

Table S1. Retrieved *AtBOB1* homologs across eukaryotes*AtBOB1* homologs in plants and algae

Organism	Locus ID	Gene name	Uniprot ID	Number of exons	Protein length (aa)	Protein domains & positions	Maximum organ expression	Intracellular localization (found/predicted)	Functions (found/predicted)	References
<i>Arabidopsis thaliana</i>	<i>At4g27890</i>	<i>BOBBER 2 (BOB2)</i>	A0A5S9XWX5, Q9STN7	3	293	CS (131-220); p23_NUDC_like (136-220)	root, stem, flower, silique, seed	cytoplasm	unfolded protein binding, protein folding, response to stress	Jurkuta et al. (2009); Perez et al. (2009)
<i>Arabidopsis thaliana</i>	<i>At5g53400</i>	<i>BOBBER1 (BOB1)</i>	Q9LV09	6	304	CS (142-231); p23_NUDC_like (147-231)	root, shoot, flower, silique, seed	cytoplasm, cytoplasmic granules	protein folding, response to heat, pollen development, response to high light intensity, embryonic pattern specification, leaf morphogenesis, inflorescence meristem growth, developmental process, response to endoplasmic reticulum stress, response to hydrogen peroxide, stamen morphogenesis, specification of floral organ number	Jurkuta et al. (2009); Perez et al. (2009); Kaplinsky (2009)
<i>Arabidopsis thaliana</i>	<i>At5g58740</i>	<i>NMig1</i>	Q8VXX3, A0A178UER9	5	158	CS (16-104); p23_NUDC_like (21-104)	root, flower, silique, seed	cytoplasm, nucleus	unfolded protein binding, protein folding, response to stress, root development	Velinov et al. (2020); Velinov et al. (2021)
<i>Brassica napus</i>	<i>GSBRNA2T00004948001</i>	<i>BnaA10g29540D</i>	A0A078IM25	5	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Brassica napus</i>	<i>GSBRNA2T00044314001</i>	<i>BnaA03g48890D</i>	A0A078GZ49	2	287	CS (126-215); p23_NUDC_like (131-215)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Brassica napus</i>	<i>GSBRNA2T00044313001</i>	<i>BnaA03g48880D</i>	A0A078GXE8	2	308	CS (148-238); p23_NUDC_like (153-235)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Brassica napus</i>	<i>GSBRNA2T00094192001</i>	<i>BnaC03g34480D</i>	A0A078IU54	2	209	CS (47-136); p23_NUDC_like (52-133)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Brassica napus</i>	<i>GSBRNA2T00006266001</i>	<i>BnaC01g20510D</i>	A0A078G219	3	226	CS (64-153); p23_NUDC_like (69-153)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Brassica rapa subsp. pekinensis</i>	<i>Bra002621</i>	<i>Bra002621</i>	A0A397XSX1	5	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm	response to stress	
<i>Brassica rapa subsp. pekinensis</i>	<i>Bra040837</i>	<i>Bra040837</i>	M4FIA8	2	290	CS (129-218); p23_NUDC_like (134-218)			unfolded protein binding, protein folding, response to stress	
<i>Brassica rapa subsp. pekinensis</i>	<i>Bra040836</i>	<i>Bra040836</i>	A0A397L8K8	1	305	CS (145-235); p23_NUDC_like (150-232)			response to stress	

<i>Brassica rapa subsp. pekinensis</i>	Bra026300	Bra026300	M4EBZ1	2	289	CS (127-216); p23_NUDC_like (132-216)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Brassica rapa subsp. pekinensis</i>	Bra003059	Bra003059	M4CFS7	6	279	CS (117-206); p23_NUDC_like (122-206)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Capsicum annuum</i>	T459_18329	T459_18329	A0A1U8HBB2	5	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm, nucleus	unfolded protein binding, protein folding, response to stress	
