

Supplementary text for Pazour et al., “Proteomic Analysis of a Eukaryotic Cilium”

Table S1. Flagellar proteins identified by two or more peptides.

Peptides analyzed in this work were compared to the DOE JGI v. 2 assembly of the *C. reinhardtii* genome to identify the gene models (“Cr Model”) from which the peptides were derived. These models were analyzed by BLAST searches of NCBI databases to characterize the encoded proteins (“CrFP description”). If the protein was not functionally characterized in *C. reinhardtii* or any other species, and was identified by 5 or more peptides, it was named FAPxxx for Flagellar Associated Protein (some models with less than 5 peptides also were named). “CrFP Peptides” gives the total number of unique peptides found for each model as well as the number of peptides found in each of the four fractions (“M+M,” membrane + matrix; “Axo,” extracted axonemes; “KCl,” KCl extract; “Tergitol,” Tergitol-insoluble; see Fig. 1). “Induction by Deflagellation” gives, for selected proteins, the fold change \pm standard deviation (SD) in transcript level following deflagellation as measured by real-time PCR. In our terminology, “0x induction,” “1x induction” and “2x induction” indicate no change, a doubling, or a tripling of transcript levels, respectively. “Human Data” indicates the human protein that best matches the *C. reinhardtii* protein, and the BLAST E value of the match (BLAST E values $\leq 1e-10$ are colored in blue); a “yes” under “Human Conserved Uncharacterized” indicates that a protein is conserved in humans but not yet characterized in any organism. “Hs/Cr Reciprocal Best Match” indicates if the human protein identifies the corresponding *C. reinhardtii* protein in a reciprocal BLAST search of the *C. reinhardtii*

genome. “Map Positions of Best Human Matches” gives, for each human protein, the NCBI gene identification number, the chromosome on which the gene is located, and the map position. “Cr/At BLAST E” gives the BLAST E score for the *A. thaliana* protein that best matches a *C. reinhardtii* protein; only those scores $\leq 1e-10$ are given.

Chlamydomonas Data			CrFP Peptides					Induction by Deflagellation		Human Data			Hs/Cr Reciprocal Best Match	Map Positions of Best Human Matches			Cr/At BLAST E
Cr Model		CrFP Description	Total Unique	M+ M	Axo	KCl	Ter git ol	Fold Change	SD (+/-)	Hs NCBI number	Cr/Hs BLAST E value	Human Conserved Unchar?		NCBI Gene ID	Chr	Map Position	
C_1150005	153556	IA1-DHC1a, Inner Dynein Arm Heavy Chain 1-alpha	106	0	6	103	6			XP_085578.6	0		146754	17	17p13.2		
C_750046	169516	DHC1b, Cytoplasmic Dynein Heavy Chain 1b	88	85	3	9	1	7.9	3.7	XP_370652.2	0	Yes	79659	11	11q21-q22.1		
C_410060	165004	HYD3, Hydrocephalus 3-Like Protein	69	0	54	6	28	6.9	2.7	XP_030075.5	0	Yes	54768	16	16q22.2		
C_10076	158922	IA1-DHC1b, Inner Dynein Arm Heavy Chain 1-beta	65	0	4	64	2	3.0	2.0	XP_085578.6	0		146754	17	17p13.2		
C_1580011	156513	CPC1, Central Pair Complex 1	56	0	46	10	33	3.4	0.2	XP_371732.1	5.00E-21	Yes	389282	5	5p13.2		
C_310047	163029	FAP43, Conserved Uncharacterized Flagellar Associated Protein	54	0	29	48	15	4.3	2.1	XP_376056.1	0.016		400954	2	2p16.3		
C_160167	157346	FAP42, Flagellar Associated Protein Similar to Adenylate/Guanylate Kinases	54	2	45	6	19			NP_000849.1	2.00E-28		2987	1	1q32-q41		
C_730051	169338	FMG-1B, Flagella Membrane Glycoprotein 1B	52	50	24	22	23	5.1	3.3	XP_379905.1	6.00E-16		402576	7	7q22		
C_80197	171127	DHC2, Dynein Heavy Chain 2	52	6	35	34	7			NP_060009.1	0		55567	16	16p13.11-p12.3		
C_730006	169293	FAP44, Conserved Uncharacterized Flagellar Associated Protein	47	1	18	43	17	2.4	1.0	NP_060808.2	4.00E-70	Yes	55779	3	3q13.2		
C_170190	157911	IFT172, Intraflagellar Transport Protein 172	47	46	0	3	3			NP_114272.4	0	Yes	26160	2	2p23.3		
C_1740007	157568	FAP33, Flagellar Associated Protein with Ankyrin Repeats	44	29	12	34	13			NP_015628.1	0.009		8989	8	8q13		
C_680086	168675	RIB72, nucleoside-diphosphokinase regulatory subunit p72	44	5	38	8	29			NP_060570.1	9.00E-96	Yes	114327	6p	6p12.3		
C_60158	168923	PC6, Central Pair Protein	42	0	36	5	22	1.2	1.0	NP_055987.1	0.17		23215	1	1q23.3		
C_2600003	161325	DHC7, Dynein Heavy Chain 7	42	1	25	27	11			XP_049952.2	0	Yes	79964	2	2p11.2		
C_680011	168600	FAP45, Flagellar Associated Protein Weakly Similar to Nasopharyngeal Epitheliu	39	1	30	5	26			NP_036469.1	1.00E-06	Yes	25790	1	1q22		
C_260018	161437	FAP46, Conserved Uncharacterized Flagellar Associated Protein	38	0	37	0	8	7.8	0.5	NP_775843	4.00E-14	Yes	255352	10	10q26.3		
C_170072	157793	FAP47, Flagellar Associated Protein with Weak Similarity to Hydrocephalus 3 Pr	35	0	31	1	10	11.5	4.2	XP_098980.4	9.00E-27	Yes	158730	X	Xp21.1		
C_1320004	154911	TUA2, alpha-2 Tubulin	35	21	30	28	22			NP_006000.2	0		7846	12	12q12-12q14.3		
C_220096	160289	ODA-DHCb, Outer Dynein Arm Heavy Chain beta	34	0	0	0	34			NP_001363.1	0	Yes	1770	17	17p12		
C_70002	169905	TUB1, beta-1 tubulin	34	24	28	29	26			NP_006079.1	0		10383	9	9q34		
C_970047	171773	FAP48, Flagellar Associated Protein Similar to Inositol 1,4,5,-tris-Phosphate Rec	33	33	0	0	5	6.3	3.8	NP_001026.1	2.00E-16	Yes	6262	1	1q42.1-q43		
C_860059	170694	RIB43a, Flagellar Protofilament Ribbon Protein	33	0	29	0	20			NP_056468.1	1.00E-26	Yes	26150	22	22q13.31		
C_410035	164979	IFT72/74, Intraflagellar Transport Protein 72 and 74	33	32	0	2	0			NP_079379.1	3.00E-31	Yes	80173	9	9p21.1		
C_1010042	152450	EF1A2, Similar to Elongation Factor 1 alpha	32	27	3	20	3			NP_001949.1	2.00E-93		1917	20	20q13.3		
C_1520005	156262	FAP49, Flagellar Associated Membrane Protein with PAS Sensory	31	3	1	30	14	-1.4	2.0	NP_689635.3	6.4		138639	9	9q22.32		
C_50194	167679	FAP51, Flagellar Associated Coiled-Coil Protein	31	0	27	0	10	5.6	0.7	XP_379895.1	9.00E-06		84176	7	7q22.1		
C_2000016	159240	FAP50, Conserved Uncharacterized Leucine-Rich Repeat Flagellar Associated Pr	31	0	31	1	10			NP_031399.2	5.00E-21	Yes	8036	10	10q25		
C_60149	168914	Cyclic Nucleotide Dependent Protein Kinase	31	16	11	23	3			NP_002721.1	3.00E-53		5566	19	19p13.1		
C_50080	167565	KLP1, Kinesin-Like Protein 1	31	16	0	29	9			NP_878905.1	1.00E-108	Yes	64147	3	3p21.31		
C_20038	162407	DHC5, Dynein Heavy Chain 5	31	1	10	26	2			NP_061720.1	0		56171	2	2q33.1		
C_30120	164620	TUA1, alpha-1 tubulin	31	20	26	23	6	7.2	5.9	NP_006000.2	0	Yes	7846	12	12q12-12q14.3		
C_630058	168135	FAP52, Conserved Uncharacterized Flagellar Associated Protein	30	0	28	5	11	12.2	4.9	NP_659491.2	1.00E-156	Yes	146845	17	17p13.1		
C_1630034	156969	FAP252, Flagellar Associated Protein	29	4	24	7	22	11.7	2.8	NP_004356.1	7.00E-05		1070	5	5q14.3		
C_120056	154633	PHOT, Putative Blue Light Receptor	29	18	12	23	4	-0.2	0.3	NP_002722.1	8.00E-46		5567	1	1p36.1		
C_360006	163907	DHC6, Dynein Heavy Chain 6	29	5	5	22	5			NP_061720.1	0	Yes	56171	2	2q33.1		
C_30001	164501	FAP53, Flagellar Associated Protein	28	0	25	1	4	3.9	3.0	NP_000436.1	0.005		5339	8	8q24		
C_1230030	154251	MST1, Mastigoneme	28	13	16	20	14	1.8	1.1	NP_689966.2	8.00E-10		222663	6p	6p21.3		
C_530081	166736	IA1-IC140, Inner Dynein Arm 11 Intermediate Chain IC140	28	0	1	26	10			NP_660155.1	8.00E-51	Yes	126820	1	1p22.3		
C_200127	159591	EF1A1, Similar to Elongation Factor 1-alpha	28	24	2	15	3	0.2	0.6	NP_001949.1	2.00E-93	Yes	1917	20	20q13.3		
C_7270001	169191	DHC9, Dynein Heavy Chain 9	28	3	25	6	2			NP_061720.1	0		56171	2	2q33.1		
C_1820018	158015	FAP55, Flagellar Associated Protein	27	0	27	0	6			NP_079005.2	0.004		79784	19	19q13.33		
C_460051	165688	FAP56, Flagellar Associated Protein	27	0	2	23	11			NP_056390.2	1.00E-06		26058	2	2q37.1		
C_160066	157246	FAP54, Conserved Uncharacterized Flagellar Associated Protein	27	0	27	0	2	6.1	3.0	BAB71089.1	2.00E-15	Yes	144535	12	12q23.1		
C_290063	162279	RSP3, Radial Spoke Protein 3	27	1	26	4	9	4.9	0.9	NP_114130.3	1.00E-52	Yes	83861	6q	6q25.3		
C_160138	157318	Enolase (2-Phosphoglycerate Dehydratase) (2-Phospho-D-Glyceratehydro-Lyase	27	21	9	22	9	-1.1	0.7	NP_001966.1	1.00E-168	Yes	2026	12	12p13		
C_70152	170055	TUB2, beta-2 tubulin	27	22	23	26	12			NP_006079.1	0	Yes	10383	9	9q34		
C_1660006	157052	MBO2, Coiled-Coil Flagellar Protein	26	0	25	0	2			XP_089747.2	3.00E-35		159686	10	10q25.1		
C_490039	166039	RSP16, Radial Spoke Protein 16	26	4	18	4	20			NP_006136.1	4.00E-57	Yes	3337	19	19p13.2		
C_870023	170753	FAP59, Conserved Uncharacterized Flagellar Associated Protein	26	1	23	4	13	5.0	3.4	XP_291028.3	1.00E-62	Yes	339829	3	3q27.2		
C_10177	159022	IFT81, Intraflagellar Transport Protein 81	26	26	0	1	0	4.1	0.9	NP_054774.2	4.00E-82	Yes	28981	12	12q24.13		
C_1000046	152378	FAP57, Conserved Uncharacterized Flagellar Associated Protein	26	0	23	16	9	7.2	3.9	NP_689711.1	1.00E-106	Yes	149465	1	1p34.1		

Chlamydomonas Data			CrFP Peptides					Induction by Deflagellation		Human Data			Hs/Cr Reciprocal Best Match	Map Positions of Best Human Matches			Cr/At BLAST E
Cr Model	CrFP Description		Total Unique	M+ M	Axo	KCl	Ter git ol	Fold Change	SD (+/-)	Hs NCBI number	Cr/Hs BLAST E value	Human Conserved Unchar?		NCBI Gene ID	Chr	Map Position	
C_560103	167100	DHC8, Dynein Heavy Chain 8	26	1	2	23	4			NP_061720.1	0		56171	2	2q33.1		
C_750045	169515	DHC1b, C-Terminal End of Cytoplasmic Dynein DHC1b	26	26	1	3	0			XP_370652.2	0		79659	11	11q21-q22.1		
C_230118	160652	FAP58, Conserved Uncharacterized Flagellar Associated Protein	26	0	23	5	8	8.9	4.6	XP_089747.2	0	Yes	159686	10	10q25.1		
C_130121	155416	RSP2, Radial Spoke Protein 2	25	3	21	10	15			NP_115748.1	3.00E-06	Yes	84332	10	10q23.1		
C_80226	171156	FAP12, Uncharacterized Protein with Lipase Domain	25	16	4	11	18	21.4	6.5	NP_631918.1	2.00E-10		221955	7	7p22.2		
C_1390012	155265	ODA5-Associated Adenylate Kinase	25	15	14	19	20			NP_000467.1	2.00E-40		203	9	9q34.1		
C_340102	163664	FAP61, Conserved Uncharacterized Flagellar Associated Protein	25	0	23	4	4	3.3	2.4	NP_056400.2	1.00E-57	Yes	26074	20	20p11.23		
C_270146	161826	FAP60, Conserved Uncharacterized Flagellar Associated Protein	25	24	0	2	0	4.7	1.1	NP_079029.2	0	Yes	79809	2	2q24.3-q31.1		
C_240002	160837	FAP62, Flagellar Associated Protein with Ankyrin Repeats	24	14	9	22	6			NP_055240.2	3.00E-09		27130	9	9q31		
C_60116	168881	Tektin	24	0	21	1	12			NP_653275.1	9.00E-20	Yes	146279	16	16p13.2		
C_20334	162703	Parkin Co-Regulated Gene Protein	24	0	19	6	18	8.8	2.8	NP_689623.1	3.00E-59	Yes	135138	6q	6q26		
C_2020016	159289	METE, Methionine Synthase Upregulated During Gametic Activation	23	23	0	0	2	-1.9	1.9	NP_777580.1	3.2		201191	17	17q21.33		
C_60141	168906	FAP63, Flagellar Associated Protein	23	0	23	0	3			XP_038150.3	0.68		23031	19	19p13.12-p13.11		
C_310084	163066	FAP5, Conserved Uncharacterized Protein	23	23	0	1	2	4.2	1.6	NP_073733.1	4.00E-04		64837	11	11q13.1		
C_160036	157216	IDA-IC138, Inner dynein arm intermediate chain IC138	23	0	0	22	3			NP_036276.1	7.00E-48		27019	9	9p21-p13		
C_120055	154632	RSP1, Radial Spoke Protein 1	23	2	20	12	8			NP_003570.1	3.00E-58		8438	1	1p32		
C_1880008	158194	FLA10, Kinesin-II Motor Protein	23	19	3	5	3			NP_004789.1	1.00E-167	Yes	9371	20	20q11.21		
C_210077	159931	FAP66, Conserved Uncharacterized Flagellar Associated Protein	23	22	0	3	1	7.3	2.5	NP_079408.2	0	Yes	57728	4	4p14		
C_670028	168520	ODA-DHcA, Outer Dynein Arm Heavy Chain alpha	23	0	0	0	23	4.1	1.6	NP_001363.1	0		1770	17	17p12		
C_230038	160572	FAP64, Conserved Uncharacterized Flagellar Associated Protein	22	0	16	13	3	6.2	1.4	XP_089747.2	7.00E-66	Yes	159686	10	10q25.1		
C_1710010	157469	ODA-DHcG, Outer Dynein Arm Heavy Chain gamma	22	0	1	0	22			NP_001362.1	0	Yes	1769	6p	6p21.31-p21.1		
C_1310009	154863	IDA5, Actin, Inner Dynein Arm Intermediate Chain	22	9	13	18	13	-0.6	0.9	NP_001605.1	0	Yes	71	17	17q25		
C_980010	171824	FAP65, Conserved Uncharacterized Flagellar Associated Protein	21	0	0	21	4	12.8	8.5	NP_919278.1	3.00E-45	Yes	255101	2	2q36.1		
C_1160041	153658	FAP250, Conserved Uncharacterized Flagellar Associated Protein Similar to NYD	21	0	16	3	7	7.6	5.1	NP_149115.1	1.00E-59	Yes	85478	12	12q13.12		
C_740003	169383	IA-IC28, Inner Dynein Arm Light Chain p28	21	8	13	16	14			NP_003453.2	3.00E-74	Yes	7802	1	1p35.1		
C_280144	162106	FAP68, Flagellar Associated Protein	20	0	16	0	14			XP_372292.1	0.25		389922	Y	Yq11.223		
C_380061	164270	FAP7, Flagellar Associated Protein	20	2	17	9	17			NP_056224.1	0.004		57634	12	12q24.33		
C_340095	163657	FAP69, Conserved Uncharacterized Flagellar Associated Protein	20	0	18	0	9	5.1	3.9	NP_079064.2	1.00E-16	Yes	79846	7	7q21.2		
C_1090038	153027	FAP67, Flagellar Associated Protein Similar to Nucleoside Diphosphate Kinase	20	5	14	2	14			NP_037462.1	1.00E-81	Yes	29922	1	1q24		
C_200042	159506	FAP71, Flagellar Associated Protein	19	0	11	3	15			NP_065875.1	0.18		57584	10	10p12.31		
C_100105	153157	FAP70, Conserved Uncharacterized Flagellar Associated Protein	19	1	1	19	2			NP_660153.2	1.00E-14	Yes	118491	10	10q22.3		
C_160226	157405	FLA8 Kinesin II Motor Protein	19	17	1	7	4			NP_004789.1	1.00E-162		9371	20	20q11.21		
C_160217	157396	EFG2, Similar to Elongation Factor 2	19	19	0	2	1			NP_001952.1	0	Yes	1938	19	19pter-q12		
C_1520029	156286	FAP72, Flagellar Associated Membrane Protein with PAS Sensory Domain	18	1	0	16	10	-0.5	3.1	XP_374998.1	6.9		22895	12	12q24.21		
C_750038	169508	FAP75, Flagellar Associated P-Loop Containing Protein	18	1	0	18	2			NP_689540.1	3.8		122481	14	14q32.31		
C_170077	157798	ODA-DC1, Outer Dynein Arm Docking Complex 1, Mr 105,000	18	0	0	0	18			NP_116255.2	6.00E-05		84952	15	15q21.2		
C_80150	171080	FAP76, Flagellar Associated Protein	18	0	17	1	5			XP_372133.1	7.00E-06	Yes	57653	9	9q22.33		
C_270111	161791	FAP74, Conserved Uncharacterized Flagellar Associated Protein	18	0	15	0	7	1.8	0.8	XP_372193.1	7.00E-25	Yes	85452	1	1p36.33		
C_970037	171763	ODA-DC2, Outer Dynein Arm Docking Complex 2, Mr 70,000	18	0	0	0	18			NP_689804.1	5.00E-28	Yes	160762	12	12q24.13		
C_650031	168312	FAP73, Conserved Uncharacterized Flagellar Associated Protein	18	0	0	16	10	6.1	2.9	NP_653282.1	6.00E-29	Yes	146849	17	17p13.1		
C_130041	155336	FAP77, Flagellar Associated Protein with Very Weak Similarity to Breast Cancer	17	0	13	5	12			NP_036367.1	0.12		22937	3	3p21.31		
C_960024	171679	FAP78, Flagellar Associated Protein	17	0	6	6	9			NP_055204.1	0.012		27043	17	17p13.3		
C_320065	163279	FAP18, High E/A/P Content Protein	17	11	4	13	8			NP_066554.2	2.00E-06		4744	22	22q12.2		
C_450112	165606	RSP9, Radial Spoke Protein 9	17	2	12	4	14			NP_689945.2	1.00E-18	Yes	221421	6p	6p21.1		
C_550076	166958	FAP39, Similar to Ca2+-Transporting ATPase	17	6	3	12	8	0.2	0.5	NP_001673.1	1.00E-154		490	12	12q21-q23		
C_640055	168243	IFT140, Intraflagellar Transport Protein 140	17	17	0	0	1	3.8	1.9	NP_055529.2	0	Yes	9742	16	16p13.3		
C_190129	158803	FAP81, Flagellar Associated Protein	16	0	13	0	10			NP_031363.1	3.00E-04		9940	3	3p22-p21.3		
C_10017	158863	FAP22, Danio Cystic Kidney Disease Gene	16	16	0	2	0	4.3	0.6	NP_079069.1	9.00E-11	Yes	23059	16	16p13.3		
C_450043	165537	FAP82, Conserved Uncharacterized Flagellar Associated Protein	16	0	14	0	5	1.8	0.8	NP_079002.3	7.00E-17	Yes	79781	2	2q37.3		
C_1000050	152382	FAP79, Flagellar Associated Protein with Ankyrin Repeats	16	16	0	2	1	-0.8	0.6	NP_066267.2	2.00E-25	Yes	288	10	10q21		
C_30061	164561	FAP251, Conserved Uncharacterized Flagellar Associated Protein	16	0	14	1	4	4.7	4.5	NP_653269.1	4.00E-58	Yes	144406	12	12q24.31		
C_1410017	155586	PF2, Dynein Regulatory Complex Protein	16	0	13	3	6			NP_001472.1	1.00E-124	Yes	2622	16	16q24.3		

