas reinhardtii], 0.0; Ser/Thr protein kinase domain, 2e-69; found in the flagellar proteome as FAP262
166958 <sup>d</sup>	118223 <sup>e</sup>	1156 AA / 124.6 kD	1137-SAGSpGSTAPLLIDPSTpPR	2	3.29	ref XP_001692057.1  plasma membrane calcium-transporting ATPase [Chlamydomonas reinhardtii], 0.0; found in the flagellar proteome as FAP39
Other flagellar associated proteins (FAP's)						
158915	137210	356 AA / 37.7 kD	285-TpPHHDGFpSPVGSppGPGSFTVQR	3	5.16	ref XP_001692711.1 , gb EDP03730.1  flagellar associated protein [Chlamydomonas reinhardtii] gb AAP04730.1  putative ankyrin-like protein [Chlamydomonas reinhardtii], 0.0; Ankyrin repeats, 7e-27; found in the flagellar proteome as FAP254
159905	143511 <sup>a</sup>	3562 AA / 388.2 kD	1619-AVSpLSQSpDHADLNDLNEVEAAESAPPR -> AVSpLSQSpDHADLNDLNEVEAAESAPPR -> AVSpLSQSpQSDHADLNDLNEVEAAESAPPR	3 3 3	4.95 4.92 4.67	ref XP_001693763.1 , gb EDP09017.1  flagellar associated protein, callose synthase-like protein [Chlamydomonas reinhardtii], 0.0; 1,3-beta-glucan synthase component, 2e-132; found in the flagellar proteome as FAP228

161985	32222 <sup>a</sup> 189686	447 AA / 45.4 kD	21- <b>GAASVVAAAQPPAGT<sub>p</sub>PRSpAR</b>	2	4.23	ref XP_001689442.1 , gb EDP09180.1  flagellar associated protein [Chlamydomonas reinhardtii], 1e-170; Ankyrin repeats, 2e-17; ion transport protein domain, 9e-13; found in the flagellar proteome as FAP230
			-> GAASpVVAAAQPPAGTPRSpAR	2	2.91	
			38-SpARIT <sub>p</sub> PRPVGAALSAAASAPAAVPALIPLDGTPALVR	3	6.58	
			-> SpARITPRPVGAALSpAAASAPAAVPALIPLDGTPALVR	3	6.21	
			-> SpARITPRPVGAALSAAASpAPAAVPALIPLDGTPALVR	3	5.81	
			-> SARIT <sub>p</sub> PRPVGAALSpAAASAPAAVPALIPLDGTPALVR	3	5.67	
			-> SARIT <sub>p</sub> PRPVGAALSAAASpAPAAVPALIPLDGTPALVR	3	5.32	
-> SARITPRPVGAALSpAAASpAPAAVPALIPLDGTPALVR	3	4.73				
164110	144551 <sup>a</sup>	459 AA / 48.8 kD	101-TSASTSANLAGVPLSQPS <sub>p</sub> TPT <sub>p</sub> HRT <sub>p</sub> PR	3	5.30	ref XP_001690814.1 , gb EDP05260.1  flagellar associated protein [Chlamydomonas reinhardtii], 0.0; EF Hand, 2e-09; found in the flagellar proteome as FAP288
			-> TSASTSANLAGVPLSQPST <sub>p</sub> PTHRT <sub>p</sub> PR	3	5.07	
			-> TSASTSANLAGVPLSQPST <sub>p</sub> PT <sub>p</sub> HRT <sub>p</sub> PR	3	5.07	
			-> TSASTSANLAGVPLSQPST <sub>p</sub> PT <sub>p</sub> HRT <sub>p</sub> PR	3	4.84	
			-> TSASTSANLAGVPLSQPS <sub>p</sub> TPT <sub>p</sub> HRT <sub>p</sub> PR	3	4.76	
			-> TSASTSANLAGVPLSQPS <sub>p</sub> TPT <sub>p</sub> HRT <sub>p</sub> PR	3	4.52	
-> TSASTSANLAGVPLSQPS <sub>p</sub> PT <sub>p</sub> PTHRT <sub>p</sub> PR	3	4.19				
171223	194620 <sup>e</sup>	1316 AA / 136.7 kD	356-STSSIGGGYSEPVGS <sub>p</sub> DGEGS <sub>p</sub> DAASAKPR	3	4.93	ref XP_001702134.1 , gb EDO97223.1  flagellar associated protein [Chlamydomonas reinhardtii], 0.0; Sterile alpha motif, 5e-08; found in the flagellar proteome as FAP190
			-> STSSIGGGYSEPVGS <sub>p</sub> DGEGSDAASpAKPR	3	4.36	
			384- <b>RVVAAPAAAAAAAAAAAAAGSpDDDDGAELSpDGDVKR</b>	3	9.68	
			-> RVVAAPAAAAAAAAAAAAAGSpDDDDGAELSpDGDVK	3	4.44	
157568	36026 <sup>a</sup>	1329 AA / 138.1 kD	1-MDGAAAAAAAAAGSpDPDLGK	2	4.92	ref XP_001699049.1 , gb EDO99103.1  flagellar associated protein [Chlamydomonas reinhardtii], 0.0; found in the flagellar proteome as FAP33; in Vs3 annotated as ANK17 with ankyrin repeats, 3e-15