<i>Capsicum annuum</i>	T459_07419	T459_07419	A0A2G2ZTM5	1	153	CS (25-120); p23_NUDC_like (30-120)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Capsicum annuum</i>	T459_07420	T459_07420	A0A2G2ZTK9	2	245	CS (60-149); p23_NUDC_like (65-149)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Capsicum annuum</i>	T459_27622	T459_27622	A0A2G2YEH3	1	117	NudC (6-110); HSP20-like chaperone (4-73)		cytoplasm	unfolded protein binding, protein folding	
<i>Capsicum annuum</i>	T459_07418	T459_07418	A0A2G2ZTL8	2	254	CS (82-171); p23_NUDC_like (87-171)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Capsicum annuum</i>	T459_16487	T459_16487	A0A2G2Z984	6	286	CS (124-213); p23_NUDC_like (129-213)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Capsicum annuum</i>	T459_09591	T459_09591	A0A1U8FZY1	6	307	CS (145-234); p23_NUDC_like (150-234)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Lactuca sativa</i>	LSAT_2X122940	LSAT_2X122940	A0A2J6M261	5	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Lactuca sativa</i>	LSAT_9X56360	LSAT_9X56360	A0A2J6KDI6	6	306	CS (144-233); p23_NUDC_like (149-233)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Solanum lycopersicum</i>	Solyc06g076940.3	SIBOBBER1 (SIBOB1)	A0A3Q7HXJ3, K4CA52	5	158	CS (16-104); p23_NUDC_like (21-104)	root, fruit, seed	cytoplasm	unfolded protein binding, protein folding, developmental process, immune response	Liu et al. (2019)
<i>Solanum lycopersicum</i>	Solyc09g092210.3	Solyc09g092210.3	A0A3Q7I8N0	3	205	CS (58-147); p23_NUDC_like (63-147)	flower, fruit	cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Solanum lycopersicum</i>	Solyc02g062410.2	SIBOBBER2 (SIBOB2)	A0A3Q7FJG8	2	226	CS (54-143); NudC (10-204); p23_NUDC_like (59-143)	flower, fruit	cytoplasm	unfolded protein binding, protein folding, response to stress	Liu et al. (2019)
<i>Solanum lycopersicum</i>	Solyc09g092200.2	Solyc09g092200.2	A0A3Q7I8G7	4	219	CS (39-135); p23_NUDC_like (44-135)	flower, fruit	cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Solanum lycopersicum</i>	Solyc06g051950.3	SIBOBBER3 (SIBOB3)	A0A3Q7HNZ6	9	347	CS (191-280); p23_NUDC_like (196-280)	flower, fruit, seed	cytoplasm	response to stress, immune response	Liu et al. (2019)

<i>Solanum lycopersicum</i>	<i>Solyc03g083390.3</i>	101255475	K4BIB5, A0A3Q7FN48	6	302	CS (140-229); p23_NUDC_like (145-229)	stem, flower, fruit, seed	cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Solanum tuberosum</i>	<i>PGSC0003DMG400030355</i>	102588480	M1CZA6	5	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm, nucleus	unfolded protein binding, protein folding, response to stress	
<i>Solanum tuberosum</i>	<i>PGSC0003DMG400026423</i>	<i>PGSC0003DMG400026423</i>	M1CI53	2	247	CS (62-151); p23_NUDC_like (67-151)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Solanum tuberosum</i>	<i>PGSC0003DMG400046575</i>	<i>PGSC0003DMG400046575</i>	M1DZP7	2	211	CS (39-128); p23_NUDC_like (44-128)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Solanum tuberosum</i>	<i>PGSC0003DMG400009123</i>	102577908	Q38HV0	6	308	CS (146-235); p23_NUDC_like (151-235)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Nicotiana tabacum</i>	<i>LOC107815638</i>	<i>LOC107815638</i>	A0A1S4C715	5	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Nicotiana tabacum</i>	<i>LOC107796635</i>	