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Cr Model	CrFP Description		Total Unique	M+ M	Axo	KCl	Ter git ol	Fold Change	SD (+/-)	Hs NCBI number	Cr/Hs BLAST E value	Human Conserved Unchar?		NCBI Gene ID	Chr	Map Position	
C_90137	172081	FAP16, Conserved Uncharacterized Protein, Similar to Echinoderm Microtubule	12	12	0	0	0	8.0	5.4	XP_376056.1	3.00E-35	Yes	400954	2	2p16.3		
C_2590004	161133	Similar to Pyruvate Kinase	12	12	0	2	3	0.8	0.1	NP_870986.1	2.00E-92		5313	1	1q21		
C_20225	162594	DHC4, Dynein Heavy Chain 4	12	0	11	0	1			NP_061720.1	0		56171	2	2q33.1		
C_1040033	152670	FAP115, Flagellar Associated Protein	11	3	10	3	10			XP_042978.3	1		84443	X	Xq22		
C_160082	157262	FAP117, Flagellar Associated Protein	11	0	6	4	11			XP_373868.2	0.003		388697	1	1q21.3		
C_460037	165674	FAP123, Flagellar Associated Protein	11	0	5	0	10			NP_835223.1	5.00E-04	Yes	90529	1	1p36.11		
C_910017	171275	FAP126, Flagellar Associated Protein	11	0	7	3	10	10.1	3.8	NP_659490.2	2.00E-04	Yes	143630	11	11p15.4		
C_200209	159673	FAP119, Conserved Uncharacterized Flagellar Associated Protein	11	0	10	3	3			XP_373675.2	2.00E-08	Yes	90835	16	16p11.2		
C_410061	165005	FAP122, Conserved Uncharacterized Flagellar Associated Protein	11	0	6	0	6	4.8	2.4	NP_115639.1	5.00E-13	Yes	84223	3	3q29		
C_3300001	163334	FAP121, Flagellar Associated Protein Similar to Guanylate Kinase	11	11	0	9	2			NP_000849.1	3.00E-13		2987	1	1q32-q41		
C_20103	162472	FAP120, Flagellar Associated Protein with Ankyrin Repeats	11	0	1	11	0			NP_066187.1	2.00E-18	Yes	287	4	4q25-q27		
C_990023	171911	FAP127, Flagellar Associated Protein Weakly Similar to Nuclear Structural Prote	11	0	10	0	5	3.3	1.7	NP_060835.1	1.00E-19	Yes	55329	15	15q21.2		
C_140070	156043	FAP116, Flagellar Associated Protein Similar to Microtubule Interacting TNF Rec	11	11	0	0	0			NP_056465.2	1.00E-25	Yes	26146	2	2q37.3		
C_70192	170095	FAP125, Flagellar Associated Protein Similar to Kinesin KIF17	11	0	10	5	6			NP_065867.1	4.00E-34		57576	1	1p36.12		
C_4220001	165072	ALD1, Fructose-Bisphosphate Aldolase	11	10	0	3	0	-0.2	0.2	NP_000025.1	3.00E-83		226	16	16q22-q24		
C_1410025	155594	PP2A, Protein Phosphatase 2a	11	5	0	7	1			NP_055040.2	1.00E-164	Yes	5518	19	19q13.41		
C_1970008	158615	FAP118, Conserved Uncharacterized Flagellar Associated Protein	11	9	0	2	0	5.9	2.8	NP_065830.1	0	Yes	57539	2	2p24.3		
C_2600004	161326	DHC7, Dynein Heavy Chain 7	11	0	7	6	0			NP_061720.1	0		56171	2	2q33.1		
C_730071	169358	FAP124, Flagellar Associated Protein Similar to Ubiquitin-Activating Enzyme	11	11	0	0	0			NP_695012.1	0	Yes	7317	X	Xp11.23		
C_850051	170615	FAP138, Flagellar Associated Colled-Coil Protein	10	10	0	0	0										
C_810062	170314	FAP137, Flagellar Associated Protein Similar to Uncharacterized VSP3 Protein	10	0	6	4	5			NP_919278.1	7.6		255101	2	2q36.1		
C_120117	154693	FAP129, Flagellar Associated Protein	10	0	9	0	2			XP_374011.1	5		389038	2	2q21.2		
C_1080026	152954	FAP130, Flagellar Associated Protein	10	0	6	0	8			XP_374600.1	1.1		392862	7	7p22.2		
C_80223	171153	FAP140, Flagellar Associated Protein	10	0	8	1	9			NP_666017.1	1		150372	22	22q13.31		
C_1010003	152411	FAP128, Flagellar Associated Protein	10	0	8	2	10			XP_087254.4	0.38		23200	3	3q27		
C_90081	172025	FAP141, Flagellar Associated Protein	10	0	8	1	7			XP_371315.1	0.25	Yes	388701	1	1q22		
C_380089	164298	SKS-C, Protein Kinase, 48K	10	9	0	1	0			NP_059127.1	0.16		53632	2	2q36.1		
C_10358	159203	FAP131, Flagellar Associated Protein Also Known as S926, Novel Nuclear-Encod	10	10	0	0	0			NP_055704.2	0.1		10531	10	10p15.3		
C_680062	168651	FAP136, Flagellar Associated Protein	10	0	5	1	10			NP_055542.1	0.048		9757	19	19q13.1		
C_80146	171076	FAP139, Flagellar Associated Colled-Coil Protein	10	0	0	9	2			XP_371227.2	0.009		9696	1	1pter-p36.11		
C_240045	160880	FAP132, Flagellar Associated Protein	10	0	6	0	9			NP_055248.1	0.001	Yes	27156	22	22q11.2		
C_80102	171032	FAP11, Flagellar Associated Protein with Similarity to TRP Channels	10	4	2	6	7			NP_000288.1	0.001		5311	4	4q21-q23		
C_590099	167468	PKD2, Similar to Polycystin-2	10	3	1	6	4	0.5	0.3	NP_057196.2	4.00E-13	Yes	9033	10	10q24		
C_540078	166850	FAP17, Flagellar Associated Protein with Ankyrin Repeats	10	10	0	0	0			NP_942592.1	2.00E-13	Yes	26057	4	4q21.1-q21.21		
C_11600002	153607	FAP37, Conserved Uncharacterized Protein	10	10	0	0	0	-7.7	4.2	NP_057161.1	2.00E-18	Yes	51651	17	17q23.2		
C_620044	168008	FAP135, Flagellar Associated Protein Similar to Calpain-Like Protein	10	0	1	9	2			NP_006606.1	9.00E-27	Yes	10753	1	1q42.11-q42.3		
C_1530011	156307	D1bLIC, Dynein 1b Light Intermediate Chain	10	7	0	5	0	7.4	1.9	NP_057092.2	4.00E-32	Yes	51626	2	2p25.1-p24.1		
C_1810005	157968	RSP6, Radial Spoke Protein 6	10	0	10	3	5			NP_110412.1	2.00E-36		81492	19	19q13.3		
C_1810004	157967	RSP4, Radial Spoke Protein 4	10	0	7	0	7	5.9	1.1	NP_110412.1	5.00E-39	Yes	81492	19	19q13.3		
C_20188	162557	FAP133, Flagellar Associated Protein Similar to Dynein Intermediate Chains	10	7	0	7	0			NP_443076.1	3.00E-56	Yes	89891	9	9q34.13		
C_380055	164264	FAP134, Conserved Uncharacterized Flagellar Associated Protein	10	0	8	0	7	8.1	4.2	NP_112584.2	6.00E-66	Yes	83450	17	17p11.2		
C_2260011	160144	PP1, Phosphatase 1	10	4	1	9	6	1.9	1.7	NP_002701.1	1.00E-153	Yes	5501	12	12q24.1-q24.2		
C_270130	161810	CDC48, Conserved AAA Domain Protein	10	9	1	2	0	-0.1	0.7	NP_009057.1	0	Yes	7415	9	9p13-p12		
C_1480018	155909	FAP142, Flagellar Associated Protein Similar to Quinone Reductase	9	9	0	0	0			XP_371661.1	0.36		79364	3	3q21.3		
C_140017	155990	FAP144, Flagellar Associated Protein	9	0	7	0	5			NP_055548.2	0.24		9765	5	5p15.2-q14.3		
C_140061	156034	FAP143, Flagellar Associated Protein	9	0	8	0	4			NP_056128.1	0.2		23365	11	11q23.3		
C_150137	156730	FAP145, Flagellar Associated Protein Weakly Similar to Translin-Associated Fact	9	0	2	6	5			NP_689598.1	0.032		130162	2	2p16.3		
C_40164	166285	FAP147, Flagellar Associated Protein Weakly Similar to Myc-Binding Protein-Ass	9	0	0	9	0			NP_115509.2	3.00E-07	Yes	84073	17	17q21.33		
C_240117	160952	ODA-DC3, Outer Dynein Arm Docking Complex 3, Mr 25,000	9	0	2	0	8			NP_003271.1	3.00E-11		7134	3	3p21.3-p14.3		
C_740074	169454	FAP31, Conserved Uncharacterized TPR-Repeat Protein	9	9	0	1	0			NP_891553.1	2.00E-13	Yes	3831	14	14q32.3		
C_30068	164568	FAP146, Conserved Uncharacterized Zinc Finger-Like Flagellar Associated Prote	9	1	3	8	7	5.4	1.0	NP_115633.2	6.00E-19	Yes	84217	1	1p34.1		
C_900027	171211	RSP10, Radial Spoke Protein 10	9	0	4	0	7			NP_543136.1	5.00E-21		89765	21	21q22.3		

