

Erratum

Dagenbach, E. M. and Endow, S. A. (2004). A new kinesin tree. *J. Cell Sci.* **117**, 3-7.

The neck analysis entries in Table 1 were not aligned correctly in both the print and online versions of this paper. The corrected Table 1 is shown below. We apologise for any inconvenience caused.

Table 1. Analysis of previously unclassified kinesin proteins for assignment to groups

Group	Proteins compared to	Protein	Motor position*	Motor sequence ID (%)	Predicted coiled-coil position†	Notes	Neck analysis‡	
At1	AtF3K23.6	AtF24M12.190	N	66.9	380-425			
		AtK1L20.9	N	67.1	383-434			
		AtT19F6.160	N	66.6	329-360			
		AtMDH9.19			52.9	None		
		AtF19H22.50	N	76.6	336-365			
		AtF7K15.60	N	55.0	385-434			
		AtF15H18.12	N	44.9	418-464		1 aa missing from alignment	
At2	AtF3K23.14	AtF3K23.6	N	100	364-393			
		AtF19H22.150	N	73.8	489-580			
		AtT21B14.15e	N	74.2	385-426			
		AtF15M7.20	N	72.0	394-432			
		AtF8K7.17	N	76.7	394-474			
Unnamed At group	AtF28P10.150	AtF3K23.14	N	100	422-513			
		AtF22M8.8	N	65.7	423-452			
Unnamed At group	AtPAKRP1	AtF5011.15	N	69.7	466-495			
		AtF28P10.150	N	100	473-524			
		AtMAL21.18	N	44.1	421-453			
Unnamed At group	AtT15B3.190	AtMDB19.17	N	89.6	439-468	Phragmoplast-associated		
		AtPAKRP1	N	100	1044-1073	Phragmoplast-associated		
Unnamed At group	AtT15B3.190	AtMGD8.20	N	64.9	494-527			
		AtK13E13.17	N	64.1	771-805			
Unnamed At group	AtT1E22.130	AtT15B3.190	N	100	578-609			
		AtMRO11.5	N	34.5	None	Grouped by bootstrap		
BimC	AnBimC	AtT1E22.130		100	None			
		PMAL3P6.13	N	37.0	None			
		HsKIF8			(53.5)		Partial sequence	
		AtKRP125a	N	50.1	(438-467) <i>P</i> =0.41			
		AtKRP125b	N	50.8	406-477		GenBank identifies as cytokinesis motor	
CENP-E	HsCENP-E	AtKRP125c	N	53.3	438-518	GenBank identifies as spindle motor		
		AtF16L2.60	N	50.1	433-523			
		DmCana	N	40.4	487-536	Kinetochore motor (Yucel et al 2000)		
		DmCmeta	N	48.1	333-374	Kinetochore motor (Yucel et al 2000)		
Chromokinesin/ KIF4	HsKIF4	AtF14P13.22	N	49.3	364-410	GenBank identifies as putative kinesin-like centromere protein		
		AtZCF125	N	51.0	359-414			
		HsNYREN62	N	50.7	467-509			
Unnamed Hs group	HsKIAA1236	AtMSL3.5	N	49.5	581-615	Group supported by neighbor-joining bootstrap value of 95% and high % sequence ID to HsKIF4		
		AtMCA23.16	N	47.2	539-573			
		AtF11CI.80	N	50.4	411-443			
KHC	DmKHC	HsKIAA1236		100	None	May not be full-length sequence		
		HsLOC343489		54.4	None			
Kip3	ScKip3	AtMAA21.110	N	40.6	374-418	Bootstrap values do not support placement in KHC group		
		PfMAL3P7.1	N	41.9	594-629			
		HsKIF18	N	47.7	None			
		AtF25II6.11	N	44.7	502-540	Bootstrap values do not support placement in Kip3 group		
		DmKlp67A	N	43.6	362-398			
		DmKIF19A	N	39.0	550-598			
		HsFLJ37300	N	45.4	420-451	DmKIF19A listed in alignment as DmKlp19A		
KRP85/95	CeOsm3	PfMAL1P2.11	N	46.6	1412-1442			
		HsKIAA1405	N	58.3	368-411	Group supported by neighbor-joining bootstrap value of 100% and high % sequence ID to CeOsm3		
		DmKIF3C	N	50.9	(351-380) <i>P</i> =0.44			