<i>LOC107796635</i>	A0A1S4AEN1	5	158	CS (16-104)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Nicotiana tabacum</i>	<i>LOC107769666</i>	<i>LOC107769666</i>	A0A1S3XWY9	1	170	CS (49-138)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Nicotiana tabacum</i>	<i>LOC107769667</i>	<i>LOC107769667</i>	A0A1S3XWY7	2	251	CS (65-154); p23_NUDC_like (54-138)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Nicotiana tabacum</i>	<i>LOC107785569</i>	<i>LOC107785569</i>	A0A1S3ZD95	1	230	CS (57-146); p23_NUDC_like (62-146)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Nicotiana tabacum</i>	<i>LOC107779500</i>	<i>LOC107779500</i>	A0A1S3YTB1	1	213	CS (46-135)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Nicotiana tabacum</i>	<i>LOC107791897</i>	<i>LOC107791897</i>	A0A1S3ZYN1	2	166	CS (46-135)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Nicotiana tabacum</i>	<i>LOC107790710</i>	<i>LOC107790710</i>	A0A1S3ZUT2	2	240	CS (67-156)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Nicotiana tabacum</i>	<i>LOC107816713</i>	<i>LOC107816713</i>	A0A1S4CA10	6	289	CS (127-216); p23_NUDC_like (132-216)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Nicotiana tabacum</i>	<i>LOC107775992</i>	<i>LOC107775992</i>	A0A1S3YGN1	6	299	CS (137-226)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Nicotiana tabacum</i>	<i>LOC107798015</i>	<i>LOC107798015</i>	A0A1S4AIB2	6	301	CS (139-228); p23_NUDC_like (144-228)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Cucumis sativus</i>	<i>Csa1G530660</i>	<i>Csa1G530660</i>	A0A0A0LV57	5	156	CS (16-104); p23_NUDC_like (21-104)		cytoplasm, nucleus	unfolded protein binding, protein folding, response to stress	
<i>Cucumis sativus</i>	<i>Csa5G139440</i>	<i>Csa5G139440</i>	A0A0A0KQ62	6	315	CS (153-242); p23_NUDC_like (158-242)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Medicago truncatula</i>	<i>MTR_3g463620</i>	<i>MTR_3g463620</i>	A0A072UXE1, I3SF11	4	180	CS (44-132); p23_NUDC_like (49-132)	root	cytoplasm, nucleus	response to stress	

<i>Medicago truncatula</i>	MTR_1g008195	25481856	A0A072VDR8	6	290	CS (128-217); p23_NUDC_like (133-217)	seed	cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Medicago truncatula</i>	MTR_1g008170	11431318	G7I4A6	6	289	CS (128-217); p23_NUDC_like (133-217)	seed	cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Medicago truncatula</i>	MTR_1g008200	11429600	G7I4A8	6	295	CS (133-222); p23_NUDC_like (138-222)	nodule	cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Glycine max</i>	GLYMA_11G175500	GLYMA_11G175500	C6SYT5, I1LLK0	5	158	CS (16-104); p23_NUDC_like (21-104)	leaf, seed	cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Glycine max</i>	GLYMA_18G063100	100306544	C6SZU0	5	158	CS (16-104); p23_NUDC_like (21-104)	nodule, seed, embryo	cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Glycine max</i>	GLYMA_06G128000	100775670	I1KAR6	6	299	CS (137-226); p23_NUDC_like (142-226)	nodule, embryo	cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Glycine max</i>	GLYMA_04G236300	100813799	C6TKE3	6	301	CS (139-228); p23_NUDC_like (144-228)	nodule, embryo	cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Eucalyptus grandis</i>	EUGRSUZ_B02255	EUGRSUZ_B02255	A0A059D4G2	5	221	CS (79-167); p23_NUDC_like (84-167)		cytoplasm, nucleus	unfolded protein binding, protein folding, response to stress	