Chlamydomonas Data			CrFP Peptides					Induction by Deflagellation		Human Data			Hs/Cr Reciprocal Best Match	Map Positions of Best Human Matches			Cr/At BLAST E
Cr Model		CrFP Description	Total Unique	M+ M	Axo	KCl	Ter git ol	Fold Change	SD (+/-)	Hs NCBI number	Cr/Hs BLAST E value	Human Conserved Unchar?		NCBI Gene ID	Chr	Map Position	
C_60061	168826	FAP148, Flagellar Associated Protein With Cation Channel Domain	9	1	1	7	5	4.9	1.8	NP_775750.1	1.00E-22	Yes	126248	19	19q13.12	3.00E-20	
C_1220044	154206	CNK2, NIMA-Related Kinase 2	9	0	1	6	5	13.0	3.2	NP_036356.1	4.00E-48		4750	4	4q33	2.00E-36	
C_1230002	154223	FAP103, Flagellar Associated Protein Similar to Nucleoside Diphosphate Kinase	9	9	1	0	1	-0.8	0.1	NP_000260.1	9.00E-53	Yes	4830	17	17q21.3	2.00E-63	
C_3230001	163162	Peptidylprolyl Isomerase, Cyclophilin 1, Similar to Radial Spoke Protein RSP12	9	9	0	0	1			NP_005720.1	5.00E-62	Yes	10105	10	10q22-q23	1.00E-68	
C_860007	170642	CAM, Calmodulin	9	7	7	5	2	0.9	1.1	NP_008819.1	7.00E-73	Yes	801	14	14q24-q31	1.00E-69	
C_200199	159663	FTT2, 14-3-3	9	8	0	2	3	-0.5	0.7	NP_006752.1	3.00E-78		7531	17	17p13.3	3.00E-80	
C_50062	167547	PKG, Similar to cGMP-Dependent Protein Kinase	9	9	0	0	0			NP_002722.1	2.00E-78	Yes	5567	1	1p36.1	1.00E-61	
C_370072	164100	ODA-IC2, Outer Dynein Arm Intermediate Chain 2	9	0	0	0	9			NP_075462.1	1.00E-154	Yes	64446	17	17q25		
C_9190001	171258	C-Terminal end of a Dynein Heavy Chain	9	1	7	2	0			NP_061720.1	1.00E-155		56171	2	2q33.1		
C_80166	171096	PF16, Central Pair Protein	9	1	6	7	2			NP_036575.1	1.00E-179	Yes	9576	10	10p12.2	4.00E-17	
C_1500033	156201	FAP152, Flagellar Associated Protein	8	4	5	4	3										
C_1520004	156261	FAP153, Flagellar Associated Protein	8	0	0	8	1										
C_510089	166541	FAP162, Flagellar Associated Protein	8	8	0	0	0										
C_1520007	156264	FAP154, Flagellar Associated Protein with PAS Sensory Domain	8	1	1	8	2	-1.4	0.1	XP_377910.1	5.5		402228	5	5q31.1		
C_430092	165311	HRP1, Putative Cell Wall Protein	8	0	5	6	6			NP_005839.1	1.9		10260	15	15q22.2		
C_810060	170312	FAP40, Flagellar Associated Protein	8	2	6	7	4			NP_775853.2	1.9		283209	11	11q13.3		
C_240009	160844	FAP158, Flagellar Associated Protein Similar to Pherophorin I	8	1	5	7	1			NP_004378.1	0.96		1482	5	5q34		
C_1010068	152476	FAP149, Flagellar Associated Protein	8	0	6	0	5			NP_006776.1	0.36	Yes	10892	18	18q21		
C_350006	163741	FAP159, Leucine-Rich Repeat Flagellar Associated Protein	8	0	0	7	1			XP_085383.7	0.041		146206	16	16q22.1		
C_510069	166521	FAP161, Flagellar Associated Protein	8	1	7	2	0			NP_775799.1	0.031	Yes	161502	15	15q24.3		
C_1170006	153680	FAP150, Similar to Pherophorin-dz1 Protein	8	3	7	5	2			NP_064516.2	0.022		56893	1	1q21		
C_840032	170527	FAP249, Flagellar Associated Protein with Ankyrin Repeats	8	8	0	0	0			NP_848605.1	6.00E-07		255239	11	11q23.2		
C_830019	170435	RSP11, Radial Spoke Protein 11	8	0	6	1	5			NP_114122.2	3.00E-07	Yes	83853	5	5p15.31		
C_2350009	160451	FAP157, Conserved Uncharacterized Flagellar Associated Protein	8	0	0	6	4	9.9	4.4	XP_209941.2	8.00E-12	Yes	286207	9	9q34.13		
C_40010	166131	PF20, Central Pair Associated WD-Repeat Protein	8	2	0	8	0			NP_078808.2	2.00E-16		79582	2	2q35		
C_990019	171907	FAP164, Flagellar Associated Protein with Ankyrin Repeats	8	8	0	0	0	1.8	3.1	NP_659431.5	2.00E-16	Yes	200539	2	2q11.2	1.00E-12	
C_6980002	168690	FAP163, Conserved Uncharacterized WD-Repeat Flagellar Associated Protein	8	8	0	0	0	2.4	0.9	NP_060521.2	7.00E-19	Yes	55112	7	7q36.3		
C_1800011	157940	FAP155, Flagellar Associated Protein Similar to t-Complex-Associated Testis Exp	8	0	5	0	7	9.8	5.5	NP_872345.1	4.00E-19	Yes	202500	6p	6p21.1		
C_180190	158418	FAP156, Flagellar Associated Rab-like GTPase	8	8	0	0	0			NP_006851.1	9.00E-29	Yes	11020	22	22q13.1	1.00E-16	
C_780049	169795	ODA-LC7, Outer Dynein Arm Light Chain 7	8	2	1	5	6			NP_570967.1	1.00E-30	Yes	83657	16	16q23.3		
C_10352	159197	DIP13, Deflagellation Inducible Protein, 13KD	8	4	1	8	5			NP_003722.1	2.00E-32	Yes	8636	9	9q34.3		
C_40146	166267	Similar to Elongation Factor 3	8	7	0	0	1			NP_009120.1	4.00E-43		10061	7	7q36	4.00E-43	
C_2020008	159281	ODA-LC8, Outer Dynein Arm Light Chain 8, 8KD	8	5	7	2	2	4.9	1.7	NP_542408.1	5.00E-44	Yes	140735	17	17q23.2	5.00E-33	
C_140184	156157	PGK, Phosphoglycerate Kinase	8	8	0	0	0	-1.2	1.1	NP_000282.1	1.00E-103	Yes	5230	X	Xq13	1.00E-166	
C_30059	164559	FAP160, Conserved Uncharacterized Coil-Coil Flagellar Associated Protein	8	0	0	8	0	-7.4	9.4	NP_056031.2	1.00E-118	Yes	23262	5	5q21.2	1.00E-125	
C_120077	154654	SAH1, Similar to Adenosylhomocysteinase (S-Adenosyl-L-Homocysteine Hydroly	8	8	1	0	0			NP_000678.1	1.00E-133	Yes	191	20	20cen-q13.1	0	
C_140091	156064	FAP151, Flagellar Associated Protein Similar to Non-Transporter ABC Protein	8	0	1	8	0	-0.7	1.8	NP_009120.1	1.00E-162	Yes	10061	7	7q36	1.00E-168	
C_420012	165102	PKHD1-1, Similar to Fibrocystin	8	3	8	0	1	-0.2	0.1	NP_803875.1	0	Yes	93035	8	8q23.2		
C_950024	171599	DHC11, Dynein Heavy Chain 11	8	0	6	3	0			NP_061720.1	0		56171	2	2q33.1		
C_10275	159120	FAP171, Flagellar Associated Protein	7	1	1	7	2										
C_1100048	153321	FAP165, Flagellar Associated Protein	7	7	0	0	0			NP_872313.1	8.8		144501	12	12q13.13		
C_400020	164828	FAP176, Flagellar Associated Protein	7	0	0	4	5			NP_031397.1	7.9		8019	9	9q34		
C_1510025	156234	FAP170, Flagellar Associated Protein Weakly Similar to Flagellar Membrane Gly	7	7	2	2	0			NP_115514.2	4.1		84078	13	13q13.3		
C_14920001	155932	FAP168, Flagellar Associated Protein	7	0	0	7	0			NP_597713.1	0.47		134549	5	5q31.1		
C_120038	154615	FAP166, Flagellar Associated Protein	7	0	7	0	3			NP_115674.1	0.19		84258	19	19q13.41		
C_1150014	153565	Similar to Carbonic Anhydrase	7	3	0	1	4			NP_001667.2	0.039		479	13	13q11-q12.1	9.00E-13	
C_940050	171550	FAP177, Flagellar Associated Protein	7	3	0	0	4			NP_003473.1	0.038		8085	12	12q12-q14		
C_160110	157290	FAP169, Flagellar Associated Protein	7	0	5	0	3			NP_116264.2	0.008		84961	17	17q21.2		
C_310134	163116	FAP173, Conserved Uncharacterized Flagellar Associated Protein	7	6	0	4	0	2.2	2.0	NP_038470.1	8.00E-07	Yes	30968	9	9p13.1	8.00E-77	
C_2310002	160383	FAP172, Flagellar Associated Protein	7	0	6	1	5	5.4	3.7	XP_371082.1	8.00E-11	Yes	55036	17	17q25.3		
C_20048	162417	FAP174, Flagellar Associated Protein Similar to Myc-Binding Protein	7	0	7	2	0			NP_036465.1	2.00E-13	Yes	26292	1	1p33-p32.2		
C_380098	164307	ODA-LC3, Outer Dynein Arm Light Chain 3, 16KD	7	0	0	0	7			NP_057700.2	1.00E-14		51314	7	7p14.1		

Chlamydomonas Data			CrFP Peptides					Induction by Deflagellation		Human Data			Hs/Cr Reciprocal Best Match	Map Positions of Best Human Matches			Cr/At BLAST E
Cr Model	CrFP Description		Total Unique	M+ M	Axo	KCl	Ter git ol	Fold Change	SD (+/-)	Hs NCBI number	Cr/Hs BLAST E value	Human Conserved Unchar?		NCBI Gene ID	Chr	Map Position	
C_660055	168434	FAP178, Flagellar Associated Protein Similar to Testis and Spermatogenesis Cel	7	1	1	5	5	11.9	4.8	NP_653245.2	2.00E-21	Yes	132851	4	4q34.2		
C_40173	166294	Similar to Importin Alpha 2	7	0	5	1	1			NP_002258.2	1.00E-21		3839	13	13q14.3		
C_730054	169341	FMG-1A, Flagella Membrane Glycoprotein 1A	7	7	2	3	0			XP_379905.1	4.00E-24		402576	7	7q22		
C_680013	168602	ODA-LC1, Outer Dynein Arm Light Chain 1	7	0	1	0	7			NP_113615.1	4.00E-34	Yes	83544	14	14q24.3		
C_380021	164230	Similar to Protein Phosphatase 2C	7	7	0	0	0			NP_055721.3	2.00E-38	Yes	22843	17	17q23.2		
C_120075	154652	FAP167, IFT80, Intraflagellar Transport protein 80	7	6	0	1	0	7.2	2.3	XP_028413.4	2.00E-53	Yes	57560	3	3q25.33-q26.1		
C_1630013	156948	IFT57, Intraflagellar Transport Protein 57	7	7	0	1	0			NP_060480.1	2.00E-57	Yes	55081	3	3q13.13		
C_360070	163971	FAP175, Flagellar Associated Conserved Uncharacterized Protein with Ankyrin R	7	1	1	6	0	2.2	2.7	NP_066187.1	2.00E-73	Yes	287	4	4q25-q27		
C_670076	168568	Similar to Arginyl-tRNA Synthetase	7	7	0	0	0			NP_002878.2	1.00E-133	Yes	5917	5	5q35.1		
C_1660005	157051	FAP193, Coiled-Coil Flagellar Associated Protein	6	0	6	0	0										
C_2440005	160775	FAP201, Flagellar Associated Protein	6	0	4	0	5										
C_550052	166934	FAP209, Flagellar Associated Protein	6	0	6	0	0										
C_1920001	158482	FAP195, Flagellar Associated Protein	6	0	0	6	0			XP_049349.11	7.2		26033	10	10q26		
C_300076	162889	FAP205, Flagellar Associated Protein	6	0	3	2	6			XP_113706.5	6.3		196385	12	12q24.31		
C_50195	167680	FAP211, Flagellar Associated Protein	6	1	5	5	2			NP_004930.1	4.5		1653	2	2p24		
C_270009	161689	Phosphoglyceromutase	6	6	0	0	0	-1.2	1.1	NP_003312.3	3		7284	16	16p11.2		
C_1150042	153593	FAP182, Flagellar Associated Protein	6	0	5	0	3			NP_954871.1	2.7		80320	17	17q21.32		
C_50197	167682	FAP212, Flagellar Associated Protein	6	0	0	6	0			NP_000525.1	2.4		5378	2	2q31.1		
C_1100042	153315	FAP181, Flagellar Associated Coiled-Coil Protein	6	6	0	0	0			NP_620714.1	1.6		219931	11	11q13.1-q13.2		
C_1340007	155018	FAP188, Flagellar Associated Protein	6	0	3	0	4			XP_042833.3	1.5		23060	15	15q22.1		
C_3380004	163387	FAP206, Flagellar Associated Protein	6	0	5	1	2			NP_061900.1	0.57		54502	4	4p13-p12		
C_650036	168317	FAP213, Coiled-Coil Flagellar Associated Protein	6	0	0	3	6			XP_050478.1	0.36		57477	X	Xp11.23		
C_110075	153900	FAP186, Uncharacterized Flagellar Associated Protein	6	1	1	5	0			NP_056492.1	0.16		26751	2	2p25.3		
C_220159	160352	FAP199, Lipase-Domain Containing Flagellar Associated Protein	6	0	5	2	4			NP_005725.2	0.13		10114	11	11p13		
C_1180025	153741	FAP183, Flagellar Associated Protein	6	0	6	0	0			NP_005176.1	0.048		810	10	10pter-p13		
C_240010	160845	FAP202, Flagellar Associated Protein Similar to Pherophorin I	6	0	5	5	0			XP_038150.3	0.045		23031	19	19p13.12-p13.11		
C_1480002	155893	FAP191, Flagellar Associated Protein Similar to Quinone Reductase	6	6	0	0	1			XP_371661.1	0.025		79364	3	3q21.3		
C_50085	167570	FAP210, Flagellar Associated Protein	6	0	6	1	0			XP_291020.1	0.006		339809	2	15q11.2		
C_650056	168337	FAP214, Flagellar Associated Protein with Ca2+-Dependent Phospholipid-Bindin	6	6	0	0	0			NP_056107.1	1.00E-06		23344	12	12q13.13		
C_1020027	152520	FAP179, Flagellar Associated Protein Weakly Similar to Glutathione S-Transfere	6	2	2	4	2			NP_000843.1	6.00E-07		2950	11	11q13		
C_2000002	159226	FAP197, Flagellar Associated Protein Weakly Similar to Plectin	6	0	0	5	1			NP_006435.1	2.00E-07		10592	9	9q31.2		
C_1250022	154341	FAP187, Uncharacterized Flagellar Associated Protein	6	0	6	0	0	1.4	1.1	NP_006444.2	3.00E-08		10607	16	16p13.3		
C_2340004	160430	FAP200, Flagellar Associated Protein with Weak Calmodulin Similarity	6	0	4	0	4			NP_115704.1	7.00E-09		84288	1	1q44		
C_150052	156645	FAP192, Conserved Uncharacterized Flagellar Associated Protein	6	0	5	0	2	9.2	2.8	NP_073621.1	6.00E-11	Yes	64799	15	15q22.31		
C_110068	153893	FAP185, Conserved Uncharacterized Flagellar Associated Protein	6	6	0	0	0			NP_073733.1	1.00E-11	Yes	64837	11	11q13.1		
C_10320001	152554	FAP180, Flagellar Associated Protein Similar to Uridylate and Adenylate Kinases	6	3	0	6	1			NP_000467.1	3.00E-12		203	9	9q34.1		
C_2810005	161894	FAP203, Flagellar Associated Protein Weakly Similar to Heat Shock Protein 70	6	2	4	3	1			NP_005338.1	1.00E-13		3309	9	9q33-q34.1		
C_70195	170098	Similar to HSP70	6	0	6	0	0			NP_005338.1	6.00E-14		3309	9	9q33-q34.1		
C_30222	164722	ODA-LC6, Outer Dynein Arm Light Chain 6, 11KD	6	0	1	0	6			NP_542408.1	2.00E-14		140735	17	17q23.2		
C_160143	157323	FAP194, Flagellar Associated Protein Similar to Central Pair Protein PF16	6	0	4	3	0			NP_036575.1	1.00E-17		9576	10	10p12.2		
C_860086	170721	FAP215, Conserved Uncharacterized Flagellar Associated Protein	6	6	0	0	0	0.9	0.5	NP_002517.1	3.00E-24		4907	6q	6q14-q21		
C_480009	165900	FAP208, Flagellar Associated Protein with Ankyrin Repeats	6	6	0	0	2			NP_689983.1	2.00E-24	Yes	255119	4	4q21.3		
C_20323	162692	RSP12, Radial Spoke Protein 12	6	0	5	0	5			NP_775943.1	9.00E-25	Yes	285755	6q	6q21		
C_110027	153853	FAP184, Conserved Uncharacterized Flagellar Associated Protein	6	0	4	2	3	5.4	3.0	NP_699207.1	5.00E-26	Yes	257236	4	4p16.1		
C_450085	156579	FAP207, Conserved Uncharacterized Flagellar Associated Protein	6	0	4	1	5	7.2	2.4	NP_776254.1	1.00E-27	Yes	283385	12	12q24.31		
C_3310003	163344	Dynein Heavy Chain, Similar to DHC9, All peptides are also found in DHC9	6	1	5	3	1			NP_061720.1	1.00E-31		56171	2	2q33.1		
C_10310	159155	FAP196, Conserved Uncharacterized Flagellar Associated Protein	6	0	0	6	0	7.3	1.1	NP_659491.2	6.00E-35	Yes	146845	17	17p13.1		
C_1500009	156177	VFL2, Caltractin / Centrin, 20 kD Calcium-Binding Protein	6	0	4	5	4	3.5	1.8	NP_004335.1	8.00E-40	Yes	1069	X	Xq28		
C_220104	160297	FAP198, Conserved Uncharacterized Flagellar Associated Protein	6	0	3	0	6	14.6	3.9	NP_653208.2	9.00E-48	Yes	124637	17	17p13.2		
C_1780022	157697	ARL2, Similar to ADP-Ribosylation Factor-Like Protein, DrScorpion	6	6	0	0	0	0.8	0.3	NP_004302.1	1.00E-54	Yes	403	10	10q23.3		
C_13770001	155160	FAP189, Conserved Uncharacterized Coiled-Coil Flagellar Associated Protein	6	0	5	5	0			XP_089747.2	9.00E-56	Yes	159686	10	10q25.1		
C_2130007	159749	FAP32, Conserved Uncharacterized Flagellar Associated Protein	6	6	0	0	0	5.2	1.3	NP_064538.2	2.00E-62	Yes	56912	11	11q23.3		

