

Table S1. Flagellar enriched gene cluster

Predicted function	JGI Peptide ID	Proteomics Hit	Predicted homolog
IFT (Intraflagellar transport)	79669		FLA3/Kinesin-associated protein 3
	63939		FLA2/FLA8 (kinesin 2 homolog)
	62977		IFT20
	77715		IFT52
	45002	Yes	IFT57
	77945		IFT80
	63280	Yes	IFT88
	71180		IFT122
	48798		IFT140
BBS (Transport to flagellar base)	65179		BBS1
	71257		BBS2
	44202		BBS3
	28891		BBS4
	34252		BBS5
	68114		BBS7
	80979		BBS8
	80972		BBS9
Structural components	39221	Yes	Alpha-tubulin
	56065		Alpha-tubulin
	56236		Alpha-tubulin
	83350		Beta-tubulin
	55423	Yes	Beta-tubulin
	56391		Beta-tubulin
	78637		ODA9 (outer arm dynein intermediate chain)
	80259	Yes	D1bLIC (dynein light intermediate chain)
	81548	Yes	ODA1 (p66 outer dynein arm docking complex protein)
	30532		ODA12
	81047	Yes	RIB72
	83064	Yes	RIB43A-domain containing protein
	49798	Yes	Radial spoke protein 4
	44954	Yes	Radial spoke-head-like
	30562	Yes	PF16
	952		PF20/SPG16
	82851	Yes	PACRG
	55564		Flagellar calmodulin (CAM1)
64648		KLP1 (kinesin-9)	
General MT associated	72175	Yes	Katanan P80
	83220		katanin p60
	62120		CLASP-like
	71898		DIP13
	64818	Yes	XRP2
FAPP	4601	Yes	FAP9
	50227		FAP14
	62998		FAP22

	81229		FAP32
	67854	Yes	FAP45
	68117		FAP50
	59637	Yes	FAP52
	380	Yes	FAP59
	50399		FAP60
	73596		FAP61
	29690		FAP66
	33146		FAP67
	62358		FAP69
	70274		FAP70
	79290		FAP82
	46605	Yes	FAP91
	79626	Yes	FAP116
	32701		FAP118.
	74561		FAP134
	65873		FAP161
	61993		FAP259
	54982		FAP253
	29188	Yes	FAP251
Unknown	32341		Kinase
	66608		Guanylate cyclase
	63921		MOT17
	56610		MOT25
	73917		MOT51
	63091	Yes	SSA4
	67046		SSA20 (chymotrypsin-like domain)
	74042		Leucine-rich repeats
	56805		Unknown
	60926		RABL2A
	79456	Yes	ARL3
	68064		ARL13
Other	80690		DYF13
	56340		POC7/UNC119/HRG4.
	29950		Nucleoside diphosphate kinase (flagellate-specific domain structure)
	69688	Yes	DPY30
	78184		FKB12
	78645	Yes	PDE14

Genes contained in the flagella-enriched gene cluster are classified by predicted function (left).

Gene information for each protein ID in the second column can be found at: <http://genome.jgi-psf.org/NaeGr1/NaeGr1.home.html>. Genes with hits in the proteomic analysis of *Naegleria* flagella are indicated in the second column with a “Yes”. Predicted orthologs of each gene are listed on the far right.