<i>Eucalyptus grandis</i>	EUGRSUZ_A01460	EUGRSUZ_A01460	A0A059DEY7	7	407	CS (245-334); p23_NUDC_like (250-334)		cytoplasm, membrane	unfolded protein binding, protein folding, response to stress	
<i>Juglans regia</i>	LOC109002082	LOC109002082	A0A6P9EDV6	6	180	CS (24-123); p23_NUDC_like (29-123)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Juglans regia</i>	LOC109015374	LOC109015374	A0A6P9EFR4	5	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Juglans regia</i>	LOC108980108	LOC108980108	A0A2I4DH47	1	280	CS (118-207); p23_NUDC_like (123-207)		cytoplasm, nucleus	unfolded protein binding, protein folding, response to stress	
<i>Juglans regia</i>	LOC108982868	LOC108982868	A0A2I4DRW5	6	296	CS (134-223); p23_NUDC_like (139-223)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Juglans regia</i>	LOC109013205	LOC109013205	A0A2I4H3N7	6	296	CS (134-223); p23_NUDC_like (139-223)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Theobroma cacao</i>	TCM_041625	TCM_041625	A0A061GV77	5	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Theobroma cacao</i>	TCM_021712	TCM_021712	A0A061EYB6	1	174	CS (12-101); p23_NUDC_like (18-101)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Theobroma cacao</i>	TCM_015401	TCM_015401	A0A061G2U6	6	295	CS (133-222); p23_NUDC_like (138-222)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Manihot esculenta</i>	MANES_02G119500	MANES_02G119500	A0A2C9WD44	5	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Manihot esculenta</i>	MANES_01G161700	MANES_01G161700	A0A2C9WLD1	5	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm	unfolded protein binding, protein folding, response to stress	

<i>Manihot esculenta</i>	MANES_14G006200	MANES_14G006200	A0A2C9UIQ0	6	320	CS (158-247); p23_NUDC_like (163-247)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Manihot esculenta</i>	MANES_06G160400	MANES_06G160400	A0A2C9VRD1	4	286	CS (223-286); p23_NUDC_like (228-286)		cytoplasm, membrane	unfolded protein binding, protein folding, response to stress	
<i>Manihot esculenta</i>	MANES_06G160000	MANES_06G160000	A0A2C9VST6	3	252	CS (178-252); p23_NUDC_like (183-244)			response to stress	
<i>Prunus persica</i>	PRUPE_6G057600	PRUPE_6G057600	M5W0J7	5	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm, nucleus	unfolded protein binding, protein folding, response to stress	
<i>Prunus persica</i>	PRUPE_2G310800	PRUPE_2G310800	M5XEL2	6	296	CS (16-104); p23_NUDC_like (21-104)		cytoplasm, endoplasmic reticulum, membrane	calcium ion binding, unfolded protein binding, unfolded protein binding, endoplasmic reticulum calcium ion homeostasis, protein folding, response to stress	
<i>Erythranthe guttata</i>	MIMGU_mgv1a015421mg	MIMGU_mgv1a015421mg	A0A022RC76	6	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Erythranthe guttata</i>	MIMGU_mgv1a010735mg	MIMGU_mgv1a010735mg	A0A022PVU0	6	303	CS (141-230); p23_NUDC_like (146-230)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Erythranthe guttata</i>	MIMGU_mgv1a011251mg	MIMGU_mgv1a011251mg	A0A022QB71	6	288	CS (126-215); p23_NUDC_like (131-215)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Helianthus annuus</i>	HannXRQ_Ch07g0202931	HannXRQ_Ch07g0202931	A0A251UEM1	5	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Helianthus