Chlamydomonas Data		CrFP Peptides					Induction by Deflagellation		Human Data			Hs/Cr Reciprocal Best Match	Map Positions of Best Human Matches			Cr/At BLAST E
Cr Model	CrFP Description	Total Unique	M+ M	Axo	KCl	Ter git ol	Fold Change	SD (+/-)	Hs NCBI number	Cr/Hs BLAST E value	Human Conserved Unchar?		NCBI Gene ID	Chr	Map Position	
C_20138	162507 PRX4, Similar to Peroxiredoxin 4	6	6	1	2	1			NP_006397.1	4.00E-75	Yes	10549	X	Xp22.13	1.00E-60	
C_1150031	153582 Malate dehydrogenase	6	5	1	1	0			NP_005909.2	1.00E-96		4191	7	7p12.3-q11.2	1.00E-127	
C_20061	162430 FAP204, Flagellar Associated Protein Similar to GTP-Binding Protein	6	6	0	0	0	0.1	0.4	NP_037473.2	1.00E-124	Yes	29789	2	2q31.1	1.00E-152	
C_490046	166046 GSK3, Glycogen Synthase Kinase 3	6	5	0	0	2	0.2	0.7	NP_063937.1	1.00E-129	Yes	2931	19	19q13.31	1.00E-156	
C_70224	170127 Similar to Alcohol Dehydrogenase	6	6	0	0	0			NP_000662.2	1.00E-134	Yes	128	4	4q21-q25	1.00E-147	
C_110180	154005 Similar to T-complex protein 1 epsilon subunit, putative chaperonin	6	6	0	0	0			NP_036205.1	0	Yes	22948	5	5p15.31	0	
C_280023	161985 FAP230, Flagellar Associated Protein	5	0	4	2	0			NP_055922.1	7.5		23133	X	Xp11.22		
C_800011	170165 FAP245, Flagellar Associated Protein	5	0	0	5	0			NP_891554.1	4.6		79778	7	7p22.3		
C_330118	163516 FAP233, Flagellar Associated Protein	5	0	2	5	0			NP_055614.1	3.1		9843	X	Xq11-q12		
C_1610019	156865 FAP222, Flagellar Associated Protein	5	0	4	0	4			NP_006097.1	2.8		10413	11	11q13		
C_970003	171729 FAP248, Flagellar Associated Protein	5	5	0	0	0			XP_378730.1	2.3		400638	17		17	
C_1410022	155591 FAP221, Coiled-Coil Flagellar Associated Protein	5	0	5	0	0			NP_079345.1	1.9		80139	8	8p11.23		
C_3200003	163131 Hydroxyproline-Rich Glycoprotein GAS29	5	0	5	2	1			XP_374501.1	1.9		392762	7	7q22		
C_640033	168221 FAP242, Coiled-Coil Flagellar Associated Protein	5	0	0	5	0			NP_055566.2	1.8		9788	8	8p22		
C_780008	169754 FAP244, Flagellar Associated Protein	5	0	0	5	0			NP_009041.2	1.1		7011	14	14q11.2		
C_210051	159905 FAP228, Flagellar Associated Protein Similar to Callose Synthase	5	1	0	4	1			NP_000079.1	1		1277	17	17q21.3-q22.1	1.00E-111	
C_410059	165003 FAP235, Flagellar Associated Protein	5	3	0	0	2			NP_056996.1	0.89		51059	8	8q24.3		
C_1230028	154249 FAP219, Flagellar Associated Protein	5	0	4	0	4			NP_006292.2	0.32		7786	12	12q13		
C_100149	153201 FAP217, Flagellar Associated Coiled-Coil Protein	5	0	0	4	3			XP_208993.3	0.093		284069	17	17q21.31		
C_1010019	152427 FAP216, Flagellar Associated EF-Hand Protein	5	0	2	0	4			NP_739576.1	0.065		80352	6p	6p21.3		
C_1270021	154445 FAP220, Flagellar Associated Protein	5	1	3	0	3			XP_034872.4	0.047		23176	5	5q31		
C_7160001	169099 FAP243, Coiled-Coil Flagellar Associated Protein	5	0	4	0	2			NP_057323.2	0.024		51168	17	17p11.2		
C_540077	166849 FAP239, Flagellar Associated Coiled-Coil Protein	5	0	0	4	3			NP_003010.3	0.004		6441	10	10q22.2-q23.1		
C_430115	165334 FAP237, Conserved Uncharacterized Flagellar Associated Protein	5	0	5	0	0	-6.2	7.6	NP_060034.8	0.003		55576	12	12q23.3		
C_1510005	156214 IFT20, Intraflagellar Transport Protein 20	5	5	0	0	0			NP_777547.1	4.00E-04	Yes	90410	17	17q11.2		
C_570086	167212 FAP240, Flagellar Associated Protein	5	0	0	5	0			NP_115513.2	2.00E-04	Yes	84077	3	3p25.1		
C_110161	153986 FAP218, Flagellar Associated Protein	5	5	0	0	0			NP_060693.1	1.00E-04		55743	12	12q24.33		
C_50183	167668 FAP241, Flagellar Associated Protein	5	0	1	1	3			XP_208835.4	1.00E-04		283767	15	15q11.2		
C_180158	158386 FAP225, Flagellar Associated Protein	5	0	0	2	4			NP_056363.2	4.00E-05		667	6p	6p12-p11		
C_430069	165288 FAP236, Conserved Uncharacterized Flagellar Associated Protein	5	0	2	0	5	17.1	5.8	XP_208809.2	2.00E-08		283726	15	15q25.1		
C_490074	166074 FAP238, Flagellar Associated Protein	5	0	3	3	0			NP_056390.2	2.00E-09		26058	2	2q37.1		
C_250115	161253 FAP9, Weakly Similar to RABs	5	5	0	0	0	8.7	3.6	NP_073614.1	3.00E-12	Yes	64792	7	7q22.1		
C_10189	159034 FAP227, Flagellar Associated Protein with Similarity to Conserved Region in Tes	5	0	2	0	5	2.8	0.9	NP_919246.1	1.00E-12	Yes	378464	2	2p22.3	2.00E-12	
C_320063	163277 FAP232, Conserved Uncharacterized Flagellar Associated Protein	5	5	0	0	0	4.6	2.5	NP_057210.1	1.00E-13	Yes	51668	1	1p32.1-p33		
C_20056	162425 FAP231, Flagellar Associated Protein with Ankyrin Repeats	5	0	3	0	4			NP_065210.1	1.00E-13	Yes	286	8	8p11.1		
C_80051	170981 Tctex2b, Similar to ODA-LC2	5	3	0	4	2	10.6	1.7	NP_689986.1	8.00E-19		255758	3	3q29		
C_350031	163766 FAP234, Conserved Uncharacterized Flagellar Associated Protein	5	0	0	5	0	3.5	1.5	NP_940901.1	3.00E-23	Yes	341883	14	14q23.1		
C_10119	158965 FAP226, Flagellar Associated Protein Similar to Calpain	5	5	0	0	0	20.3	8.6	NP_005623.1	4.00E-24		6650	16	16p13.3	5.00E-17	
C_8400002	170482 FAP246, Conserved Uncharacterized Leucine-Rich Repeat Flagellar Associated P	5	0	5	0	0	12.7	7.6	NP_653249.1	1.00E-28	Yes	136332	7	7q33	3.00E-14	
C_230098	160632 FAP229, Flagellar Associated Protein Similar to FK506-Binding Proteins	5	5	0	0	0			NP_000792.1	1.00E-39	Yes	2280	20	20p13	3.00E-28	
C_190063	158737 FAP224, Conserved Uncharacterized Flagellar Associated Protein	5	5	0	0	0	-0.4	0.3	NP_054757.1	3.00E-50	Yes	28969	7	7p21.2	2.00E-84	
C_170065	157786 FAP223, Flagellar Associated Protein Similar to Calcium-Dependent Protein Kinase	5	5	0	0	0			NP_003647.1	1.00E-61		8536	3	3p25.3	1.00E-136	
C_520009	166572 NADP-Malate Dehydrogenase	5	2	1	4	0			NP_005908.1	5.00E-65		4190	2	2p13.3	1.00E-141	
C_960034	171689 FAP247, Flagellar Associated Protein Similar to Serine-Threonine Kinase	5	1	0	5	1	8.7	2.1	NP_003150.1	3.00E-85	Yes	6792	X	Xp22	6.00E-46	
C_1220040	154202 RABD1, RAB-like GTP-Binding Protein YPTC1	5	4	0	0	3			NP_004152.1	1.00E-90	Yes	5861	2	2p14	8.00E-90	
C_80101	171031 RAB1, RAB-like GTP-Binding Protein YPTC4	5	4	0	0	2			NP_002856.1	2.00E-93	Yes	5862	8	8q12.1	1.00E-101	
C_1260018	154393 IFT52, Intraflagellar Transport Protein 52	5	5	0	1	0			NP_057088.1	1.00E-102	Yes	51098	20	20q12-q13.1		
C_700061	169064 Similar to Calcium Transporting ATPases	5	0	0	2	3	0.6	0.6	NP_001674.1	1.00E-154		491	3	3p26-p25	1.00E-153	
C_810057	170309 Hypothetical Protein	4	0	1	0	4										
C_610008	167871 Coiled-Coil Protein	4	0	4	0	0			NP_005817.1	9.6		10236	1	1p36.11		
C_300007	162820 Similar to Pherophorin II	4	0	4	0	0			NP_004548.2	5.4		4855	6p	6p21.3		
C_880018	170820 Oxygen-Evolving Enhancer Protein 2	4	0	4	0	0			XP_376112.1	5.2		400993	2	12q14.1	1.00E-56	

Chlamydomonas Data			CrFP Peptides					Induction by Deflagellation		Human Data			Hs/Cr Reciprocal Best Match	Map Positions of Best Human Matches			Cr/At BLAST E
Cr Model		CrFP Description	Total Unique	M+ M	Axo	KCl	Ter git ol	Fold Change	SD (+/-)	Hs NCBI number	Cr/Hs BLAST E value	Human Conserved Unchar?		NCBI Gene ID	Chr	Map Position	
C_1550010	156389	Similar to Pherophorin	4	0	2	1	2			NP_071389.1	4.1		63939	20	20q13.2-q13.33		
C_1190051	153824	TPR-Domain Protein	4	0	0	2	2			NP_056360.2	3.9		26024	7	7q22.1		
C_3380002	163385	Hypothetical Protein	4	4	0	0	0			NP_003038.2	3.7		6548	1	1p36.1-p35		
C_1150015	153566	Hypothetical Protein	4	1	1	0	3			NP_061324.1	2.9		55966	1	1p36.31		
C_170123	157844	Hypothetical Protein	4	0	3	2	1			NP_065134.1	2.7		57122	12	12q14.3		
C_300008	162821	Similar to Pherophorin	4	1	2	3	1			NP_722520.1	2.1		161882	16	16q24.2		
C_590018	167387	Coiled-Coil Protein	4	0	4	3	3			NP_000881.3	1.8		3762	11	11q24		
C_1120048	153437	Hypothetical Protein	4	0	1	0	4	21.6	4.1	NP_444279.1	1.1		116840	17	17p13.2		
C_640058	168246	Hypothetical Protein	4	0	0	4	0			NP_001798.1	0.83		1056	9	9q34.3		
C_300058	162871	Hypothetical Protein	4	0	0	4	0			NP_005210.2	0.61		1729	5	5q31		
C_1040042	152679	Hypothetical Protein	4	0	4	1	3			NP_060353.2	0.5		64743	X	Xp11.23		
C_1620003	156889	Hypothetical Protein	4	0	0	0	4			XP_042833.3	0.23		23060	15	15q22.1		
C_340008	163570	Hypothetical Protein	4	0	1	0	3			NP_001931.1	0.11		1822	12	12p13.31		
C_20104	162473	Hypothetical Protein	4	0	0	4	0			NP_115859.2	0.079		7148	6p	6p21.3		
C_1250031	154350	Coiled-Coil Protein	4	0	0	4	0			NP_055892.1	0.066		23098	17	17q11		
C_16120001	156840	Hypothetical Protein	4	0	0	4	0			NP_056281.1	0.061		25930	3	3p21.3		
C_680050	168639	Hypothetical Protein	4	0	1	3	1			NP_940881.1	0.049		284355	19	19q13.33		
C_730021	169308	Coiled-Coil Protein	4	0	2	1	1			NP_653316.2	0.026		151651	3	3p24.3		
C_70106	170009	Hypothetical Protein	4	0	0	4	1			NP_002947.1	0.009		6249	12	12q24.3		
C_1530026	156322	Coiled-Coil EF-Hand Protein	4	0	3	0	1			NP_002696.2	0.007		5493	16	16p13.3		
C_10167	159012	Hypothetical Protein	4	0	2	0	3	5.1	3.0	NP_714918.1	0.004		158297	9	9p22.1		
C_60207	168972	Hypothetical Protein	4	4	0	0	0			NP_079279.2	0.002		80070	12	12q12		
C_900007	171191	Similar to Putative Protease/Amidase	4	4	0	0	0			NP_872418.1	0.001	Yes	347862	11	11p15.5		
C_1230005	154226	Similar to Calcium-Binding Protein	4	4	0	0	0			NP_059118.1	0.001		51806	10	10p15.1	2.00E-11	
C_250030	161168	Hypothetical Protein	4	0	0	3	4			NP_689919.1	7.00E-04	Yes	219557	7	7q21.13	5.00E-11	
C_170175	157896	EF-Hand Protein	4	1	4	0	0			NP_777283.1	4.00E-04		26289	1	1p31		
C_210041	159895	Similar to Zinc-Finger Proteins	4	0	4	0	0			NP_877952.1	7.00E-07	Yes	51593	7	7q21	2.00E-11	
C_1410021	155590	Similar to Oxidoreductase/Dehydrogenase	4	4	0	0	0			NP_057095.1	3.00E-07		51102	1	1pter-p22.3	5.00E-11	
C_40157	166278	Similar to Hyalin	4	0	4	1	0			XP_370601.2	2.00E-07		387740	11	11p15.5		
C_140037	156010	Weakly Similar to Protein Phosphatase Regulatory Subunit	4	2	0	3	0	1.0	0.6	NP_068778.1	1.00E-07	Yes	6992	6p	6p21.3		
C_1830001	158033	Coiled-Coil Protein	4	0	0	4	0			NP_002465.1	4.00E-10		4629	16	16p13.13-p13.12		
C_8820002	170794	Thioredoxin H	4	4	0	1	0			NP_003320.1	3.00E-11		7295	9	9q31	1.00E-14	
C_680027	168616	Leucine-Rich Repeat Coiled-Coil Protein	4	4	0	0	0			NP_874365.1	1.00E-11	Yes	23513	8	8q24.3		
C_530068	166723	Conserved Uncharacterized Protein with Ankyrin Repeats	4	4	0	0	0	-12.9	13.4	XP_042860.6	3.00E-13	Yes	23243	3	3p25.1	1.00E-24	
C_70068	169971	DLC7b, Roadblock-Like Dynein Light Chain	4	2	3	3	2			NP_570967.1	8.00E-16		83657	16	16q23.3		
C_680036	168625	Similar to Importin Alpha 1b	4	4	0	0	0			XP_379894.1	1.00E-16		402569	7	7q22	7.00E-15	
C_1070035	152894	Conserved Uncharacterized Protein	4	0	4	3	0	-11.0	18.4	XP_379967.1	2.00E-18	Yes	23145	7	7q36.1		
C_370102	164130	Leucine-Rich Repeat Protein	4	4	0	0	0			NP_694992.1	1.00E-19	Yes	255252	15	15q14	7.00E-38	
C_1910003	158455	Similar to MAP3K delta-1 Protein Kinase	4	4	0	0	0			NP_003179.1	2.00E-20		6885	6q	6q16.1-q16.3	5.00E-25	
C_1020054	152547	Similar to Glutathione S-Transferase	4	3	2	1	1			NP_000843.1	2.00E-24	Yes	2950	11	11q13		
C_10069	158915	Conserved Uncharacterized Protein with Ankyrin Repeats	4	4	0	0	0	1.4	0.4	NP_710181.1	3.00E-25	Yes	91526	2	2q33.1	1.00E-17	
C_2230003	160091	Similar to Peroxiredoxin	4	4	0	0	0			NP_036226.1	6.00E-34	Yes	25824	11	11q13	8.00E-40	
C_1610014	156860	Similar to Polyubiquitin	4	4	0	1	0			NP_003324.1	1.00E-36		7311	19	19p13.1-p12	3.00E-37	
C_4130001	164925	Similar to Nascent Polypeptide Associated Complex alpha Chain	4	3	0	2	0			NP_005585.1	7.00E-42	Yes	4666	12	12q23-q24.1	3.00E-41	
C_900058	171242	Similar to cob(I)alamin adenosyltransferase	4	4	0	0	0			NP_443077.1	2.00E-42	Yes	326625	12	12q24		
C_860056	170691	Similar to Calmodulin	4	4	1	2	1			NP_008819.1	6.00E-46		801	14	14q24-q31	8.00E-46	
C_100034	153086	FA2, Protein Kinase	4	0	0	4	0			NP_003148.1	4.00E-50		6787	3	3p21.1	9.00E-43	
C_130172	155467	Conserved Uncharacterized Protein	4	1	0	3	0	9.1	3.4	XP_375682.1	2.00E-50	Yes	9731	1	1p36.32		
C_450030	165524	Similar to Calcium-Dependent protein Kinase	4	4	0	0	0	-0.2	0.7	NP_742126.1	7.00E-55		817	4	4q26	1.00E-137	
C_30158	164658	Similar to Asparaginyl-tRNA Synthetase	4	4	0	0	0	-10.6	14.6	NP_078954.3	2.00E-62	Yes	79731	11	11q13.4	1.00E-162	
C_10830001	152917	ARFA1a, ADP-ribosylation factor 1	4	4	0	1	0	0.7	0.3	NP_001649.1	8.00E-87		375	1	1q42	3.00E-94	
C_80137	171067	Similar to GDP dissociation inhibitor GDI1	4	4	0	0	0			NP_001484.1	1.00E-111	Yes	2664	X	Xq28	8.00E-82	

