

Supplemental Table S2.

Genes upregulated 100% or more at t=30 or 45 min. Entries in bold indicate genes with prior information about flagellar association, based on localization, comparative genomics, upregulation, or proteomics, as indicated in columns 2-5.

gene ID	known flagellar protein	known FABP	known upregulated message	human ciliary proteome	t=30	t=45	t=120	protein description
152411					492.99%	215.92%	8.84%	hypothetical protein
152476					158.73%	74.96%	-10.42%	hypothetical protein
152888					110.40%	62.27%	1.76%	hypothetical protein
152954					255.78%	93.46%	15.25%	hypothetical protein
153027	X			X	175.08%	141.24%	1.52%	nucleoside diphosphate kinase
153565					215.40%	37.33%	-14.22%	CAH6 carbonic anhydrase (chloroplast)
153566					164.91%	115.85%	-18.52%	hypothetical protein
153592					176.88%	79.07%	-13.47%	hypothetical protein
153593					293.91%	209.62%	14.90%	novel
153658		X	X		220.27%	157.04%	-1.71%	testis expressed gene NYD-SP28
153853		X	X		196.25%	75.98%	7.61%	novel
153940					152.48%	31.91%	-7.81%	novel
154005	X				480.27%	138.69%	0.56%	T-complex protein 1 epsilon subunit CCT5
154182					165.43%	43.94%	45.27%	novel, KH domain
154226					249.99%	56.24%	-17.53%	EF-hand protein
154231					208.96%	56.70%	46.69%	no homology
154393	X	X	X		168.36%	81.09%	5.86%	IFT52/BLD1
154652	X	X		X	142.16%	43.96%	-5.14%	IFT80/Che-2
154693					429.81%	258.94%	34.09%	no homology
154954					115.69%	48.13%	5.47%	novel
155018					173.93%	127.25%	7.47%	PI3 kinase
155023	X				1382.52%	151.30%	6%	HSP70A (flagellar)
155083					367.92%	168.46%	-15.56%	no homology
155160		X			282.70%	119.66%	14.73%	novel

155242				128.92%	60.59%	42.36%	CPN2 tubulin folding cofactor B
155336				385.30%	148.08%	21.32%	no homology
155586	X	X	X	207.12%	129.09%	-3.74%	PF2 dynein regulatory complex, Growth arrest protein 8
155801				126.71%	183.47%	-3.02%	novel
155853				1266.57%	436.70%	-21.79%	HSP22B (cytosolic)
155875				1853.32%	860.83%	5.12%	HSP22A (cytosolic)
155958				258.36%	53.31%	32.11%	AAA ATPase
155967	X			218.21%	116.10%	46.04%	T-complex prot 1 delta subunit, CCT4
155990				317.95%	140.30%	-17.98%	no homology
156034				183.87%	83.64%	-1.67%	no homology
156038				506.54%	188.67%	13.91%	glucan 1,4-alpha-glucosidase
156043		X	X	116.06%	48.75%	9.94%	MIP-T3 microtubule-interacting protein
156201				154.62%	69.47%	3.32%	no homology
156214	X	X		183.92%	37.02%	-1.71%	IFT20
156232	X			647.07%	299.32%	18.47%	FMG1A
156234	X			156.09%	74.42%	22.96%	FMG1A-like
156354				138.18%	38.46%	29.05%	cytochrome p450 family
156724				452.53%	226.27%	44.25%	Reptin
156757				176.86%	91.89%	-3.34%	no homology
156769	X			365.47%	135.25%	33.76%	T-complex protein 1 alpha subunit CCT1
156828				123.32%	66.01%	-13.58%	hypothetical protein
156865				308.67%	187%	63.77%	no homology
156948	X	X	X	232.55%	56.82%	19%	IFT57
156969				500.02%	221.96%	27.80%	calcium-binding EF hand protein
157068	X			466.31%	152.34%	52.90%	T-complex protein 1 beta subunit CCT2
157193				115.91%	102.96%	-13.63%	novel
157216	X	X		144.01%	67.19%	11.71%	dynein intermediate chain IC138
157312				237.91%	57.59%	4.55%	novel, putative phosphatase
157731				314.14%	55.55%	40.04%	DnaJ chaperone
157798	X		X	127.93%	33.57%	1%	ODA3
157896		X		172.83%	130.06%	-1.73%	novel