annuus</i>	HannXRQ_Ch08g0221811	HannXRQ_Ch08g0221811	A0A251U4P2	5	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Helianthus annuus</i>	HannXRQ_Ch09g0267241	BOB1	A0A251TY55	6	293	CS (131-220)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Populus trichocarpa</i>	POPTR_003G100900v3	POPTR_003G100900	B9GZU9	1	272	CS (103-192); p23_NUDC_like (109-192)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Populus trichocarpa</i>	POPTR_001G132500v3	POPTR_001G132500	A0A2K2BWX2	1	261	CS (104-193)			response to stress	
<i>Populus trichocarpa</i>	POPTR_015G013900v3	POPTR_015G013900	A0A2K1XGH3	6	300	CS (138-227)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Populus trichocarpa</i>	POPTR_012G014100v3	POPTR_012G014100	A0A2K1Y782	6	289	CS (127-216)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Ricinus communis</i>	RCOM_0612440	RCOM_0612440	B9SI21	6	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Ricinus communis</i>	RCOM_0169970	RCOM_0169970	B9T3X1	3	87			cytoplasm	unfolded protein binding, protein folding	
<i>Ricinus communis</i>	RCOM_0597500	RCOM_0597500	B9SJ06	2	209	CS (47-136); p23_NUDC_like (53-135)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Ricinus communis</i>	RCOM_1579230	RCOM_1579230	B9RIH7	6	307	CS (151-240); p23_NUDC_like (156-240)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Gossypium hirsutum</i>	LOC107936543	LOC107936543	A0A1U8MGZ5	5	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm	unfolded protein binding, protein folding, response to stress	

<i>Gossypium hirsutum</i>	LOC107891963	LOC107891963	A0A1U8I2D0	5	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Gossypium hirsutum</i>	LOC107946804	LOC107946804	A0A1U8NCM9	1	269	CS (107-196); p23_NUDC_like (111-194)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Gossypium hirsutum</i>	LOC107947245	LOC107947245	A0A1U8NE51	6	291	CS (129-218); p23_NUDC_like (134-218)			response to stress	
<i>Gossypium hirsutum</i>	LOC107930277	LOC107930277	A0A1U8LS30	6	289	CS (127-216); p23_NUDC_like (132-216)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Gossypium hirsutum</i>	LOC107929622	LOC107929622	A0A1U8LPU0	6	296	CS (134-223); p23_NUDC_like (139-223)			response to stress	
<i>Gossypium hirsutum</i>	LOC107894867	LOC107894867	A0A1U8IGS2	7	285	CS (123-212); p23_NUDC_like (128-212)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Gossypium hirsutum</i>	LOC107944939	LOC107944939	A0A1U8N5J0	1	270	CS (111-200); p23_NUDC_like (116-200)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Gossypium hirsutum</i>	LOC107944267	LOC107944267	A0A1U8N3B4	1	269	CS (111-200); p23_NUDC_like (116-200)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Gossypium hirsutum</i>	LOC107890769	LOC107890769	A0A1U8HXR4	6	289	CS (127-216); p23_NUDC_like (132-216)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Vitis vinifera</i>	VIT_12s0142g00120	VIT_12s0142g00120	D7TR32	6	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Vitis vinifera</i>	VIT_16s0098g00370	VIT_16s0098g00370	E0CVH6	6	289	CS (127-216); p23_NUDC_like (132-216)		cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Nelumbo nucifera</i>	LOC104601263	LOC104601263	A0A1U8AKM9	5	130	CS (16-104); p23_NUDC_like (21-104)				