Chlamydomonas Data		CrFP Peptides					Induction by Deflagellation		Human Data			Hs/Cr Reciprocal Best Match	Map Positions of Best Human Matches			Cr/At BLAST E
Cr Model	CrFP Description	Total Unique	M+ M	Axo	KCl	Ter git ol	Fold Change	SD (+/-)	Hs NCBI number	Cr/Hs BLAST E value	Human Conserved Unchar?		NCBI Gene ID	Chr	Map Position	
C_620048	168012 KAP, Kinesin II associated Protein	4	3	0	2	0			NP_055785.2	1.00E-127		Yes	22920	1	1q23.3	
C_190067	158741 Similar to Eukaryotic Initiation Factor 4A	4	4	0	1	0	0.2	0.3	NP_001958.1	1.00E-159		Yes	1974	3	3q28	0
C_110095	153920 Coiled-Coil Protein	3	0	3	0	0										
C_1610008	156854 Hypothetical Protein	3	0	0	3	0										
C_6620002	168371 Hypothetical Protein	3	0	0	3	1										
C_730023	169310 Coiled-Coil Protein	3	0	0	2	1										
C_810061	170313 Hypothetical Protein	3	0	1	2	0										
C_290113	162329 Similar to DNA-Binding Protein HU	3	0	0	3	0			NP_000044.1	9.3			540	13	13q14.2-q21	
C_1420029	155634 Hypothetical Protein	3	0	0	3	0			NP_003176.1	6.3			6874	20	20q13.33	
C_590014	167383 Hypothetical Protein	3	2	1	0	2			NP_945342.1	5.2			284252	18	18q12.1	
C_440077	165440 Coiled-Coil Protein	3	0	0	3	0			NP_057048.1	3.7			51673	16	16q22.1	
C_200178	159642 Hydroxyproline-Rich Glycoprotein	3	0	2	3	0			NP_689722.1	3.5			150244	22	22q11.23	
C_2700003	161585 Hypothetical Membrane Protein	3	1	0	0	2			XP_370836.1	3.5			388079	15	15q11.2	
C_100189	153241 RSP7, Radial Spoke Protein 7	3	1	2	0	0			NP_006152.2	2.6			4762	5	5q23-q31	2.00E-52
C_1970006	158613 Hypothetical Protein, Similar to CrPKD2	3	0	0	2	1			NP_922932.1	2.5			345667	5	5q12.3	
C_120148	154724 Hypothetical Protein	3	0	2	0	1			NP_851853.1	1.9			221496	6p	6p21.31	
C_1460023	155804 Isocitrate Lyase	3	3	0	0	0			XP_371471.1	1.9			758	22	22q13.31	7.00E-22
C_1540029	156369 Hypothetical Protein	3	3	0	0	0			NP_077306.1	1.8			11000	1	1q22	
C_130122	155417 Profilin	3	3	0	0	0			NP_000482.2	1.6		Yes	713	1	1p36.3-p34.1	2.00E-20
C_200130	159594 Hypothetical Protein With Insulin-Like Domain	3	3	0	0	1			NP_699193.1	1.5			167681	6q	6q15	
C_170162	157883 Similar to Hydroxyproline-Rich Glycoprotein GAS28 Precursor	3	0	3	0	0			NP_057425.2	1.4			51196	10	10q23	
C_950023	171598 Model Next to Dynein Heavy Chain 11, Probably Not Dynein	3	0	3	0	0			XP_036299.7	0.72			57648	1	1p34.3	
C_170032	157753 Membrane Protein with PAS Sensory Domain (three peptides)	3	1	1	1	0	1.0	0.5	NP_003710.1	0.69			8622	5	5q14.1	
C_1800020	157949 Conserved Uncharacterized Protein	3	3	0	0	0	-2.8	1.9	XP_209509.2	0.51			285193	2	2q37.3	
C_1810016	157979 Coiled-Coil Protein	3	0	0	3	0			XP_371463.1	0.24			388891	22	22q12.2	
C_1080051	152979 Hypothetical Protein	3	2	0	0	1			XP_291314.2	0.19			26267	9	9p13.1	
C_10174	159019 Hypothetical Protein	3	2	0	2	0			NP_056972.1	0.19			51361	1	1p32.1	
C_100035	153087 WD40-Repeat Containing Protein	3	0	3	0	0			NP_061942.2	0.18			54554	3	3q21.1	
C_340077	163639 Hypothetical Protein	3	0	0	0	3			XP_292943.3	0.12			344148	2	2q21.2	
C_80196	171126 Similar to Hydroxyproline Rich Glycoprotein Vsp6	3	0	3	1	0			XP_375369.1	0.11			400546	16	16q22.3	
C_520017	166580 Hypothetical Protein	3	0	2	0	1			NP_001421.2	0.046			2034	2	2p21-p16	
C_130029	155324 Coiled-Coil EF-Hand Protein	3	3	0	0	0			NP_003091.2	0.02			6643	5	5q23	
C_160190	157369 Weak Similarity to Conserved Uncharacterized Protein	3	0	0	2	3	4.7	2.1	NP_001804.1	0.012			1062	4	4q24-q25	
C_10366	159211 Hypothetical Protein	3	0	0	3	0			NP_005563.1	0.009			4000	1	1q21.2-q21.3	
C_13140001	154849 Hypothetical Protein	3	3	0	0	3			XP_371086.1	0.003			388432	17	17q25.3	
C_240120	160955 Coiled-Coil Protein	3	0	0	2	2			NP_060041.1	0.001			55580	2	2p16.3	
C_450017	165511 Hypothetical Protein	3	0	0	3	0			NP_056151.1	0.001			23390	12	12q21.1	
C_250097	161235 Hypothetical Protein	3	0	3	0	0			XP_378177.1	5.00E-04			399700	17	17q11.2	
C_430065	165284 Hypothetical Protein	3	1	0	3	0			NP_055892.1	2.00E-04			23098	17	17q11	
FAP41	192034 Hypothetical Protein	3	0	3	3	2			XP_379905.1	6.00E-05			402576	7	7q22	
C_310066	163048 Hypothetical Protein with Weak Similarity to Elongation Factor 1 gamma	3	3	0	0	0			NP_001395.1	3.00E-05			1937	11	11q12.3	
C_2340009	160435 Coiled-Coil Protein	3	3	0	0	0			XP_209505.3	2.00E-06			285188	2	2q37.3	
C_4990001	166000 Hypothetical Protein	3	0	0	3	0			XP_370927.1	1.00E-06		Yes	146310	16	16p13.3	
C_6350001	168070 Conserved Uncharacterized Protein	3	0	2	0	1			NP_620151.1	3.00E-07		Yes	128153	1	1q41	
C_740063	169443 Hypothetical Protein Protein with FAS Domains	3	3	0	0	0			NP_000349.1	2.00E-07			7045	5	5q31	
C_770050	169700 Leucine-Rich-Repeat Coiled-Coil Protein	3	3	0	0	0			NP_079337.2	7.00E-10			80131	19	19p13.3	
C_590002	167371 Similar to Monodehydroascorbate Reductase	3	3	0	0	0			NP_653305.1	1.00E-10		Yes	150209	22	22q11.21-q11.22	7.00E-80
C_40151	166272 Carbonic Anhydrase 1	3	0	3	1	0			NP_005173.1	4.00E-12			766	16	16q22.1	1.00E-12
C_870056	170786 Similar to 60S Ribosomal Protein L14 (Also Known as Hydroxyproline-Rich Glyc	3	0	0	3	0			XP_056681.4	4.00E-13		Yes	144581	12	12q14.1	2.00E-21
C_890036	170904 Similar to Glycine-Rich RNA-Binding Protein	3	3	0	0	0			NP_001271.1	3.00E-13			1153	19	19p13.3	2.00E-17
C_1500010	156178 Similar to Transmembrane ATPases	3	3	0	0	0	-2.4	1.7	NP_569730.1	1.00E-13		Yes	534	6p	6p21.3	1.00E-18
C_1570028	156484 Weakly Similar to Leucine Zipper Transcription Factor-Like Protein	3	3	0	0	0			NP_065080.1	1.00E-14		Yes	54585	3	3p21.3	

Chlamydomonas Data			CrFP Peptides					Induction by Deflagellation		Human Data			Hs/Cr Reciprocal Best Match	Map Positions of Best Human Matches			Cr/At BLAST E
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C_880050	170852	Similar to Glutaredoxin	3	3	0	0	0			NP_932066.1	2.00E-15	Yes	51022	1	1q31.2-q31.3	4.00E-21	
C_650009	168290	Similar to Glutathione S-Transferase	3	3	0	0	0			NP_665683.1	2.00E-17	Yes	2938	6p	6p12.1		
C_460056	165693	Similar to Kinases	3	0	0	3	0			NP_002410.1	5.00E-18		4296	11	11q13.1-q13.3	2.00E-17	
C_1570033	156489	Similar to Spermine Synthase	3	3	0	0	0			NP_003123.1	1.00E-20		6723	1	1p36-p22	6.00E-30	
C_380086	164295	ODA-LC2, Outer Dynein Arm Light Chain 2	3	0	0	0	3			NP_689986.1	2.00E-21	Yes	255758	3	3q29		
C_1380019	155233	Similar to Structural Maintenance of Chromosomes (SMC) Proteins	3	1	1	0	1			NP_006297.2	2.00E-21		8243	X	Xp11.22-p11.21	6.00E-25	
C_10363	159208	FAP13, Conserved Uncharacterized Protein	3	3	0	0	0	3.9	2.7	NP_004795.1	1.00E-21	Yes	9391	2	2q11.2	3.00E-15	
C_510021	166473	Similar to Calcium-Dependent Protein Kinase	3	3	0	0	0			NP_004746.2	3.00E-24		9252	14	14q31-q32.1	3.00E-26	
C_20021	162390	Similar to Transcriptional Coactivator-Like Protein	3	1	0	3	0			NP_003783.1	4.00E-27	Yes	8721	9	9q34.3	3.00E-33	
C_330103	163501	Similar to Ran-binding protein 1, RanBP1	3	3	0	0	0			NP_002873.1	3.00E-28	Yes	5902	22	22q11.21	1.00E-36	
C_380105	164314	Ribosomal Protein S27	3	3	0	0	0			NP_057004.1	4.00E-32	Yes	51065	15	15q22.1	1.00E-40	
C_360048	163949	Ubiquitin-Conjugating Enzyme E2 Isoform	3	3	0	0	0			NP_003340.1	7.00E-37	Yes	387522	20	20q13.2	4.00E-51	
C_610033	167896	Similar to Translation Initiation Factor 5A	3	3	0	0	0			NP_001961.1	3.00E-38	Yes	1984	17	17p13-p12	4.00E-50	
C_610051	167914	Similar to Alpha-Soluble NSF Attachment Protein	3	3	0	0	0	-0.2	0.3	XP_371393.1	8.00E-40	Yes	63908	20	20p12.3-p11.21	6.00E-59	
C_850045	170609	Similar to Putative Serine Protease	3	3	0	0	0			NP_006016.1	2.00E-40	Yes	8909	12	12q13.1	3.00E-40	
C_1580014	156516	Similar to SNF2/RAD54 Family Proteins	3	3	0	0	0	-0.1	0.1	XP_372231.1	2.00E-51	Yes	54821	X	Xq13.1	1.00E-59	
C_1010056	152464	Conserved Uncharacterized Protein	3	3	0	0	0	2.1	1.3	NP_478144.1	9.00E-57	Yes	57718	14	14q32.2		
C_330025	163423	Similar to Polyubiquitin	3	3	0	0	0			NP_066289.1	1.00E-60	Yes	7316	12	12q24.3	3.00E-60	
C_1140007	153495	Conserved Uncharacterized Protein	3	3	0	0	0			NP_057046.1	1.00E-61	Yes	51077	14	14q24.2	1.00E-56	
C_1860010	158140	Similar to Glycyl-tRNA Synthetase	3	3	0	0	0			NP_002038.1	5.00E-63	Yes	2617	7	7p15	3.00E-75	
C_370121	164149	FAP253, Conserved Uncharacterized Flagellar Associated Protein	3	0	1	0	3	7.1	5.3	NP_849149.2	2.00E-63	Yes	154865	7	7q31.33		
C_160077	157257	RABF1, Similar to GTP-Binding Protein Rab5	3	2	0	0	1			NP_958842.1	9.00E-64	Yes	5878	17	17q21.2	1.00E-65	
C_180161	158389	Similar to Protein Phosphatase	3	3	0	0	0	-0.5	0.9	NP_002700.1	6.00E-64		5500	2	2p23	0	
C_410080	165024	Similar to Ubiquitin-Conjugating Enzyme	3	3	0	0	0	-0.5	0.7	NP_003339.1	1.00E-65	Yes	7334	12	12q22	3.00E-74	
C_90122	172066	RABG1, RAB-like GTP-binding protein YPTC5	3	3	0	0	0			NP_004628.4	5.00E-75	Yes	7879	3	3q21.3	7.00E-86	
C_110042	153868	Similar to RNA Helicase	3	3	0	0	0	-1.7	1.0	NP_004387.1	1.00E-78		1655	17	17q21	8.00E-83	
C_740056	169436	Similar to Cyclic Nucleotide Dependent Protein Kinase	3	3	0	0	0	-0.3	0.4	NP_006250.1	8.00E-80		5593	4	4q13.1-q21.1	1.00E-47	
C_30122	164622	RAN, Similar to RAN GTPase	3	3	0	0	0	-2.3	2.5	NP_006316.1	5.00E-84	Yes	5901	12	12q24.3	1.00E-100	
C_490009	166009	Similar to Mitogen-Activated Protein Kinase	3	2	0	1	0	0.3	0.4	NP_620603.1	2.00E-95		5598	17	17p11.2	1.00E-123	
C_230110	160644	Similar to Eukaryotic Translation Initiation Factor 6 (EIF-6) - Like Protein	3	3	0	0	0			NP_002203.1	8.00E-97	Yes	3692	20	20q12	1.00E-103	
C_18960001	158210	Beta Tubulin	3	1	1	1	2			NP_006079.1	1.00E-111		10383	9	9q34	1.00E-120	
C_750005	169475	Similar to S-Adenosylmethionine Synthetase	3	3	0	0	0			NP_005902.1	1.00E-129	Yes	4144	2	2p11.2	0	
C_420025	165115	Conserved Uncharacterized Coiled-Coil Protein	3	2	0	1	0	3.5	0.7	NP_689488.2	1.00E-132	Yes	92104	2	2q31.3		
C_190013	158687	Similar to Hydroxymethyltransferase	3	3	0	0	0			NP_005403.2	1.00E-157		6472	12	12q12-q14	0	
C_3800004	164184	Similar to UDP-Glucose Dehydrogenase	3	3	0	0	0			NP_003350.1	1.00E-160		7358	4	4p15.1	0	
C_430064	165283	Similar to UDP-Glucose Dehydrogenase	3	3	0	0	0	0.5	0.8	NP_003350.1	1.00E-161	Yes	7358	4	4p15.1	0	
C_640028	168216	Similar to Phosphoribosylformylglycinamide Synthase	3	0	3	0	0			NP_036525.1	0	Yes	5198	17	17p13.1	0	
C_580059	167319	Conserved Uncharacterized Protein	2	0	2	0	0	-0.5	0.8								
C_130037	155332	Hypothetical Protein	2	2	0	0	0										
C_1510023	156232	Hypothetical Protein	2	2	0	0	0										
C_160035	157215	Inner Dynein Arm 11 intermediate chain IC138 piece, see C_160036	2	0	0	2	0										
C_22160001	160050	Hypothetical Protein	2	0	0	2	0										
C_2280008	160180	Hypothetical Protein	2	2	0	2	0										
C_500069	166413	Coiled-Coil Protein	2	0	1	0	2										
C_5490001	166772	Coiled-Coil Protein (Mostly Xs)	2	0	0	2	1										
C_690046	168738	Hypothetical Protein	2	2	0	0	0										
C_760066	169637	Hypothetical Protein	2	0	0	1	1										
C_450120	165614	Similar to Hydroxyproline-Rich Glycoprotein GAS29 Precursor	2	0	0	2	0			XP_371403.1	9.8		388802	20	20q13.32		
C_1750005	157593	Hypothetical Protein	2	0	1	0	2			NP_037497.1	9.6		26088	22	22q13.31		
C_840010	170505	Coiled-Coil Protein	2	2	0	0	0			NP_076980.1	7.7		79042	19	19q13.4		
C_1610018	156864	Hypothetical Protein	2	2	0	0	0			NP_073585.6	7.6		64759	7	7p12.3		
C_940039	171539	Similar to Gametolysin and Autolysin	2	0	2	1	0			XP_371309.1	6.5		23248	1	1q21.3		

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Cr Model		CrFP Description	Total Unique	M+ M	Axo	KCl	Ter git ol	Fold Change	SD (+/-)	Hs NCBI number	Cr/Hs BLAST E value	Human Conserved Unchar?		NCBI Gene ID	Chr	Map Position	
C_330027	163425	Similar to Sexual Inducer Glycoprotein	2	0	0	2	0			NP_060693.1	6.1		55743	12	12q24.33		
C_70041	169944	Light-Harvesting Chlorophyll-a/b Binding Protein LhcII-3	2	1	0	0	1			NP_004703.1	5.7		9146	17	17q25		
C_290114	162330	Similar to HU DNA-Binding Proteins	2	0	0	2	0			NP_057484.3	5		25764	15	15q15.1		
C_2620005	161345	Hypothetical Protein	2	1	1	2	0			NP_938026.1	4.2		349136	7	7q36.1		
C_830020	170436	Hypothetical Protein	2	0	0	2	0			NP_065955.1	4		57664	19	19q13.33		
C_110216	154041	Hypothetical Protein	2	0	2	0	1			XP_374042.1	3.8	Yes	389131	3	3p14.1		
C_40156	166277	Hypothetical Protein	2	2	0	0	0			NP_689591.1	3.8		127943	1	1q23.1		
C_90072	172016	Hypothetical Protein	2	2	0	0	0			NP_000453.2	3.6		7337	15	15q11-q13		
C_450104	165598	Conserved Uncharacterized Protein	2	2	0	0	0	-4.8	5.7	NP_057552.1	3.4	Yes	51241	14	14q24.1		
C_30259	164759	Hypothetical Protein	2	0	2	0	0			NP_005145.2	3.3		9101	15	15q15.3		
C_1500014	156182	Hypothetical Protein	2	0	2	0	0			XP_375408.1	2.4		9912	17	17p12		
C_90194	172138	Hypothetical Protein	2	0	0	0	2			NP_853517.1	2.4		353288	17	17q21.2		
C_220001	160194	GP1_Hydroxyproline-Rich Glycoprotein1	2	0	0	2	0			NP_000278.2	2.2		5190	6p	6p21.1		
C_160106	157286	Cytochrome C	2	2	0	0	0			NP_003473.1	2.1		8085	12	12q12-q14		
C_660012	168391	Ribulose Biphosphate Carboxylase	2	2	0	0	0			NP_001922.2	2.1		1737	11	11q23.1		
C_270048	161728	Hypothetical Protein	2	0	0	0	2			NP_056531.1	1.9		50488	17	17p13.3		
C_880036	170838	Hypothetical Protein	2	0	0	2	0			NP_079223.2	1.6		80012	3	3q26.31		
C_1050039	152733	Hypothetical Protein	2	2	0	0	0			NP_115915.1	1.5		84618	1	1p34.3-p33		
C_430114	165333	Hypothetical Protein	2	0	2	0	0			NP_776176.2	1.1		283848	16	16q22.1		
C_2370001	160482	Hypothetical Protein	2	0	0	0	2			NP_872586.1	1		245806	6q	6q22.31		
C_380028	164237	Hypothetical Protein	2	0	0	2	0			NP_620706.1	0.91		6601	12	12q13-q14		
C_10250	159095	Similar to Pherophorin I	2	0	2	2	0			NP_941961.1	0.86		386674	21	21q22.3		
C_330021	163419	Hypothetical Protein	2	0	0	2	0			NP_037403.1	0.86		27344	X	Xp11.23		
C_1360002	155121	Conserved Uncharacterized Protein	2	2	0	0	0	0.1	0.2	NP_065733.1	0.76		57412	10	10q24.33		
C_910052	171310	Hypothetical Protein	2	2	0	0	0			NP_055877.3	0.76		23082	10	10q24.32		
C_1060014	152783	Coiled-Coil Protein	2	0	2	0	0			NP_057285.3	0.73		51421	3	3q21-q22		
C_920029	171369	Hypothetical Protein	2	1	0	1	0			XP_375922.1	0.65	Yes	400848	20	20q13.32		
C_420076	165166	Hypothetical Protein	2	0	1	2	0			NP_942136.1	0.61		31	17	17q21		
C_400074	164882	Weak Similarity to cGMP-Dependent Protein Kinases	2	0	0	2	0			XP_032278.5	0.6		23094	19	19q13.13		
C_1780007	157682	Conserved Uncharacterized Protein	2	2	0	0	0	-0.5	0.1	XP_113625.5	0.56	Yes	195977	10	10q11.22		
C_70109	170012	Universal Stress-Domain Containing Protein	2	2	0	0	0			NP_001886.1	0.52		1457	20	20p13		
C_1710011	157470	Hypothetical Protein	2	0	2	0	1			NP_002131.2	0.49		3190	9	9q21.32-q21.33		
C_590029	167398	ODA-LC5, Outer Dynein Arm Light Chain 5, 14KD	2	0	0	0	2			NP_057323.2	0.3		51168	17	17p11.2		
C_760033	169604	Coiled-Coil Protein	2	0	2	0	1			NP_055792.1	0.3		22985	14	14q11.2		
C_130161	155456	Hypothetical Protein	2	0	0	0	2			NP_149056.1	0.29		63948	1	1p32.3		
C_100190	153242	RSP7 piece	2	0	2	0	0			NP_008989.1	0.22		11131	6p	6p12		
C_350082	163817	Similar to Pseudouridylate Synthase I	2	0	0	2	0			NP_005924.1	0.2		4297	11	11q23		
C_780027	169773	Similar to Sulfite Synthesis Pathway Protein and Ammonium Transporter Struct	2	2	0	0	0			NP_005954.2	0.19		4619	17	17p13.1		
C_170044	157765	Hypothetical Protein	2	2	0	0	0			NP_940926.1	0.15		374618	15	15q21.2		
C_40131	166252	Similar to DNA Gyrase Subunit A	2	0	2	0	0			NP_001059.2	0.13		7155	3	3p24		
C_40046	166167	Membrane Protein	2	2	0	0	0			NP_006050.2	0.083		10319	9	9q31-q34		
C_850014	170578	Hypothetical Protein	2	0	1	0	2			NP_004964.2	0.056		3720	6p	6p24-p23		
C_410117	165061	WD40-Repeat Containing Coiled-Coil Protein	2	0	2	0	2			NP_064597.1	0.055	Yes	56964	15	15q26.1		
C_3530003	163713	Hypothetical Protein	2	0	1	1	0			NP_005558.1	0.034		3959	17	17q25		
C_190100	158774	Similar to Carboxymethylenebutenolidase	2	2	0	0	0			NP_620164.1	0.014		134147	5	5p15.31		
C_14900001	155931	Hypothetical Protein	2	0	2	0	1			NP_115645.3	0.008		84229	16	16q13		
C_400024	164832	Hypothetical Protein	2	0	0	2	0			NP_055560.1	0.007		9780	16	16q24.3		
C_290071	162287	Hypothetical Protein	2	0	0	2	0			NP_659444.1	0.005		204801	19	19q13.43		
C_340127	163689	Weak Similarity to Phosphoglycerate Mutase	2	2	0	0	0			NP_116262.2	0.003		84959	11	11q24.1		
C_380091	164300	Hypothetical Protein	2	0	0	2	0			NP_006653.1	0.002		10847	16	16p11.2		
C_490022	166022	Coiled-Coil Protein	2	0	0	2	0			NP_055818.3	0.001		23015	15	15q11.2		
C_200160	159624	Conserved Uncharacterized Protein (Ubiquitin Related?)	2	2	0	0	1	0.1	0.6	NP_009037.1	0.001	Yes	5412	13	13q12-q13		