156262	16685 <sup>a</sup>	4441 AA / 466.8 kD <sup>b</sup>	853-LISEAEADRPTSpADGSpR -> LISEAEADRPTpSADGSpR -> LISEAEADRPTpSADGSpRHGAPGSPGGASDGGTTAR	3	5.17	ref XP_001696012.1 , gb EDP00961.1
156264 <sup>f</sup>				3	5.00	flagellar associated protein
				3	4.45	[Chlamydomonas reinhardtii], 2e-61; annotated as FAP49 (156262) and FAP154 (156264) in Vs2; fused as FAP154 in Vs3
153853	192295 <sup>e</sup>	490 AA / 55.1 kD	42-AGYDTpPPSGTpPDGGR -> AGYDTpPPSpGTPDGGR 57-RGGGSpRPATVDSpDDDMPMPGR	2	3.58	ref XP_001697427.1  flagellar associated protein [Chlamydomonas reinhardtii], 4e-169; found in the flagellar proteome as FAP184
				2	3.06	
				3	4.11	
153201	146112	1301 AA / 134.0 kD	583-AASpPPAVPSpPR	2	3.03	ref XP_001692474.1 , gb EDP03952.1  flagellar associated protein [Chlamydomonas reinhardtii], 0.0; found in the flagellar proteome as FAP217
153592	154591	443 AA / 47.6 kD	219-GGSpGSpGAQAAAAPTGQSFSFGAKPEAK	3	4.29	ref XP_001703197.1 , gb EDO96573.1  flagellar associated protein [Chlamydomonas reinhardtii], 3e-119; found in the flagellar proteome as FAP83
166967 <sup>c</sup>	191238	196 AA / 21.7 kD	29-LYTATQGSdVWAR -> LYTATpQGSDVWAR -> LYTpATQGSDVWAR 55- <b>SpRGSFQEGQAMVR</b>	2	3.94	ref XP_001694870.1 , gb EDP02022.1  flagellar associated protein [Chlamydomonas reinhardtii], 1e-112; found in the flagellar proteome as FAP1
				2	3.30	
				2	2.80	
				2	2.83	
156201	185409	153 AA / 16.5 kD	105-SpGANTETATpTLMR	2	2.62	ref XP_001699548.1 , flagellar associated protein [Chlamydomonas reinhardtii], 1e-41; found in the flagellar proteome as FAP152