157940	X			297.77% 145.75%	-0.56%	Tcte1, t-complex testis expressed
157967	X	X	X	382.67% 240.87%	30.47%	RSP4 flagellar radial spoke protein
158148				152.02% 45.29%	2.68%	novel, putative cytochrome p450
158210	X		X	X	434.08% 243.83%	116.95% beta tubulin
158418				170.16% 113.35%	16.29%	CHLRE_180190 Rab GTPase
158440				240.71% 55.73%	10.27%	no homology
158643				101.23% 76.69%	28.22%	novel
158809				312.27% 133.43%	21.45%	novel
158863	X	X	X	134.99% 49.99%	-2.50%	Qilin (zebrafish PKD) KIAA0643 protein
158864				239.19% 96.59%	-11.41%	novel
158900				253.65% 72.95%	23.07%	novel ATP binding
158903	X			234.68% 139.52%	35.07%	novel
159012				138.74% 60.23%	2.15%	novel
159022	X	X	X	106.16% 35.44%	-7.71%	IFT81
159126				109.98% 60.37%	6.56%	novel
159197	X	X	X	223.34% 55.54%	7.67%	DIP13 deflagellation inducible gene
159203			X	250.33% 91.21%	-6.86%	S926 upregulated message
159247		X	X	334.95% 35.71%	-20.73%	novel
159281	X			265.12% 128.04%	36.99%	FLA14 outer dynein arm light chain LC8
159506				525.19% 206.09%	103.04%	no homology
159624				186.81% 37.02%	75.96%	novel
159673				286.31% 94.93%	-3.32%	novel
159749	X	X	X	212.19% 180.48%	37.70%	hypothetical protein Q9NQC8
159848				144.16% 43.34%	1.45%	novel
159948				120.52% 43.68%	-38.04%	novel
160014				271.79% 200.16%	3.91%	novel
160067				353.50% 94.99%	60%	novel
160123				280.30% 209.34%	29.38%	Hsp100 family chaperone
160204				149.61% 31.50%	12.33%	novel
160297	X	X		371.12% 219.34%	83.35%	FABP CG15429 (prototypical cilia class)
160572				197.53% 57.03%	-1.68%	novel

160880				X	159.01%	84%	6.24%	rhabdoid tumor deleted region protein 1
160881					126.56%	45.41%	22.13%	HSP22F
160936					159.66%	146.61%	-2.10%	novel
160952	X				676.09%	213.18%	43.84%	ODA14
160953					172.70%	45.41%	22.13%	HSP22E
160955					148.37%	106.98%	10.39%	novel
160959					177.04%	29.33%	-29.08%	novel
161089					129.58%	90.76%	20.68%	UBC4 E2 ubiquitin conjugating enzyme
161174					266.08%	105.31%	12.98%	novel
161213					268.67%	128.11%	2%	centrin-like EF-hand protein
161490				X	119.95%	54.42%	11.10%	novel
161556					481.47%	163.93%	15.97%	unknown P-loop protein
161600					100.05%	45.07%	6.85%	novel
161728					350.65%	113.56%	-8.83%	novel P-loop protein
161985					140.90%	60.60%	2.23%	novel
162279	X	X	X		143.86%	56.65%	6.06%	RSP3
162390					425.99%	124.27%	34.97%	helix-turn-helix transcription factor
162417				X	477.88%	175.80%	78.92%	c-myc binding protein MYCBP/AMY-1
162425					125.61%	73.73%	-4.88%	novel
162449		X			178.70%	91.19%	-3.76%	novel
162472					113.29%	55.28%	-6.58%	novel
162692					200.82%	87.98%	14.62%	novel
162703		X	X	X	724.23%	436.64%	87.70%	PACRG parkin co-regulated gene
162999					154.73%	83.90%	57.87%	DnaJ protein
163048					145.60%	53.08%	23.77%	EF1G elongation factor
163083					197.86%	52.69%	6.72%	novel
163193		X	X		161.35%	80.24%	-6.28%	FABP CG4525 (compartment class)
163279					134.65%	84.89%	-13.89%	novel
163322					144.14%	71.86%	26.63%	novel
163462	X				414.85%	187.67%	23.46%	T-complex protein 1 zeta subunit CCT6
163587	X				209.71%	120.55%	64.97%	T-complex protein1 theta subunit CCT8