Chlamydomonas Data			CrFP Peptides					Induction by Deflagellation		Human Data			Hs/Cr Reciprocal Best Match	Map Positions of Best Human Matches			Cr/At BLAST E
Cr Model	CrFP Description		Total Unique	M+ M	Axo	KCl	Ter git ol	Fold Change	SD (+/-)	Hs NCBI number	Cr/Hs BLAST E value	Human Conserved Unchar?		NCBI Gene ID	Chr	Map Position	
C_370082	164110	EF Hand Containing Protein	2	0	0	2	0			NP_004049.1	3.00E-04		828	19	19p13.3		
C_710066	169170	Low Complexity Protein with Similarity to Spider Silk Fibroin	2	0	2	1	0			NP_003176.1	2.00E-04		6874	20	20q13.33		
C_1140049	153537	Conserved Uncharacterized Protein	2	2	0	0	0	0.8	1.2	NP_899199.1	2.00E-04		440	7	7q21.3	2.00E-13	
C_21180001	159694	Hypothetical Protein	2	0	2	1	1			NP_659475.1	1.00E-04		92749	2	2p24.1		
C_200124	159588	Conserved Uncharacterized Protein	2	2	0	0	0			NP_056492.1	8.00E-05	Yes	26751	2	2p25.3		
C_90082	172026	Hypothetical Protein	2	0	1	1	0			NP_689711.1	3.00E-05		149465	1	1p34.1		
C_180170	158398	Similar to Subtilisin-Like Serine Proteases	2	0	2	0	0			NP_002561.1	2.00E-05		5046	15	15q26		
C_760002	169573	Similar to Calcium-Dependent Protein Kinase	2	2	0	0	0			NP_008819.1	2.00E-05		801	14	14q24-q31		
C_740022	169402	Hypothetical Protein	2	0	2	0	0			NP_689658.1	1.00E-05	Yes	145483	14	14q24.2		
C_1720008	157501	Hypothetical Protein with Ankyrin Repeats	2	2	0	0	0			NP_940683.1	2.00E-06		157567	8	8q22.3		
C_10043	158889	EF-Hand Containing Protein	2	0	1	1	0			NP_008819.1	2.00E-06		801	14	14q24-q31		
C_750013	169483	Hypothetical Protein	2	2	0	0	0			NP_443105.1	4.00E-08	Yes	112752	14	14q24.3		
C_640017	168205	Conserved Uncharacterized Protein with von Willebrand Factor Type A Domain	2	2	0	0	0	8.0	1.0	NP_002209.2	1.00E-09	Yes	3700	3	3p21-p14		
C_90120	172064	Leucine-Rich Repeat Protein	2	0	0	2	0			XP_057296.2	1.00E-10	Yes	116064	3	3q13.33		
C_520027	166590	Similar to RNA-Binding Protein	2	0	0	0	2			NP_006267.34	8.00E-11		6432	2	2p22.1	3.00E-23	
C_710063	169167	Weakly Similar to ER Protein	2	2	0	0	0			NP_076994.1	3.00E-11		79070	13	13q33		
C_130074	155369	Similar to Formyltetrahydrofolate Deformylase	2	2	0	0	0			NP_000810.1	3.00E-11		2618	21	21q22.11	7.00E-34	
C_2280002	160174	Similar to Protein Phosphatase	2	0	0	2	0			NP_055449.1	3.00E-12		9647	22	22q11.22	1.00E-13	
C_120019	154596	Similar to mannitol dehydrogenase	2	2	0	0	0			NP_000664.1	1.00E-12		131	4	4q23-q24	1.00E-110	
C_3850002	164198	Conserved Uncharacterized Protein	2	2	0	0	0	1.1	0.6	NP_776245.1	2.00E-13	Yes	122664	14	14q11.2		
C_330101	163499	Similar to Phosphoribosyl Pyrophosphate Synthase	2	2	0	0	0			NP_002755.1	1.00E-14		5631	X	Xq21-q27	1.00E-118	
C_1650017	157030	Similar to Hydroxyproline-Rich Glycoprotein VSP4	2	2	0	0	0			NP_940999.1	5.00E-16		9632	10	10q22.3	2.00E-27	
C_440064	165427	Similar to Nuclear Transport Factor 2	2	2	0	0	0			NP_005787.1	3.00E-17	Yes	10204	16	16q22.1	4.00E-35	
C_950050	171624	Similar to Inositol Hexaphosphate Kinase H	2	2	0	0	0			NP_689416.1	3.00E-19	Yes	253430	10	10q21.2-q21.3	4.00E-34	
C_420024	165114	Coiled-Coil Protein With Similarity to Prefoldins	2	2	0	0	0			NP_036526.2	2.00E-19	Yes	5202	1	1q23.1	3.00E-24	
C_180045	158273	ODA-LC4, Outer Dynein Arm Light Chain 4	2	0	0	0	2			NP_004057.1	4.00E-20		1068	18	18p11.32	3.00E-20	
C_860028	170663	Conserved Uncharacterized Protein	2	0	0	2	0			NP_060225.4	2.00E-20	Yes	54888	5	5p15.32	3.00E-21	
C_120080	154657	Similar to Adenosine Kinase	2	2	0	0	0	0.3	0.7	NP_006712.2	1.00E-23	Yes	132	10	10q22	4.00E-33	
C_80041	170971	Similar to Pre-Acrosome Localization Protein 1	2	1	0	0	1			XP_045581.6	1.00E-24	Yes	22994	17	17q25.3		
C_150073	156666	Conserved Uncharacterized Protein	2	1	0	1	0	2.3	0.9	NP_849172.1	1.00E-24	Yes	197358	16	16p13.3	3.00E-16	
C_1690015	157167	Similar to Tetrahydrofolate Synthase	2	2	0	0	0			NP_005947.2	5.00E-29		4522	14	14q24	4.00E-33	
C_1010057	152465	Similar to Phosphodiesterase	2	0	0	2	0			NP_000915.1	2.00E-29		5153	12	12q13		
C_1110009	153341	Similar to V-type proton-ATPase	2	2	0	0	0			NP_001687.1	1.00E-29	Yes	529	22	22q11.1	3.00E-46	
C_1140006	153494	Similar to Protease Inhibitor	2	2	0	0	0	0.2	0.4	NP_006208.1	8.00E-30	Yes	5276	3	3q26.1-q26.2	7.00E-23	
C_450071	165565	Similar to Calcium/Calmodulin-Dependent Kinase	2	2	0	0	0			NP_741960.1	6.00E-30		815	5	5q33.1		
C_240149	160984	Methionine Sulfoxide Reductase Domain-Containing Protein	2	2	0	0	0			NP_932346.1	2.00E-30	Yes	253827	12	12q14.1	2.00E-43	
C_1130006	153457	Similar to Phosphomannomutase	2	2	0	0	0			NP_000294.1	8.00E-31	Yes	5373	16	16p13.3-p13.2	3.00E-41	
C_10057	158903	Conserved Uncharacterized Protein	2	0	2	0	0	6.6	3.0	NP_054876.2	2.00E-35	Yes	29070	16	16q13		
C_520010	166573	Similar to Protein Phosphatase 2C	2	2	0	0	0			NP_002698.1	2.00E-36	Yes	5496	2	2p23.3	2.00E-39	
C_1020014	152507	EB1, microtubule-associated protein EB1	2	2	0	0	0	0.1	0.7	NP_036458.2	2.00E-37	Yes	22924	2	2p23.3-p23.1	9.00E-56	
C_170018	157739	Histone 2B	2	0	1	1	0			NP_003510.1	5.00E-38		8340	6p	6p22-p21.3	1.00E-41	
C_200153	159617	Histone H2B-1	2	0	2	1	0			NP_003510.1	5.00E-38		8340	6p	6p22-p21.3	1.00E-41	
C_270192	161872	Histone H2B	2	0	0	2	0			NP_003510.1	5.00E-38		8340	6p	6p22-p21.3	1.00E-41	
C_1190030	153803	Similar to Histone H2B	2	0	0	2	0			NP_003510.1	2.00E-38		8340	6p	6p22-p21.3	3.00E-40	
C_930018	171433	Histone H4	2	0	2	1	0			NP_003539.1	1.00E-38		8370	1	1q21	5.00E-39	
C_590093	167462	Histone H4	2	0	2	1	0			NP_003539.1	4.00E-39	Yes	8370	1	1q21	2.00E-39	
C_1120033	153422	Similar to Protein Tyrosine Phosphatase	2	2	0	0	0			NP_689635.3	2.00E-42	Yes	138639	9	9q22.32		
C_1090042	153031	Similar to Spermidine Synthase	2	2	0	0	0			NP_003123.1	1.00E-43	Yes	6723	1	1p36-p22	3.00E-51	
C_350045	163780	Similar to AAA-Type ATPase With P-Loop	2	2	0	0	0			NP_006787.1	2.00E-44		10939	18	18p11	2.00E-49	
C_650077	168358	Conserved Uncharacterized Protein	2	0	0	2	0	13.1	5.0	NP_775836.1	9.00E-46	Yes	222967	7	7p22.2	6.00E-25	
C_870039	170769	Conserved Uncharacterized Protein Similar to Tubulin-Tyrosine Ligase	2	0	0	2	1	4.4	2.3	XP_092778.3	1.00E-47	Yes	164395	20	20q11.21		
C_970056	171782	ARL6, ADP-Ribosylation Factor-Like Protein 6 (2 overlapping peptides)	2	2	0	0	0			NP_816931.1	7.00E-48	Yes	84100	3	3q12.1	1.00E-29	

Chlamydomonas Data			CrFP Peptides					Induction by Deflagellation		Human Data			Hs/Cr Reciprocal Best Match	Map Positions of Best Human Matches			Cr/At BLAST E
Cr Model		CrFP Description	Total Unique	M+ M	Axo	KCl	Ter git ol	Fold Change	SD (+/-)	Hs NCBI number	Cr/Hs BLAST E value	Human Conserved Unchar?		NCBI Gene ID	Chr	Map Position	
C_980036	171850	Similar to Phosphoglycerate Kinase	2	2	0	0	0			NP_000282.1	2.00E-48		5230	X	Xq13	1.00E-68	
C_790036	169861	Histone H2A	2	0	2	2	0			NP_003508.1	4.00E-50	Yes	8338	1	1q21-q23	1.00E-53	
C_1440036	155716	Histone H2A	2	0	1	2	0			NP_003508.1	4.00E-50		8338	1	1q21-q23	1.00E-53	
C_270185	161865	Ribosomal Protein S18	2	0	0	2	0			NP_072045.1	2.00E-55	Yes	6222	6p	6p21.3	1.00E-62	
C_70066	169969	Similar to Ubiquitin-Conjugating Enzyme	2	2	0	0	0	0.7	0.6	NP_003333.1	3.00E-58	Yes	7326	17	17p13.3	2.00E-70	
C_1160048	153665	Similar to Protein Kinases	2	0	0	2	0	0.1	0.2	NP_620407.1	1.00E-58		5594	22	22q11.21	6.00E-61	
C_130042	155337	Similar to 40S Ribosomal Protein	2	2	0	0	0			NP_002286.2	7.00E-63	Yes	3921	3	3p21.3	7.00E-77	
C_160119	157299	CNK6, NIMA-related kinase 6	2	1	0	1	0			NP_598001.1	1.00E-64		140609	1	1q31.3	5.00E-33	
C_20112	162481	60S Ribosomal Protein L10a	2	1	0	2	0			NP_009035.3	3.00E-65	Yes	4736	6p	6p21.3-p21.2	1.00E-71	
C_680032	168621	Similar to Nucleoredoxin	2	1	1	0	0			NP_071908.2	4.00E-67	Yes	64359	17	17p13.3	4.00E-43	
C_1350009	155077	Similar to Protein Kinases	2	1	0	1	0	16.3	7.2	NP_003150.1	8.00E-70		6792	X	Xp22	1.00E-42	
C_800022	170176	Similar to Calcium/Calmodulin-Dependent Protein Kinase	2	2	0	0	0	-1.2	0.9	NP_065130.1	1.00E-71	Yes	57118	10	10p14	3.00E-54	
C_960029	171684	Similar to Echinoderm Microtubule Associated Protein Like 5	2	0	0	2	0			NP_899243.1	3.00E-73		161436	14	14q31.3		
C_680023	168612	Similar to Fructose-Bisphosphate Aldolase	2	2	0	0	0	-7.5	4.3	NP_005156.1	2.00E-82		230	17	17cen-q12	2.00E-92	
C_1620015	156900	ARFA1b, ADP-Ribosylation Factor 1 (two peptides)	2	2	0	0	0	0.1	0.5	NP_001649.1	8.00E-87	Yes	375	1	1q42	3.00E-94	
C_20102	162471	Similar to 40S ribosomal protein S3	2	0	0	2	0			NP_000996.2	2.00E-95	Yes	6188	11	11q13.3-q13.5	1.00E-104	
C_50032	167517	Similar to GTP-Binding Protein	2	2	0	0	0			NP_037473.2	1.00E-105	Yes	29789	2	2q31.1	1.00E-115	
C_590104	167473	Similar to Dihydrofolate Reductase-Thymidylate Synthase	2	2	0	0	0			NP_001062.1	1.00E-107	Yes	7298	18	18p11.32	1.00E-132	
C_340079	163641	Similar to dUDP-Glucose 4-6-Dehydratase	2	2	0	0	0			NP_079352.2	1.00E-110	Yes	80146	2	2q12.3	1.00E-136	
C_60170	168935	Similar to Protein Kinase	2	0	0	2	0	7.8	2.3	NP_005897.1	1.00E-119	Yes	4117	6q	6q22	1.00E-120	
C_430028	165247	Guanine Nucleotide-Binding Protein Beta Subunit-Like Protein	2	2	0	0	0			NP_006089.1	1.00E-130	Yes	10399	5	5q35.3	1.00E-125	
C_600078	167820	Similar to Aspartate-tRNA Ligase	2	2	0	0	0			NP_001340.1	1.00E-133	Yes	1615	2	2q22.1	1.00E-147	
C_270078	161758	DHC3, Dynein Heavy Chain 3	2	0	1	1	0			NP_061720.1	1.00E-140		56171	2	2q33.1		
C_1280003	154475	Similar to Importin alpha Subunit	2	2	0	0	0			NP_002260.2	1.00E-157	Yes	3841	6q	6q22.31	0	
C_430080	165299	Similar to Phosphoglucomutase	2	2	0	0	0			NP_002624.2	1.00E-166	Yes	5236	1	1p31	0	
C_50178	167663	Similar to Vacuolar ATP Synthase Subunit B	2	2	0	0	0	-3.4	2.8	NP_001684.2	0	Yes	526	8	8p22-p21	0	
C_270044	161724	Similar to Threonyl-tRNA Synthetase	2	2	0	0	0			NP_689547.2	0	Yes	123283	15	15q26.3	0	
C_730014	169301	Similar to Heat Shock Protein	2	2	0	0	0			NP_005339.2	0	Yes	3320	14	14q32.33	0	

Table S2. Flagellar proteins identified by a single peptide.

