

Sequence comparison of fungal alpha-tubulins

Protein alignment for selected fungal α -tubulins:

Human K-alpha-1 sequence included (upper line, underline, *italics*) but not used to calculate consensus sequence (**bold**)

	1		50
<i>NP_006073-HsA1</i>	(1)	<u>MRECI</u> <u>SI</u> <u>THV</u> <u>GQAGV</u> <u>QIGNACWELYCLEHGIQPDG</u> <u>QMPSD</u> ----	<u>KTIGGGD</u>
AAA35180-ScA1	(1)	<u>MREVIS</u> <u>INVGQAGCQIGNACWELYSLEHG</u> <u>IKPDGHLE</u> <u>DGLS</u> --	<u>KPK</u> -GGE
P87066-CaA	(1)	<u>MREVIS</u> <u>INVGQAGCQIGNACWELYSQEHG</u> <u>IRPDGYLQ</u> <u>EGLD</u> --	<u>RPK</u> -GGE
AAA35350-SpA1	(1)	<u>MREVIS</u> <u>VHVGQAGVQIGNACWELYCLEHGI</u> <u>GPDGF</u> <u>PTENSEVH</u> <u>KNNSYLN</u>	
AW444429-AbAlpt (T3)	(1)	-----	
BAE55852-AorA1	(1)	<u>MREVIS</u> <u>LNVGQAGCQIAN</u> <u>SCWELYCLEHGIQPDG</u> <u>YLTEE</u> ----	<u>RKKEDPD</u>
XP_750005-AfuA1	(1)	<u>MREVIS</u> <u>LNVGQAGCQIAN</u> <u>SCWELYCLEHGIQPDG</u> <u>YLTEE</u> ----	<u>RKKADPD</u>
XP_657920-AniA1	(1)	<u>MREVIS</u> <u>LNVGQAGCQIAN</u> <u>SCWELYCLEHGIQPDG</u> <u>YLTEE</u> ----	<u>RKKEDPD</u>
Consensus	(1)	MREVISLNVGQAGCQIANACWELYCLEHGI PDGYLTE	R K D
	51		100
<i>NP_006073-HsA1</i>	(47)	<u>DSFN</u> <u>TFFSETGAGKHV</u> <u>PRAV</u> <u>FVDLEPTV</u> <u>IDEVRTGTYRQ</u> <u>LFHPEQLITGK</u>	
AAA35180-ScA1	(48)	<u>EGFSTFFHETGYGK</u> <u>FVPRAI</u> <u>YVDLEPNV</u> <u>IDEVRNGPYK</u> <u>DLFHPEQL</u> <u>LSGK</u>	
P87066-CaA	(48)	<u>EGFSTFFSETG</u> <u>SGKYV</u> <u>PRAI</u> <u>YVDLEPNV</u> <u>IDEVRTG</u> <u>VYKDLFHPEQL</u> <u>IAGK</u>	
AAA35350-SpA1	(51)	<u>DGFG</u> <u>TFFSETGQ</u> <u>GKVF</u> <u>PRSI</u> <u>YVDLEPNV</u> <u>IDQVRTG</u> <u>PYKDLFHPEQ</u> <u>MVTGK</u>	
AW444429-AbAlpt (T3)	(1)	-----	
BAE55852-AorA1	(47)	<u>HGFSTFFSETGQ</u> <u>GKYV</u> <u>PRTI</u> <u>YADLEPNV</u> <u>VDEV</u> <u>RTGTYR</u> <u>TLFHPEN</u> <u>MITGK</u>	
XP_750005-AfuA1	(47)	<u>HGFSTFFSETGQ</u> <u>GKYV</u> <u>PRTI</u> <u>YCDLEPNV</u> <u>VDEV</u> <u>RTGTYR</u> <u>SLFHPEN</u> <u>MITGK</u>	
XP_657920-AniA1	(47)	<u>HGFSTFFSETGQ</u> <u>GKYV</u> <u>PRTI</u> <u>YADLEPNV</u> <u>VDEV</u> <u>RTGTYR</u> <u>SLFHPEN</u> <u>LITGK</u>	
Consensus	(51)	GFSTFFSETGQGKYVPRTIY DLEPNVIDEVRTG YK LFHPENLITGK	