163755				196.05%	89.62%	67.90%	novel
163765				300%	80.53%	-15.66%	novel
164079				241.56%	101.96%	74.68%	SKP1 E3 ubiquitin ligase
164100	X	X		170.31%	81%	4.73%	ODA6
164108				137.16%	44.60%	16.23%	plasma membrane Ca-transport ATPase 9
164110				132.17%	51.83%	-15.68%	novel
164149		X	X	117.95%	77.94%	6.19%	novel
164270				207.92%	101.28%	14.40%	novel
164295	X	X		159.93%	88.85%	15.33%	ODA12
164296	X			374.62%	145.98%	93.62%	axonemal dynein light chain DNAL4
164307	X	X		316.27%	133.37%	-5.76%	DLC3 outer arm light chain 3
164442				204.79%	73.43%	35.41%	no homology
164501				142.10%	74.73%	43.15%	novel
164561		X	X	129.22%	93.45%	24.46%	novel
164568		X		255.91%	123.45%	25.82%	zinc finger, MYND domain containing protein
164620	X		X	X	345.71%	192.45%	114.43% TUA1 alpha tubulin
164722	X		X	430.58%	330.93%	40.97%	ODA13 outer dynein arm docking complex protein
164832				112.69%	79.80%	14.56%	novel
164954				126.28%	97.08%	16.78%	novel
164979	X	X		221.01%	104.70%	30.23%	IFT74/72
165023	X			510.23%	167.20%	32.89%	T-complex protein 1 eta subunit CCT7
165057		X		576.51%	136.48%	-2.35%	FABP CG31623 (motility class)
165138				185.83%	109.37%	1.81%	novel
165606		X	X	X	389.99%	208.84%	67.13% hypothetical protein Q9H1X1
165719		X		106.92%	90.20%	13.70%	novel
165743				114.97%	56.46%	-5.46%	novel
165780				545.77%	38.01%	-13.90%	CLPB2 chaperone Hsp101 type
166022				149.81%	96.61%	38.17%	novel
166039		X		426%	172.13%	6.85%	FABP CG11035 (prototypical cilia class) DnaJ protein
166074				286.01%	127.81%	11.13%	novel EF hand protein
166081				209.37%	62.50%	-19.28%	novel ATP-binding

166131	X	X	X	118.52%	43.45%	31.97%	PF20 central pair protein
166294				116.92%	145.14%	-2.50%	novel
166301				142.13%	34.39%	-27.52%	novel
166390				202.10%	86.01%	27.74%	novel
166776				169.57%	57.35%	8.34%	HSP22C
166783				185.38%	96.35%	11.59%	novel
166839				264.39%	61.81%	10.16%	SPT2 serine palmitoyltransferase
166849				159.42%	89.85%	4.34%	novel
166905				177.27%	96.70%	5.20%	novel
166967				186.34%	186.79%	27.75%	novel
166968				121.83%	79.78%	-7.20%	CHLRE_550086 Rab-type G protein
167072				102.40%	65.46%	20.36%	novel
167154				102.70%	35.13%	24.32%	novel
167190		X		88.59%	105.02%	-14.73%	Tbx1
167311				222.15%	55.70%	4.70%	HSP70E
167565	X			248.19%	90.70%	-0.66%	KLP1 central pair kinesin
167670				121.97%	13.23%	31.83%	novel, sterol c14-reductase like
167696				124.48%	83.25%	9.49%	novel
167776		X	X	110.06%	37.10%	33.84%	Dpy-30
168135		X		319.14%	143.27%	29.38%	FABP CG10064 (motility class),WD40 repeats
168312		X		197.51%	103.01%	18.12%	FABP
168339		X	X	443.10%	126.61%	-7.46%	FABP CG18675 (motility class)
168434		X		269.73%	135.18%	6.97%	TSARG2 testis & spermatogenesis prot. 2
168471				338.39%	95.90%	89.74%	no homology
168546				80.11%	203.34%	27.97%	novel
168596				275.69%	76.52%	38.48%	cytochrome p450-like
168600		X	X	338.88%	65.74%	-6.63%	nasopharyngeal epithelia specific protein
168602	X	X		337.65%	246.55%	26.75%	DLC1 outer arm light chain 1
168662				402.16%	53.02%	20.39%	novel
168675	X	X		377.18%	152.45%	26.45%	Rib72 flagellar pf ribbon protein
168790	X		X	610.32%	166.01%	14.31%	RSP23 p61 nucleoside diphosphate kinase