Table 1. Continued

Group	Proteins compared to	Protein	Motor position*	Motor sequence ID (%)	Predicted coiled-coil position†	Notes	Neck analysis‡
MCAK/ KIF2	HsMCAK	HsKlp17q22	Central	67.7	None		
		DmKlp59D	Central	61.7	None		
		AtMGL6.9	Central	52.1	705-741		
MKLP1	DmPAV	AtMSL1.9	Central	53.3	596-627		
		PtL2165w	(Central)	45.3	None	Motor towards N terminus	
		HsKlpMPP1	N	33.2	568-607		
Unc104/ KIF1	CeUnc104	HsRabK6	N	27.0	680-718	Bootstrap values and % sequence ID to DmPav do not support placement in MKLP1 group	
		AtT20H2.17	(N)	13.5	(839-868)		P=0.49
		HsKIF1B	N	70.6	504-533		
C-Terminal motor	AtKATD	HsGAKIN	N	58.5	612-644	Sequence only ~65 aa longer than motor domain, may not be full length	
		HsRBKIN1	N	57.5	391-420		
		HsKIF16B	N	49.7	None		P<0.4
C-Terminal motor	AtKATD	AtT12M4.14	N	67.3	750-788	Coiled-coil after motor domain Groups with AtKatD by bootstrap	+ + + G+ KICNKSNECITGS
		AtF15H18.10	C	62.1	433-523		++L N + +L+GN NQKLFNELQELKGN
		AtF25P22.28	C	63.8	352-444		++L N + +L+GN NRKLFNELQELKGN
		AtF24D7.17	C	62.1	285-384		+ L+N V +L+GN NRRLYNEVQELKGN
		AtK1013.11	C	61.5	276-331		+ L+N V +L+GN NRRLYNEVQELKGN
		AtF14P13.9	Central	55.8	None	Neck present Groups with AtKatD by bootstrap	++L+N V DL+GN NRKLYNMVQDLKGN
		HsKIFC2	C	37.8	270-320	C-terminal motor	+ +L+GN PAGCPGRPELPELKGN
		AtT9I22.5	C	39.9	388-430	C-terminal motor Neck present	RKEL+N + + +GN RKELYNHIEQETKGN
		AtF15A18.10	N	51.9	375-410	Coiled-coil after motor domain Neck present	RK L+N V++L+GN RKRYLYNEVIELKGN
		AtT9N14.6	C	52.0	341-373		RKEL+N +++L+GN RKELYNKILELKGN
		AtF15F15.20	C	42.2	35-78	C-terminal motor Neck present	RK++ N ++D +G+ RKQVLNKI IDTKGS
		AtF12B17.180	C	36.4	57-92	C-terminal motor Neck present	+K L N ++ +GN KKRFLFNDLLTAKGN
		AtMNA5.20	C	33.8	52-85	C-terminal motor Neck present	+K L N ++ +GN KKRFLFNDLLTAKGN
		AtC17L7.110	C	44.5	383-413	C-terminal motor Neck present	RK+LHNT+++L+GN RKKLHNTILELKGN

*Position of motor domain in protein and/or relative to predicted coiled-coil.

†Coiled-coil predicted by PAIRCOIL ($P \geq 50\%$). Coiled-coil position is that closest to the end of the motor domain for N-terminal motors and the beginning of the motor domain for C-terminal motors.

‡Sequence similarity to DmNcd neck, the region adjacent to the beginning of the conserved motor domain (RKELHNTVMDLRGN; top); sequence at bottom from corresponding region of protein under analysis.