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		101	150
<i>NP_006073-HsA1</i>	(97)	EDAANNYARGHYTIGKEIIDLVLDRIRKLADQCTGLQGFLVFHSFGGGTG	
AAA35180-ScA1	(98)	EDAANNYARGHYTVGREILGDVLDRIRKLADQCDGLQGFLFTHSLGGGTG	
P87066-CaA	(98)	EDAANNYARGHYTVGREILDDILDRVRRMSDQCDGLQGFLFTHSLGGGTG	
AAA35350-SpA1	(101)	EDASNNYARGHYTVGKEMIDSVLERIRRMADNCSGLQGFLVFHSFGGGTG	
AW444429-AbAlpt (T3)	(1)	-----	
BAE55852-AorA1	(97)	EDASNNYARGHYTVGKEMIDQLDKVRRVADNCAGLQGFLVFHSFGGGTG	
XP_750005-AfuA1	(97)	EDASNNYARGHYTVGKEMIDQLDKVRRVADNCAGLQGFLVFHSFGGGTG	
XP_657920-AniA1	(97)	EDASNNYARGHYTVGKEMIDQLDKVRRMADSCSGLQGFLVFHSFGGGTG	
Consensus	(101)	EDASNNYARGHYTVGKEMID VLDKVRRMADNCAGLQGFLVFHSFGGGTG	
		151	200
<i>NP_006073-HsA1</i>	(147)	SGFTSLLMERLSVDYGKSKLEFSIYPAPQVSTAVVEPYNSILTTHTTLE	
AAA35180-ScA1	(148)	SGLGSLLLEELSAEYGGKSKLEFAVYPAPQVSTSVVEPYNTVLTTHTTLE	
P87066-CaA	(148)	SGLGSLLLEQLSLDYGGKSKLEFAVYPAPQVSTSVVEPYNTVLTTHTTLE	
AAA35350-SpA1	(151)	SGLGTLLLERLNMEYGGKSNLQFSVYPAPQVSTSVVEPYNSVLTTHATLD	
AW444429-AbAlpt (T3)	(1)	----TRPLERLSTDYGGKSKLEFSVYPAPTLANSVVEPYNSVLTTHTTLE	
BAE55852-AorA1	(147)	SGFGALLMERLSVDYGKSKLEFCVYPAPQNATSVVEPYNSILTTHTTLE	
XP_750005-AfuA1	(147)	SGFGALLMERLSVDYGKSKLEFCVYPAPQNATSVVEPYNSILTTHTTLE	
XP_657920-AniA1	(147)	SGFGALLMERLSVDYGKSKLEFCVYPAPQNATSVVEPYNSILTTHTTLE	
Consensus	(151)	SG GALLLERLSVDYGKSKLEFAVYPAPQVATSVVEPYNSVLTTHTTLE	
		201	250
<i>NP_006073-HsA1</i>	(197)	HSDCAFVMVDNEAIYDICRRNLDIERPTYTNLNRLISQIVSSITASLRFDG	
AAA35180-ScA1	(198)	HADCTFMVDNEAIYDMCKRNLDIRPFSANLNNLIAQVVSSVTASLRFDG	
P87066-CaA	(198)	HADCTFMVDNEAIYDMCRNLDIARPNFSSLNNLIAQVVSSVTASLRFDG	
AAA35350-SpA1	(201)	NSDCTFMVDNEACYDICRRNLDIERPTYENLNRLIAQVVSSITASLRFAG	
AW444429-AbAlpt (T3)	(47)	HSDCSFMVDNEAIYDIKKNLNITSPSLVNLNRLIAQVVSSITASLRFDG	
BAE55852-AorA1	(197)	HSDCSFMVDNEAIYDICRRNLGIERPSYENLNRLIAQVVSSITASLRFDG	
XP_750005-AfuA1	(197)	HSDCSFMVDNEAIYDICRRNLGIERPSYENLNRLIAQVVSSITASLRFDG	
XP_657920-AniA1	(197)	HSDCSFMVDNEAIYDICRRNLGIERPSYENLNRLIAQVVSSITASLRFDG	
Consensus	(201)	HSDCSFMVDNEAIYDICRRNL IERPSYENLNRLIAQVVSSITASLRFDG	