168881	X	X		X	108.69%	73.91%	8.98%	Tektin
168906					349.32%	121.42%	29.29%	no homology
168911					271.06%	153.50%	12.28%	novel WD-40 protein
168935					135.04%	78.06%	-0.89%	MAK kinase
168989					272.98%	189.69%	26.96%	heat shock protein
169068					164.29%	86.32%	9.11%	novel
169116					222.48%	92.28%	15.73%	Pontin
169215					168.84%	88.41%	-6.15%	novel
169301	X			X	1759.65%	356.88%	10.26%	HSP90A (flagellar)
169310					123.35%	69.96%	12.28%	novel
169383	X	X			165.46%	54.52%	26.03%	IDA4
169414					158.50%	102.92%	48.36%	phosphatase
169511					169.75%	59.21%	-3.15%	HSP70B
169604					349.35%	106.49%	28.33%	no homology
169795	X	X			251.48%	142.96%	15.57%	DLC7a outer arm light chain 7
169905	X		X	X	418.67%	214.58%	97.42%	TUB1 beta tubulin
169971	X	X			464.30%	333.20%	71.19%	DLC7b dynein light chain, roadblock-like
169998					291.16%	166.31%	22.81%	novel
170001					377.83%	172.12%	24.71%	no homology
170055	X		X	X	418.67%	214.58%	97.42%	TUB2 beta tubulin
170098					119.65%	105.06%	12.65%	HSP70-like protein
170205					110.37%	30.37%	-38.62%	novel
170392					490.28%	98.97%	0.03%	TULP2, Tubby-like protein 2
170435	X			X	120.21%	30.94%	-29.68%	AKAP-associated sperm protein
170693					179.30%	73.50%	22.10%	CPN10 chaperone
170694	X	X			270.91%	119%	0.63%	Rib43a flagellar pf ribbon protein
170718					211.70%	64.45%	50.86%	myo-inositol-1-phosphase synthase
170981	X	X			248.61%	81.67%	-9.67%	Tctex2b, homology to outer arm light chain lc2
171050					100.70%	74.86%	7.61%	novel
171096	X			X	367.77%	123.03%	-4.21%	PF16 flagellar central pair protein, SPAG6
171102		X	X	X	431.10%	197.22%	16.93%	Mus musculus testis-specific cDNA AK017056

171153				123.45%	90.10%	-16.73%	novel
171156				948.01%	324.86%	18.60%	novel
171226	X	X		164.74%	45.98%	-8.08%	Tctex1 inner arm dlc
171275				338.27%	237.46%	12.93%	no homology
171680	X	X		289.52%	139.73%	23.18%	ODA9 flagellar outer arm IC78
171729				86.56%	147.55%	19.07%	novel
171752				260.13%	57.31%	37.90%	SC5D delta7-sterol-C5 desaturase
171782	X	X		243.78%	57.89%	31.03%	ARL6/BBS3
171911		X	X	153.40%	43.84%	-9.11%	meiosis-specific nuclear structural protein
172025				416.26%	171.33%	4.41%	no homology