C. reinhardtii gene models identified by a single peptide, and the biochemical fraction where the peptide was found. The same peptide may have been found in more than one fraction.

Cr Model	M+M	Axo	KCl	Tergitol	Total
C_100045	0	1	1	1	1
C_10003	1	0	0	0	1
C_100039	0	0	1	0	1
C_10006	1	0	0	0	1
C_10025	0	0	1	0	1
C_10052	0	0	1	0	1
C_10090	0	0	0	1	1
C_10100	0	0	1	0	1
C_1010013	1	0	0	0	1
C_1010029	1	0	0	0	1
C_1010062	1	0	0	0	1
C_1010067	1	0	0	0	1
C_10152	1	0	0	0	1
C_10169	1	0	0	0	1
C_10182	1	1	0	0	1
C_1020007	0	0	1	0	1
C_1020028	0	0	1	0	1
C_1020035	0	1	0	0	1
C_10211	1	0	0	0	1
C_10251	0	1	1	0	1
C_10266	1	0	0	0	1
C_10279	0	0	0	1	1
C_10287	0	0	0	1	1
C_10291	0	1	0	0	1
C_10295	1	0	1	1	1
C_1030046	0	0	1	0	1
C_10329	1	0	0	0	1
C_10336	1	0	0	0	1
C_10350	1	0	0	0	1
C_1040032	0	0	1	0	1
C_1050004	1	0	0	0	1
C_1050033	0	1	0	0	1
C_1060006	0	1	0	0	1
C_1060013	0	1	0	0	1
C_1060023	0	0	1	0	1
C_1060035	0	1	1	0	1
C_1060069	1	0	0	0	1
C_1070012	1	0	0	1	1
C_1070013	1	0	0	0	1
C_1070029	0	0	0	1	1
C_1070032	0	0	0	1	1
C_1070052	0	0	1	0	1
C_1080030	0	1	0	0	1
C_1090026	0	0	1	0	1
C_1100018	1	0	0	0	1
C_1100030	1	0	0	0	1
C_110081	0	1	0	0	1
C_110096	1	0	0	0	1
C_110097	1	0	0	0	1
C_110109	0	1	1	0	1
C_110154	1	0	0	0	1
C_110166	0	1	0	0	1
C_110185	0	1	0	0	1
C_110217	1	0	0	0	1
C_1120028	0	0	0	1	1
C_11280001	0	1	0	1	1
C_1130003	1	0	0	0	1
C_1130004	0	1	0	0	1
C_11320001	0	0	0	1	1
C_1140004	1	0	0	0	1
C_1140028	1	0	0	0	1
C_1140044	0	0	1	0	1
C_1150026	1	0	0	0	1
C_11830001	0	0	0	1	1
C_1190017	0	1	0	0	1
C_11950001	1	0	0	0	1
C_1200042	1	0	0	0	1
C_120128	1	0	0	0	1
C_120208	0	0	0	1	1
C_1220008	0	0	0	1	1
C_1220019	0	0	0	1	1
C_12280002	0	1	0	0	1
C_1250043	1	0	0	0	1
C_1260027	1	0	0	0	1
C_1270017	0	1	0	0	1
C_1280044	0	0	1	0	1
C_130028	1	0	0	0	1
C_130057	0	0	1	0	1
C_130059	1	0	0	0	1
C_130092	1	0	0	0	1
C_130102	1	0	1	0	1
C_130105	0	0	0	1	1

Cr Model	M+M	Axo	KCl	Tergitol	Total
C_130138	1	0	0	0	1
C_130171	0	0	0	1	1
C_130174	1	0	0	0	1
C_130178	0	1	0	0	1
C_1310010	0	1	0	0	1
C_1310044	0	1	0	0	1
C_13220001	1	0	0	0	1
C_13340001	1	0	0	0	1
C_1340006	1	1	0	0	1
C_1340016	0	0	1	0	1
C_1350001	0	0	1	0	1
C_1350007	1	0	0	0	1
C_1350015	1	0	0	0	1
C_1360020	1	0	0	0	1
C_1370024	1	0	0	0	1
C_1390032	0	1	0	0	1
C_13980001	0	0	1	0	1
C_1400020	0	0	1	0	1
C_140161	1	0	0	0	1
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C_1440012	0	1	0	0	1
C_1450010	1	1	0	0	1
C_1470031	0	0	1	0	1
C_14780001	1	0	0	0	1
C_1490013	0	1	0	0	1
C_1500032	0	0	1	0	1
C_150046	0	1	0	0	1
C_150056	0	0	1	0	1
C_150095	1	0	0	0	1
C_150101	1	1	1	0	1
C_150121	0	0	1	0	1
C_150126	0	1	0	0	1
C_150145	0	0	0	1	1
C_150183	0	1	0	0	1
C_150206	1	0	0	0	1
C_1530028	0	0	0	1	1
C_1530029	1	0	0	0	1
C_1540003	0	0	1	0	1
C_1550003	1	0	0	0	1
C_1560005	0	0	1	0	1
C_1560015	1	0	0	0	1
C_1570032	0	1	0	0	1
C_1580045	1	0	0	0	1
C_1590034	0	1	0	0	1
C_1600015	0	1	0	0	1
C_160025	1	0	0	0	1
C_160052	1	0	0	0	1
C_160054	0	0	0	1	1
C_160057	0	1	0	0	1
C_160059	0	1	0	1	1
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C_160233	0	1	0	0	1
C_16200001	0	1	0	1	1
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C_16370001	0	0	1	0	1
C_1640016	0	0	0	1	1
C_1660026	1	0	0	0	1
C_1670004	1	0	0	0	1
C_1670008	0	0	1	0	1
C_1680001	0	0	0	1	1
C_1680019	1	0	0	0	1
C_170029	1	0	0	0	1
C_170067	1	0	0	0	1
C_170151	1	0	0	0	1
C_170166	0	1	0	0	1
C_1710005	0	0	1	0	1
C_1720001	1	0	0	0	1
C_1720010	1	0	0	0	1
C_1730028	0	0	0	1	1
C_1740001	1	0	0	1	1
C_1740005	0	1	0	0	1
C_1750017	0	1	0	0	1
C_1760016	0	0	1	0	1
C_1780004	1	0	0	0	1
C_1800006	1	0	0	0	1
C_180010	1	0	0	0	1
C_180023	0	0	1	0	1
C_180024	0	0	0	1	1
C_180092	1	0	0	0	1
C_180129	0	0	1	0	1

Cr Model	M+M	Axo	KCl	Tergitol	Total
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C_18060001	1	0	0	0	1
C_1830006	1	0	0	0	1
C_1830008	1	0	0	0	1
C_1840004	1	0	0	0	1
C_1840021	1	0	0	0	1
C_1900004	0	0	0	1	1
C_1900005	0	0	0	1	1
C_190058	0	0	1	0	1
C_190059	1	0	0	0	1
C_190065	1	0	0	0	1
C_190092	0	0	1	0	1
C_190123	0	1	0	0	1
C_190160	1	0	0	0	1
C_1910001	0	1	0	0	1
C_1910013	1	0	0	0	1
C_1940010	0	0	1	0	1
C_1950006	1	0	0	0	1
C_1990007	1	0	0	0	1
C_200069	1	0	0	0	1
C_200118	1	0	0	0	1
C_200135	1	0	0	0	1
C_20087	0	1	0	0	1
C_20092	1	0	0	0	1
C_2010002	0	0	1	0	1
C_20170	0	0	0	1	1
C_2020014	0	0	0	1	1
C_20220	0	1	0	0	1
C_20337	1	0	0	0	1
C_20344	0	0	0	1	1
C_2080004	0	0	0	1	1
C_210028	1	0	0	0	1
C_210044	1	0	0	0	1
C_210078	0	1	0	0	1
C_21090001	0	0	1	0	1
C_2180009	1	0	0	0	1
C_220011	1	0	0	0	1
C_220035	1	0	0	0	1
C_220061	0	0	1	0	1
C_2260006	0	0	1	0	1
C_22660001	0	0	1	0	1
C_230026	0	0	1	0	1
C_230073	1	0	0	0	1
C_2320005	0	0	1	0	1
C_23270001	0	1	1	1	1
C_2330007	1	0	0	0	1
C_2330008	0	1	0	0	1
C_2340003	0	1	0	0	1
C_2390007	0	0	1	0	1
C_2390008	1	0	0	0	1
C_240059	1	1	0	0	1
C_240063	1	0	0	0	1
C_240081	0	0	1	0	1
C_240101	0	1	0	0	1
C_2470005	0	1	0	0	1
C_2490002	0	0	1	0	1
C_250005	0	1	0	0	1
C_250011	0	1	0	0	1
C_250079	1	0	0	0	1
C_250096	0	1	0	0	1
C_250102	0	0	1	0	1
C_250150	1	0	1	0	1
C_250153	1	0	0	0	1
C_250155	1	0	0	0	1
C_2580004	0	1	0	0	1
C_260006	1	0	0	0	1
C_260034	0	1	0	1	1
C_260061	0	1	1	0	1
C_260113	1	0	0	0	1
C_260129	0	0	1	0	1
C_260136	1	0	0	0	1
C_260142	0	0	1	0	1
C_270058	1	0	0	0	1
C_270076	1	0	0	0	1
C_270079	0	0	1	0	1
C_270190	1	0	0	0	1
C_280156	0	0	1	0	1
C_2810006	0	0	1	0	1
C_28770001	0	1	0	1	1
C_290013	1	0	0	0	1
C_290058	0	0	1	0	1
C_290139	0	0	1	0	1

Cr Model	M+M	Axo	KCl	Tergitol	Total
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C_300067	0	0	1	0	1
C_300107	1	0	0	0	1
C_300124	0	0	0	1	1
C_30104	1	0	0	0	1
C_30146	0	0	1	0	1
C_30151	0	0	1	0	1
C_30163	1	0	0	0	1
C_30170	0	0	1	0	1
C_30226	1	0	0	0	1
C_30244	1	0	0	0	1
C_30264	0	0	1	0	1
C_310004	0	0	1	0	1
C_310113	0	0	1	0	1
C_310122	0	0	0	1	1
C_31370001	1	0	0	0	1
C_320086	0	0	0	1	1
C_320094	0	0	0	1	1
C_3210005	0	0	0	1	1
C_3260004	0	0	0	1	1
C_3290001	0	0	0	1	1
C_330032	0	1	0	0	1
C_340046	1	0	0	0	1
C_3420001	0	1	0	0	1
C_3460006	0	1	0	0	1
C_350016	0	1	0	0	1
C_360053	0	0	0	1	1
C_360057	0	0	0	1	1
C_360058	1	0	0	0	1
C_3660004	0	0	1	0	1
C_370025	0	1	0	0	1
C_370031	1	0	0	0	1
C_370032	1	0	0	0	1
C_370118	1	0	0	0	1
C_3750001	0	0	1	0	1
C_380024	0	0	1	0	1
C_380110	1	0	0	0	1
C_3830002	0	1	0	0	1
C_3850001	1	0	0	0	1
C_390048	0	1	0	0	1
C_390055	1	0	0	0	1
C_390096	0	1	0	0	1
C_40016	1	0	0	0	1
C_40050	0	0	0	1	1
C_40108	1	0	0	0	1
C_40152	0	0	1	0	1
C_40184	1	0	0	0	1
C_40192	0	1	0	0	1
C_410010	0	1	0	0	1
C_410024	0	0	0	1	1
C_410091	0	1	0	0	1
C_410099	0	1	0	0	1
C_410110	0	0	1	0	1
C_410111	0	0	1	0	1
C_420023	1	0	0	0	1
C_420083	1	0	0	0	1
C_430009	1	0	0	0	1
C_430031	0	0	0	1	1
C_430055	0	0	1	0	1
C_430090	0	0	0	1	1
C_430093	0	0	1	0	1
C_430112	1	0	0	0	1
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C_440088	0	0	1	0	1
C_4450002	0	1	0	0	1
C_450022	1	0	1	0	1
C_450095	1	0	0	0	1
C_460013	1	0	0	0	1
C_460022	0	1	0	0	1
C_460067	1	0	0	0	1
C_460096	1	0	0	0	1
C_470046	0	0	0	1	1
C_480005	1	0	0	0	1
C_480011	1	0	0	0	1
C_480013	1	0	0	0	1
C_480016	0	1	0	0	1
C_4850001	0	0	1	0	1
C_490011	1	0	0	0	1
C_490015	0	1	0	0	1
C_490023	1	0	0	0	1

Cr Model	M+M	Axo	KCl	Tergitol	Total
C_490043	0	0	1	0	1
C_490057	0	0	1	0	1
C_490068	1	0	0	0	1
C_490071	1	0	0	1	1
C_490077	0	0	1	0	1
C_500045	0	0	1	0	1
C_50015	1	0	0	0	1
C_50072	1	0	0	0	1
C_50074	0	1	1	0	1
C_50129	1	0	0	0	1
C_510015	1	0	0	0	1
C_510025	0	1	0	0	1
C_510029	1	0	0	0	1
C_530010	1	0	0	0	1
C_530018	0	1	0	0	1
C_530027	0	1	0	0	1
C_530045	0	0	1	0	1
C_530086	1	0	0	0	1
C_5310001	1	0	0	0	1
C_540079	1	0	0	0	1
C_550011	1	0	0	0	1
C_550022	0	1	1	0	1
C_560024	1	0	0	0	1
C_560051	1	0	0	0	1
C_570019	1	0	0	0	1
C_570075	1	0	0	0	1
C_570077	1	0	1	0	1
C_580083	1	0	0	0	1
C_580084	1	0	0	0	1
C_590030	0	0	1	0	1
C_590032	1	0	0	0	1
C_590035	0	0	1	0	1
C_5990003	1	0	0	0	1
C_600055	0	0	0	1	1
C_600064	0	1	0	0	1
C_600069	0	0	1	0	1
C_600084	0	0	1	0	1
C_60022	1	0	0	0	1
C_60028	1	0	0	0	1
C_60040	1	0	0	0	1
C_60057	1	0	0	0	1
C_60100	1	0	0	0	1
C_60181	1	0	0	0	1
C_60194	0	0	1	1	1
C_6060001	1	0	0	0	1
C_610015	0	1	0	0	1
C_620063	0	0	1	0	1
C_620071	0	0	1	0	1
C_630021	1	0	0	0	1
C_630066	0	0	1	0	1
C_630074	0	1	1	0	1
C_640039	1	0	0	0	1
C_650001	1	0	0	0	1
C_650060	0	0	1	0	1
C_650070	1	0	0	1	1
C_660026	0	1	0	0	1
C_660031	0	0	1	0	1
C_660053	1	0	0	0	1
C_660057	0	1	0	0	1
C_660087	0	0	0	1	1
C_670021	1	0	0	0	1
C_670023	0	0	1	0	1
C_670053	0	0	1	0	1
C_670061	0	0	1	0	1
C_680038	0	1	0	1	1
C_680061	1	0	0	1	1
C_690016	0	0	1	0	1
C_690031	0	0	1	0	1
C_700009	0	1	0	0	1
C_700024	0	0	0	1	1
C_70027	0	1	0	0	1
C_70040	0	1	0	0	1
C_70050	1	0	0	0	1
C_70098	0	0	1	0	1
C_70113	1	0	0	0	1
C_70116	1	0	0	0	1
C_70146	0	1	0	0	1
C_70188	1	0	0	0	1
C_70216	0	0	1	0	1
C_710026	0	0	1	0	1
C_720007	0	0	1	0	1
C_720034	1	0	1	0	1

Cr Model	M+M	Axo	KCl	Tergitol	Total
C_720049	0	0	0	1	1
C_730040	1	0	0	0	1
C_730056	1	0	0	0	1
C_740034	1	0	0	0	1
C_740040	1	0	0	0	1
C_750008	0	0	1	0	1
C_750058	0	0	0	1	1
C_750080	0	1	1	0	1
C_750085	0	0	0	1	1
C_760010	0	0	1	0	1
C_760043	0	0	1	0	1
C_770018	1	0	0	0	1
C_770032	0	1	0	0	1
C_770033	1	0	0	0	1
C_7720001	1	0	0	0	1
C_780034	1	0	0	0	1
C_7870001	0	0	1	0	1
C_800006	1	0	0	0	1
C_800056	0	0	1	0	1
C_80103	1	0	0	0	1
C_80114	0	0	1	0	1
C_80121	0	0	0	1	1
C_80171	1	0	0	0	1
C_80190	1	0	0	0	1
C_80208	0	1	0	0	1
C_80227	1	1	0	0	1
C_820013	0	1	0	0	1
C_8210001	1	0	0	0	1
C_830010	0	1	0	0	1
C_850013	1	0	0	0	1
C_850039	0	0	1	0	1
C_850040	0	1	0	0	1
C_860024	1	0	0	0	1
C_860038	1	0	0	0	1
C_860039	1	0	0	0	1
C_860050	0	0	1	0	1
C_860065	0	0	0	1	1
C_860080	1	0	0	0	1
C_870044	0	0	1	0	1
C_8780001	0	1	0	0	1
C_880027	0	0	1	0	1
C_900006	1	0	0	0	1
C_900008	0	1	0	0	1
C_900012	0	0	1	0	1
C_900020	0	0	1	0	1
C_900042	1	0	1	0	1
C_90015	0	0	1	0	1
C_90101	0	1	0	0	1
C_90121	1	0	0	0	1
C_90144	1	0	0	0	1
C_90154	1	0	0	0	1
C_90159	1	0	0	0	1
C_910056	0	0	0	1	1
C_910058	1	0	0	0	1
C_910063	0	0	1	0	1
C_910066	1	0	0	0	1
C_920039	1	0	0	0	1
C_930010	1	0	0	0	1
C_930020	0	1	0	0	1
C_930045	0	0	1	0	1
C_9470001	0	0	0	1	1
C_950008	0	1	0	0	1
C_950026	0	1	0	0	1
C_950041	0	0	0	1	1
C_960005	0	1	1	0	1
C_960018	1	0	0	0	1
C_960038	0	0	1	0	1
C_960053	1	0	0	0	1
C_970048	1	0	0	0	1
C_970057	1	0	0	0	1
C_980038	0	1	1	0	1
C_990053	1	0	0	0	1

Table S3. Known *C. reinhardtii* flagellar proteins.