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		251	300
<i>NP_006073-HsA1</i>	(247)	ALNVDLT EFQTNLVPYPR IHFPLATYAPVISA EKAYHEQL SV AEITNACF	
AAA35180-ScA1	(248)	SLNVDLNEFQTNLVPYPR IHFPLVSYSPVL SKSKAFHESNSVS EITNACF	
P87066-CaA	(248)	SLNVDLNEFQTNLVPYPR IHFPLVSYAPVF SKSRATHEANSVS EITQSCF	
AAA35350-SpA1	(251)	SLNVDLNEFQTNLVPYPR IHFPLVTYSPIV SAAKAFHESNSVQ EITNQCF	
AW444429-AbAlpt (T3)	(97)	SLNVDLNEFQTNLVP FPR-----	
BAE55852-AorA1	(247)	SLNVDLNEFQTNLVPYPR IHFPLVAYAPVISA AKASHEANSVNEIT MSCF	
XP_750005-AfuA1	(247)	SLNVDLNEFQTNLVPYPR IHFPLVAYAPVISA AKASHEANSVNEIT SACF	
XP_657920-AniA1	(247)	SLNVDLNEFQTNLVPYPR IHFPLVAYS SPVISADKASHEANSVQ DITMSCF	
Consensus	(251)	SLNVDLNEFQTNLVPYPR IHFPLVAYAPVISA AKASHEANSVNEIT SCF	
		301	350
<i>NP_006073-HsA1</i>	(297)	EPANQMVKCDPR HGKYMAC CLLYRGD VVPKDV NAAIATIKTKRS IQFVDW	
AAA35180-ScA1	(298)	EPGNQMVKCDPRD GKYMAT CLLYRGD VVTG DVQRAVEQVKNKKT VQLVDW	
P87066-CaA	(298)	EPGNQMVKCDPRT GKYMAT CLLYRGD VVTR DVQNAVAQVKS SKKT VQLVDW	
AAA35350-SpA1	(301)	EPYNQMVKCDPRT GRYMAT CLLYRGD VIPR DVQAAVTSIK SRRT IQFVDW	
AW444429-AbAlpt (T3)	(115)	-----	
BAE55852-AorA1	(297)	EPNNQMVKCDPR NGKYMAT CLLYRGD VVPK ETHAAVATL KTKRT IQFVDW	
XP_750005-AfuA1	(297)	EPNNQMVKCDPR NGKYMAT CLLYRGD VVPK ETHAAVATL KTKRT IQFVDW	
XP_657920-AniA1	(297)	EPNNQMVKCDPR NGKYMAT CLLYRGD VVPK ETHAAVATL KTKRT IQFVDW	
Consensus	(301)	EP NQMVKCDPR GK YMATCLLYRGD VVPK D AAVATL KTKRT IQFVDW	
		351	400
<i>NP_006073-HsA1</i>	(347)	CPTGFKVGIN YQPPTV VPGGDLAKVQ RAVC MLSNTT AI AEAWARLD HKFD	
AAA35180-ScA1	(348)	CPTGFKIGICYE PPTAT PNSQLAT VDRAV CMLSNTT SI AEAWKRI DRKFD	
P87066-CaA	(348)	CPTGFKIGICYQ PPTA IKGSEL ASASRAVC MLSNTT AI AEAWRR IDRKFD	
AAA35350-SpA1	(351)	CPTGFKIGICYE PPQH VPGSGI AKVNR AVCMLSNTT SI AEAWSRL DHKFD	
AW444429-AbAlpt (T3)	(115)	-----	
BAE55852-AorA1	(347)	CPTGFKIGICYQ PPK QVPNGDLAN LSRAVC MLSNTT AI SEAWSAL DHKFD	
XP_750005-AfuA1	(347)	CPTGFKIGICYQ PP QQVPGGDLAK LDRAV CMLSNTT AI AEAWSAL DHKFD	
XP_657920-AniA1	(347)	CPTGFKIGICYQ PP QQVPGGDLAK VNR AVCMLSNTT AI SEAWSAL DHKFD	
Consensus	(351)	CPTGFKIGICYQ PP VP DLA V RAV CMLSNTT AI AEAWS LDHKFD	



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		401		450
	<i>NP_006073-HsA1</i>	(397)	<i>LMYAKRAFVHWYVGGEGEEGFSEAREDMAALEKDYEEVGVDSVEGEGEE</i>	
	AAA35180-ScA1	(398)	<i>LMYAKRAFVHWYVGGEGEEGFTTEAREDLAALERDYIEVGADSYAEEEEF</i>	
	P87066-CaA	(398)	<i>LMYSKRAFVHWYVGGEGEEGFTTEAREDLAALERDYIEVGTDSFPEEEEE</i>	
	AAA35350-SpA1	(401)	<i>LMYSKRAFVHWYVGGEGEEGFSEAREDLAALERDYEEVGVQDSMDNEMYE</i>	
	AW444429-AbAlpt (T3)	(115)	-----	
	BAE55852-AorA1	(397)	<i>LMYSKRAFVHWYVGGEGEEGFSEAREDLAALERDYEEVASDSLSEEEVA</i>	
	XP_750005-AfuA1	(397)	<i>LMYSKRAFVHWYVGGEGEEGFSEAREDLAALERDYEEVAADSMDEEVEA</i>	
	XP_657920-AniA1	(397)	<i>LMYSKRAFVHWYVGGEGEEGFSEAREDLAALERDYEEVASDSLSEEEGEE</i>	
	Consensus	(401)	LMYSKRAFVHWYVGGEGEEGFSEAREDLAALERDYEEVAADSLDEE E	
		451		
	<i>NP_006073-HsA1</i>	(447)	<i>EGEEY</i>	
	AAA35180-ScA1	(448)	-----	
	P87066-CaA	(448)	Y----	
	AAA35350-SpA1	(451)	ADEEY	
	AW444429-AbAlpt (T3)	(115)	-----	
	BAE55852-AorA1	(447)	EY---	
	XP_750005-AfuA1	(447)	EY---	
	XP_657920-AniA1	(447)	VEY--	
	Consensus	(451)		