169069	190974 <sup>a</sup>	904 AA / 97.9 kD	557-VEAPASpSpVGDPAEYGTGVR	2	2.87	ref XP_001694550.1 , gb EDP02545.1  flagellar associated protein [Chlamydomonas reinhardtii], 2e-96; found in the flagellar proteome as FAP93
			589-GWQPEEEPVKEHHSpEAGSpDEDGDNTVASK	3	4.66	
158015	144113	1122 AA / 111.5 kD	481-VAALAAQVAALKGSpRPPSpAAEEK	3	7.53	ref XP_001703395.1 , gb EDP06077.1  flagellar associated protein [Chlamydomonas reinhardtii], 0.0; found in the flagellar proteome as FAP55
163279	142968	515 AA / 54.6 kD	191-AGEEGSpTSVKSpAKSpEAVGSTSVK	2	4.36	ref XP_001698509.1  flagellar associated protein [Chlamydomonas reinhardtii], 0.0; found in flagellar proteome as FAP18
			-> AGEEGSTpSVKSpAKSpEAVGSTSVK	2	4.35	
			-> AGEEGSTpSVKSpAKSpEAVGSTSVK	2	4.26	
			-> SEAVGSTpSVKSpAKSEAVGSTSVK	3	4.61	
			-> SEAVGSTpSVKSpAKSEAVGSTSVK	3	4.33	
			-> SEAVGSpTSVKSpAKSpEAVGSTSVK	2	3.87	
-> SEAVGSpTpSVKSAKSpEAVGSTSVK	3	3.62				
166285 <sup>g</sup>	196787 <sup>a</sup>	936 AA / 97.0 kD <sup>b</sup>	787-GGSpASHTpDDGAAPEPGAGLPNVEHLQPVFHDK	3	5.07	ref XP_001692304.1  flagellar associated protein [Chlamydomonas reinhardtii], 3e- 160; found in the flagellar proteome as FAP147
			-> GGSASpHTpDDGAAPEPGAGLPNVEHLQPVFHDK	3	4.99	
			-> GGSASpHTDDGAAPEPGAGLPNVEHLQPVFHDK	3	4.66	
170753	189109 <sup>a</sup>	797 AA / 90.3 kD	743-LPSpGGSNPPSLGGSpRPGSpAR	2	3.43	ref XP_001691768.1  flagellar associated protein [Chlamydomonas reinhardtii], 0.0; found in the flagellar proteome as FAP59; Vs3 protein has RecF/RecN/SMC N terminal domain, 9e-08

156043	185392 <sup>a</sup>	532 AA / 56.6 kD	241-SpASPGGEDPLNKSpGSAAPK -> SASpPGGEDPLNKSpGSAAPK -> SpASPGGEDPLNKSGSpAAPK -> SASpPGGEDPLNKSGSpAAPK	2 2 2 2	2.92 2.91 2.72 2.72	ref XP_001699472.1  flagellar associated protein [Chlamydomonas reinhardtii], 8e-135; found in the flagellar proteome as FAP116; in Vs3 annotated as similar to microtubule interacting TNF receptor-associated factor 3 interacting protein 1
158903	154904 <sup>a</sup>	409 AA / 45.3 kD	367-SVASTTQGGGAGLQPYGSGGGAAAAAALAGGEGGGGSpRGNSpAR -> SVASTTQGGGAGLQPYGSpGGGAAAAAALAGGEGGGGSpRGNSAR -> SVASTTQGGGAGLQPYGSpGGGAAAAAALAGGEGGGGSpRGNSpAR	3 3 3	6.99 6.33 6.22	ref XP_001703742.1  flagellar associated protein [Chlamydomonas reinhardtii], 2e-174; found in the flagellar proteome as FAP263
152679	194093 <sup>e</sup>	208 AA / 22.0 kD	115-ASFSSpSRPLSpPR -> ASFSSpSRPLSpPR -> ASFSpSSRPLSpPR	2 2 2	3.01 2.96 2.83	hypothetical protein, partially overlaps with ref XP_001700495.1  dbj BAE19786.2  dynein heavy chain 9 (DHC9) [Chlamydomonas reinhardtii], 6e-59

AA, number of amino acids according to (29). MW, molecular weight according to (29). z, charge. Sp, phosphorylated Ser or Dehydroalanine. Tp, phosphorylated Thr or Methyldehydroalanine. Yp, phosphorylated Tyr. Mo, oxidized Met. **Bold** writing, the phosphopeptide was identified by MS<sup>2</sup> and in addition by MS<sup>3</sup> spectra. **Bold and in parallel italics** writing, the peptide was solely identified by MS<sup>3</sup> spectra. Function and/or homologies of depicted proteins is given as determined by NCBI BLASTp along with their conserved domains and their e-values. If a peptide is marked with an arrow, the peptide above shows identical or overlapping sequences, but the phosphorylation sites may be different. <sup>a</sup> Sequence of Vs3 model differs significantly from sequence of Vs2 model, peptides were present in both. <sup>b</sup> AA, MW and the position of the first amino acids of the peptides were calculated according to the Vs3 model. <sup>c</sup> Protein was found in the cellular phosphoproteome of *C. reinhardtii*. <sup>d</sup> Two FAPs with conserved kinase or ATPase domains were included in the category enzymes. <sup>e</sup> Sequence of Vs3 model differs significantly from sequence of Vs2 model, not all peptides were present in both. <sup>f</sup> Vs2 models were combined to one model in Vs3 <sup>g</sup> Vs2 model contains unidentified amino acids.