The first column gives the accession number if the sequence has been deposited in the NCBI database. The fifth column gives the JGI v. 2 gene model number except in those cases where the sequence was provided to us as a personal communication from H. Qin, D. Cole or W. Sale as indicated. The final column summarizes the number of proteins found out of the total number of known proteins in each category. Sequences for unpublished radial spoke proteins are from P. Yang (unpublished). A hyperlinked version of this table is available from the authors.

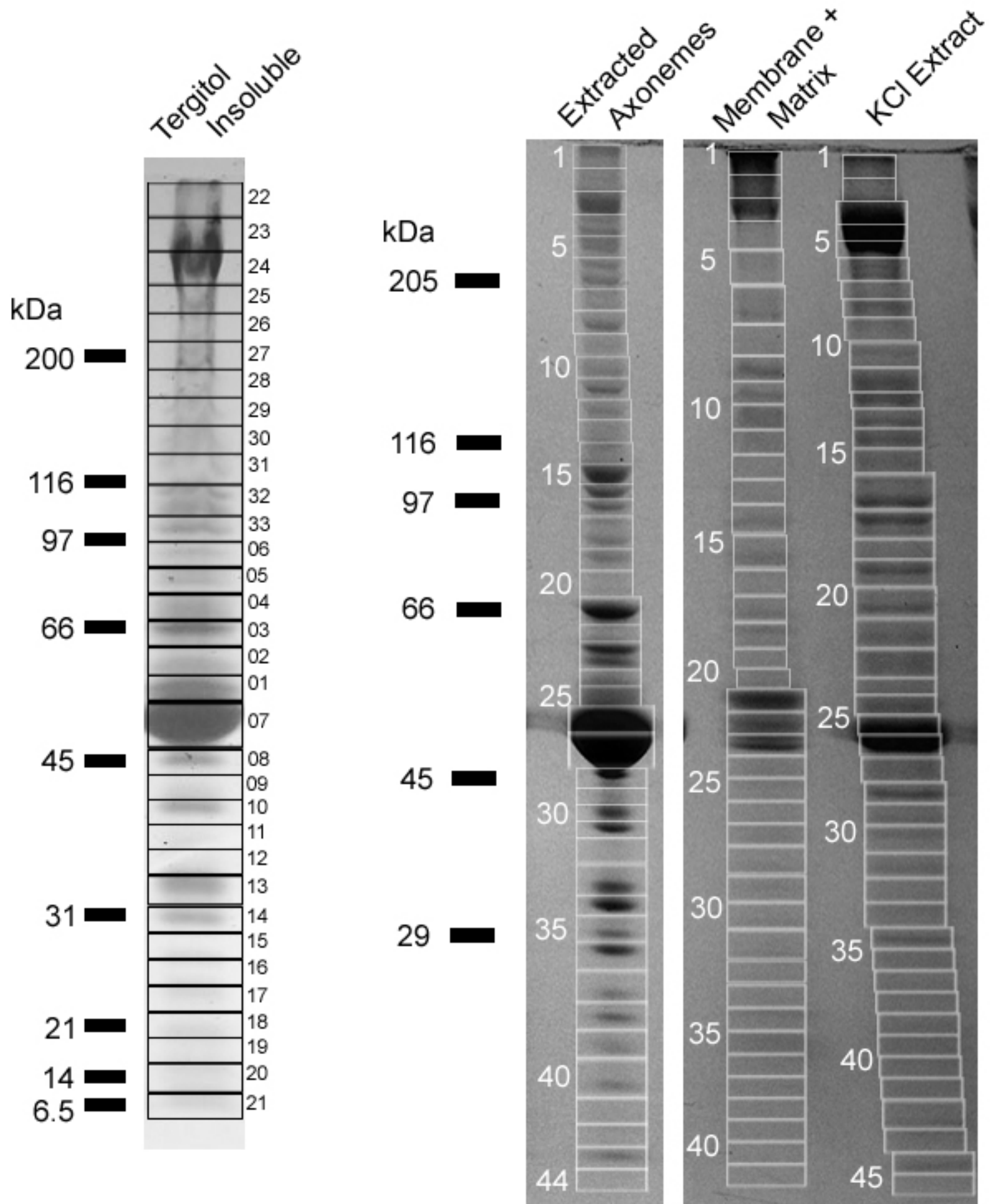
Only four of the 101 proteins in the table were not found in our proteomic study. The gene (ODA5) encoding the outer dynein arm-associated protein that is missing is not present in the genome assembly and so could not have been found by our analysis. The two peptides that match DHC3 also are encoded by other dynein heavy chains and are presumed to have originated from them. This gene was identified by PCR analysis of genomic DNA but the protein has not been shown biochemically to be in flagella and this gene was much less strongly expressed than other dynein heavy chain genes as measured by northern blot or reverse-transcriptase PCR analysis (Porter et al., 1996). The gene encoding LF4 is mostly missing from the genome assembly. The only other missing protein is p80 katanin, which was shown genetically to be involved in central pair assembly, but the abundance of the native protein is unknown (Dymek et al., 2004). Not included in the table are CALK, which is reported to be a cell body protein until gamete activation (Pan and Snell, 2000); p60 katanin, which was localized to the transition zone and may be left with the cell body when the flagella are detached (Lohret

et al., 1999); FA1, which was found associated with isolated flagella basal body apparatuses but not with isolated flagella (Finst et al., 2000); LF1 and LF3, which are found almost exclusively in the cell body (Tam et al., 2003; Nguyen et al., 2004), and FMG-1A, which has not been found in vegetative flagella (R. Bloodgood, personal communication). With the exception of FMG-1A, none of these proteins were detected in the current proteomic analysis. We found 12 peptides that are predicted by FMG-1A, but these same peptides also are encoded in FMG-1B and probably originated from it.

NCBI Accession Number	Description	Gene Name	Protein Name	JGI V2 Model ID	Number of Peptides	Found/Total
Tubulin						2/2
-alpha						
AAA33095.1	alpha-1 tubulin	TUA1	alpha tubulin	C_30120	38	
AAN87017.1	alpha-2 tubulin	TUA2	alpha tubulin	C_1320004	38	
-beta						
AAA33101.1	beta-1 tubulin	TUB1	beta tubulin	C_70002	34	
AAA33102.1	beta-2 tubulin	TUB2	beta tubulin	C_70152	34	
Outer Dynein Arm						18/19
Q39810	ODA-DHcA, Outer Dynein Arm Heavy Chain alpha	ODA11	DHC alpha	C_670028	23	
Q39565	ODA-DHcB, Outer Dynein Arm Heavy Chain beta	ODA4	DHC beta	C_220096	34	
Q39575	ODA-DHcG, Outer Dynein Arm Heavy Chain gamma	ODA2	DHC gamma	C_1710010	22	
Q39578	ODA-IC1, Outer Dynein Arm Intermediate Chain 1	ODA9	IC1, IC78	C_960025	14	
P27766	ODA-IC2, Outer Dynein Arm Intermediate Chain 2	ODA6	IC2, IC69	C_370072	9	
AA041040.1	ODA-LC1, Outer Dynein Arm Light Chain 1	DLC1	ODA-LC1	C_680013	7	
T08216	ODA-LC2, Outer Dynein Arm Light Chain 2	ODA12	ODA-LC2	C_380098	3	
Q39592	ODA-LC3, Outer Dynein Arm Light Chain 3, 16KD	DLC3	ODA-LC3	C_380098	7	
Q39584	ODA-LC4, Outer Dynein Arm Light Chain 4	DLC4	ODA-LC4	C_180045	2	
Q39591	ODA-LC5, Outer Dynein Arm Light Chain 5, 14KD	DLC5	ODA-LC5	C_590029	2	
AA80216.1	ODA-LC6, Outer Dynein Arm Light Chain 6, 11KD	ODA13	ODA-LC6	C_20222	4	
AA045881.1	ODA-LC7a, Outer Dynein Arm Light Chain 7a	ODA15	ODA-LC7a	C_780049	8	
		DLC7b	ODA-LC7b	C_70068	4	
AAA80986.1	ODA-LC8, Outer Dynein Arm Light Chain 8, 8KD	FLA14	ODA-LC8	C_2020008	8	
AA049732.1	ODA-DC1, Outer Dynein Arm Docking Complex 1, M 105,000	ODA3	ODA-DC1	C_170017	16	
AAK72125.1	ODA-DC2, Outer Dynein Arm Docking Complex 2, M 70,000	ODA1	ODA-DC2	C_970037	18	
AA049435.1	ODA-DC3, Outer Dynein Arm Docking Complex 3, M 25,000	ODA14	ODA-DC3	C_240117	9	
AA510182	ODAs-Associated Adenylate Kinase	ODAS-AK		C_1390012	25	
AY452532	ODAs, Outer Dynein Arm Protein	ODAS		C_420072	0	
Inner Dynein Arm						18/19
CAB56598.1	IA1-DHC1a, Inner Dynein Arm Heavy Chain 1-alpha	DHC11	IA1-DHC1a	C_1150005	106	
CAB99316.1	IA1-DHC1b, Inner Dynein Arm Heavy Chain 1-beta	IDA2	IA1-DHC1b/DHC10	C_10076	65	
AAC49515.1	DHC2, Dynein Heavy Chain 2	DHC2	DHC2	C_80197	52	
AAC49516.1	DHC3, Dynein Heavy Chain 3	DHC3	DHC3	C_270078	2	(not unique)
AAC49517.1	DHC4, Dynein Heavy Chain 4	DHC4	DHC4	C_20225	12	
AAC49518.1	DHC5, Dynein Heavy Chain 5	DHC5	DHC5	C_20038	31	
AAC49519.1	DHC6, Dynein Heavy Chain 6	DHC6	DHC6	C_360006	49	
AAC49520.1	DHC7, Dynein Heavy Chain 7	DHC7	DHC7	C_2600003	22	
AAC49521.1	DHC8, Dynein Heavy Chain 8	DHC8	DHC8	C_560103	26	
AAC49522.1	DHC9, Dynein Heavy Chain 9	DHC9	DHC9	C_7270001	8	
CAB39162.1	DHC11, Dynein Heavy Chain 11	DHC11	DHC11	C_950024	28	
AA045352.1	IA1-IC140, Inner Dynein Arm 11 Intermediate Chain IC140	IDA7	IC140	C_530081	28	
AA093505	IA1-IC138, Inner Dynein Arm 11 Intermediate Chain IC138	BOF5	IC138	C_160036	23	
AA093506	IA1-IC97, Inner Dynein Arm 11 Intermediate Chain IC97	IC97		W. Sak	5	
CAA88139.1	IA-IC28, Inner Dynein Arm Light Chain p28	IDA4	p28	C_740003	21	
BA094850	Actin, Inner Dynein Arm Intermediate Chain	IDA5	Actin	C_1310009	22	
T07930	Dynein Light Chain Tctex1	TCTEX1	Tctex1	C_900042	1	
DA05278	Dynein Light Chain Tctex2	TCTEX2	Tctex2	C_900051	1	
P05434	Caltractin / Centrin 20 kD Calcium-Binding Protein	VEL2	Centrin / Caltractin	C_1500009	9	
Radial Spoke						16/16
AAQ29371	RSF1, Radial Spoke Protein 1	RSF1	RSF1	C_120055	23	
P12750	RSF2, Radial Spoke Protein 2	PF24	RSF2	C_130121	25	
Q01656	RSF4, Radial Spoke Protein 4	PF1	RSF4	C_1810004	10	
		RSF5	RSF5	C_70095	15	
Q01657	RSF6, Radial Spoke Protein 6	PF26	RSF6	C_1810005	10	
		RSF7	RSF7	C_100189 + C_100190	3 + 2	
		RSF8	RSF8	C_50211	13	
		RSF9	RSF9	C_50112	17	
		RSF10	RSF10	C_900027	9	
		RSF11	RSF11	C_830019	8	
		RSF12	RSF12	C_20323	6	
		RSF15	RSF15	C_1640005 + v1 gene 2467.0	6	
		RSF16	RSF16	C_490039	26	
		RSF17	RSF17	C_420011	15	
AA515573	RSF23, Radial Spoke Protein 23	RSF23/NDK		C_60025	13	
Central Pair						6/6
P46870	KLP1, Kinesin-Like Protein 1	KLP1	KLP1	C_50080	31	
AAC49169.1	PF16, Central Pair Protein	PF16	PF16	C_80166	6	
P05107	PF20, Central Pair Associated WD-Repeat Protein	PF20	PF20	C_40010	8	
AA038856.1	PF1, Phosphatase 1	PF1a	PF1	C_2360011	10	
AAT40991	CPC1, Central Pair Complex 1	CPC1	CPC1	C_1580011	56	
AAK38270.1	PF6, Central Pair Protein	PF6	PF6	C_60158	42	
Intraflagellar Transport						20/20
P46869	FLA10, Kinesin-II Motor Protein	FLA10	Fla10 Kinesin II	C_1880008	23	
		FLA8	FLA8 Kinesin II	C_162026	19	
		KAP	KAP	C_620048	4	
CAB56748.1	DHC1b, Cytoplasmic Dynein Heavy Chain 1b	DHC1b	DHC1b	C_750046	88	
AY157841.1	D16L1C, Dynein 1b Light Intermediate Chain	D16L1C	D16L1C	C_1530011	10	
AA075748.1	IFT20, Intraflagellar Transport Protein 20	IFT20	IFT20	C_1510005	5	
		IFT27	IFT27	H. Qln / D. Cole	>5	
		IFT46	IFT46	H. Qln / D. Cole	>5	
AAL12162.1	IFT52, Intraflagellar Transport Protein 52	BLD1	IFT52	C_1260018	5	
		IFT57	IFT57	C_1630013	7	
AA092260	IFT274, Intraflagellar Transport Protein 72 and 74	IFT274	IFT27/74	C_4100035	33	
		IFT80	IFT80	C_120075	7	
AAT99262	IFT81, Intraflagellar Transport Protein 81	IFT81	IFT81	C_10177	26	
AA037228.1	IFT88, Intraflagellar Transport Protein 88	IFT88	IFT88	C_720060	14	
		IFT121	IFT121	H. Qln / D. Cole	>5	
		IFT122	IFT122	C_1190053	16	
		IFT139	IFT139	H. Qln / D. Cole	>5	
AAT95430	IFT140, Intraflagellar Transport Protein 140	IFT140	IFT140	C_640055	17	
		IFT144	IFT144	H. Qln / D. Cole	>5	
		IFT172	IFT172	C_170190	47	
Membrane Proteins						2/2
AAO25118.1	FMG-1B, Flagella Membrane Glycoprotein 1B	FMG1B	FMG1B	C_730051	52	
AA03652.1	Mastigoneme	MS1	Mastigoneme	C_1230030	28	
Miscellaneous						15/17
AA057169.1	PF2, Dynein Regulatory Complex Protein	PF2	PF2	C_1410017	16	
AAT01224	PF15, p80 Katanin	PF15	p80 Katanin	C_110001	0	
AAL86904.1	FA2, Protein Kinase	FA2	FA2	C_100034	4	
AA026968.1	EB1, microtubule-associated protein EB1	EB1	EB1	C_1020014	2	
AAT40314	CSK3, Glycogen Synthase Kinase 3	CSK3	CSK3	C_900046	6	
AA086888.1	Lf4, Long Flagella Protein	Lf4	Lf4	C_11830001	0	
P04352	Calmodulin	CAM	Calmodulin	C_860007	9	
AA027849.1	DIP13, DeFlagellation Inducible Protein, 13KD	DIP13	DIP13	C_10352	8	
P28840	HSP70, Heat Shock 70 KDa Protein	HSP70A	HSP70	C_1340012	15	
AAK54060.1	Profilin	PROF1	profilin	C_130122	3	
BAC77347	Tektin	Tektin	Tektin	C_60116	24	
AAM15771.1	MBO2, Coiled-Coil Flagellar Protein	MBO2	MBO2	C_1660006	26	
AAF34940.1	RIB43a, Flagellar Profilin/Actin Ribbon Protein	RIB43a	RIB43a	C_860059	33	
CA034041	Phototropin, Blue Light Receptor	PHOT		C_120056	29	
AA096956	Protein Kinase, 48K	SKS-C		C_380089	10	
AAM44303.1	RIB72, Nucleoside-Diphosphokinase Regulatory Subunit p72	RIB72	RIB72	C_680086	44	
		PF2a-c2	PF2a	C_1410025	11	

Figure S1. SDS-polyacrylamide gels used for the proteomic analysis.

The slides excised for analysis are indicated; the origin of each peptide relative to these slices is available on-line at <http://labs.umassmed.edu/chlamyfp/index.php>. The positions of molecular weight markers are shown to the left of the gels.



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