Positions for key feature (aligned on human sequence)

Nucleotide binding site (amino acid-position):

G10,Q11,A12,Q15,I16,D73,L74,E75,A103,A104,N105,S144,F145,G146,G147,G148,T149,G150,I175,P177,A178,N210,Y214

Taxol binding site:

E22,L23,L221,S240,S241,Y276,P278

Alpha-beta interface:

A204,N205,N206,R209,V284,E286

Beta-alpha interface:

R2,D203,T257,E258,Q260,T261,N262,P265,Y266,K330,K356



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GTPase catalytic residue:

E258

Data comes from Conserved Domains Database (CDD): cd02186.2

Citing CDD: Marchler-Bauer A, Anderson JB, Cherukuri PF, DeWeese-Scott C, Geer LY, Gwadz M, He S, Hurwitz DI, Jackson JD, Ke Z, Lanczycki CJ, Liebert CA, Liu C, Lu F, Marchler GH, Mullokandov M, Shoemaker BA, Simonyan V, Song JS, Thiessen PA, Yamashita RA, Yin JJ, Zhang D, Bryant SH (2005), "*CDD: a Conserved Domain Database for protein classification.*", **Nucleic Acids Res.** **33:** D192-6.

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Identity table (exact amino acid match - pair-wise analyses)

	AAA35180-ScA1	P87066-CaA1	AAA35350-SpA1	AW444429-AbA1	BAE55852-AorA1	XP_750005-AfuA1	XP_657920-AniA1	NP_006073-HsA1
AAA35180-ScA1	100	87	76	79	74	75	75	75
P87066-CaA1		100	75	77	77	77	77	74
AAA35350-SpA1			100	77	78	79	79	77
AW444429-AbA1				100	84	84	84	77
BAE55852-AorA1					100	97	96	79
XP_750005-AfuA1						100	95	79
XP_657920-AniA1							100	79
NP_006073-HsA1								100

Conservation table (amino-acid similarity - pair-wise analyses)

	AAA35180-ScA1	P87066-CaA1	AAA35350-SpA1	AW444429-AbA1	BAE55852-AorA1	XP_750005-AfuA1	XP_657920-AniA1	NP_006073-HsA1
AAA35180-ScA1	100	95	87	91	87	87	86	86
P87066-CaA1		100	87	91	88	87	87	87
AAA35350-SpA1			100	88	90	90	90	89
AW444429-AbA1				100	88	88	88	91
BAE55852-AorA1					100	99	98	89
XP_750005-AfuA1						100	98	89
XP_657920-AniA1							100	89
NP_006073-HsA1								100



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Accessions & Citations

Aspergillus fumigatus (Af293)

Protein: XP_750005
DNA: XM_744912
Evidence: Alpha-1 designation based on sequence homology, not supported by known biological data

Aspergillus nidulans (FGSC A4)

Protein: XP_657920
DNA: XM_652828
Evidence: Alpha-1, designation based on sequence homology, see *Aspergillus nidulans* Gene Index (AnGI) sequence TC5521, also called TUBA (see Oakley BR, 2004. *Fungal Genet. Biol.* 41: 420-7)

Aspergillus oryzae (RIB40)

Protein: BAE55852
DNA: AP007151
Evidence: Homolog based on sequence. Sequence was transcribed/translated from whole genome DNA sequence.

Candida albicans (ATCC 10231)

Protein: P87066 & BAE55852 & AAA53194
DNA: U38534
Evidence: Homolog of TUB1. *Daly et al.* 1997. *Gene* 187: 151-158.



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Saccharomyces cerevisiae

Protein: P09733
DNA: M28429
Evidence: TUB1 shown to be primary α -tubulin (see Schatz *et al.* 1986, Mol. Cell Biol. 6: 3711-3721)

Schizosaccharomyces pombe

Protein: AAA35350 is equivalent to P04688, nda2.
DNA: K02841
Evidence: Homolog Nda2 equivalent to TUB1 is primary alpha-tubulin. (see Toda *et al.* 1984. Cell 37: 233-242. & Adachi *et al.* 1986. Mol. Cell Biol. 6: 2168-2178).

Agaricus bisporus

Protein: NONE – translated from EST sequence
DNA: AW444429
Evidence: Homolog of α 1 based on short EST sequence (see Ospina-Giraldo *et al.* 2000. Fungal Genet. 29: 81-94)

Homo sapiens

Protein: NP_006073
DNA: NM_006082 (is Ref.Seq. Entry)
Evidence:
Unigene: Hs.524390