<i>Nelumbo nucifera</i>	LOC104604013	LOC104604013	A0A1U8AHB1	6	315	CS (153-242); p23_NUDC_like (158-242)		cytoplasm	unfolded protein binding, protein folding	
<i>Musa acuminata subsp. malaccensis</i>	GSMUA_Achr6G27580_001 (Ma06_t29350.1)	103989249	A0A804JLS5	5	158	CS (16-104)				
<i>Musa acuminata subsp. malaccensis</i>	GSMUA_Achr2G07330_001 (Ma02_t09250.1)	103976403	A0A804I0W5		282	CS (120-209)				
<i>Musa acuminata subsp. malaccensis</i>	GSMUA_Achr11G13090_001 (Ma11_t11290.1)	103971323	A0A804L6P6	6	306	CS (144-233); p23_NUDC_like (149-233)				
<i>Brachypodium distachyon</i>	BRADI_5g07310v3	100828146	I1IWY1	5	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm, nucleus	unfolded protein binding, protein folding	
<i>Brachypodium distachyon</i>	BRADI_1g45080v3	100832845	I1GZi6	6	322	CS (170-259); p23_NUDC_like (175-259)		cytoplasm	unfolded protein binding, protein folding	
<i>Brachypodium distachyon</i>	BRADI_2g05060v3	100839208	I1HCN3	6	183	CS (21-110); p23_NUDC_like (26-110)		cytoplasm	unfolded protein binding, protein folding	
<i>Hordeum vulgare subsp. vulgare</i>	HORVU2Hr1G068470 (HORVU.MOREX.r3.2HG016129 0)		F2CY14	5	158	CS (16-104)		cytoplasm, nucleus	unfolded protein binding, protein folding	

<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	HORVU3Hr1G110760 (HORVU.MOREX.r3.3HG0323660)		A0A8I6Y2S2	2	217	CS (54-143)				
<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	HORVU3Hr1G110720 (HORVU.MOREX.r3.3HG0323630)		A0A8I6XCL8	1	214	CS (54-143)				
<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	HORVU7Hr1G038520 (HORVU.MOREX.r3.7HG0666750)		F2E732	6	307	CS (145-234)				
<i>Triticum aestivum</i>	<i>TraesCS2A02G279900</i>		A0A3B6AZB0	5	158	CS (16-104); p23_NUDC_like (21-104)	root, endosperm, shoot axis, stigma and ovary	cytoplasm	unfolded protein binding, protein folding	
<i>Triticum aestivum</i>	<i>TraesCS2B02G296900</i>		A0A3B6C6B1	6	158	CS (16-104); p23_NUDC_like (21-104)	root, leaf, embryo	cytoplasm	unfolded protein binding, protein folding	
<i>Triticum aestivum</i>	<i>TraesCS2D02G278900</i>		A0A3B6DDH6	5	158	CS (16-104); p23_NUDC_like (21-104)	root	cytoplasm	unfolded protein binding, protein folding	
<i>Triticum aestivum</i>	<i>TraesCS3B02G566300</i>	<i>TRAES_3BF052700020CFD_c1</i>	W5D4R8	2	214	CS (51-140); p23_NUDC_like (56-140)		cytoplasm	unfolded protein binding, protein folding	
<i>Triticum aestivum</i>	<i>TraesCS3B02G566200</i>	<i>TRAES_3BF052700030CFD_c1</i>	W5D6E5	1	219	CS (56-145); p23_NUDC_like (61-145)		cytoplasm	unfolded protein binding, protein folding	
<i>Triticum aestivum</i>	<i>TraesCS3D02G509500</i>	<i>TraesCS3D02G509500</i>	A0A3B6H3F0	2	214	CS (51-140); p23_NUDC_like (56-140)		cytoplasm	unfolded protein binding, protein folding	
<i>Triticum aestivum</i>	<i>TraesCS3A02G503000</i>	<i>TraesCS3A02G503000</i>	A0A3B6ERA3	2	168	CS (48-137); p23_NUDC_like (53-137)		cytoplasm	unfolded protein binding, protein folding	
<i>Triticum aestivum</i>	<i>TraesCS3D02G509300</i>	<i>TraesCS3D02G509300</i>	A0A3B6H6D2	1	214	CS (51-140); p23_NUDC_like (56-140)		cytoplasm	unfolded protein binding, protein folding	
<i>Triticum aestivum</i>	<i>TraesCS3A02G502900</i>	<i>TraesCS3A02G502900</i>	A0A3B6EQH3	1	215	CS (52-141); p23_NUDC_like (57-141)		cytoplasm	unfolded protein binding, protein folding	
<i>Triticum aestivum</i>	<i>TraesCS7A02G189600</i>	<i>TraesCS7A02G189600</i>	A0A3B6RFV2	6	316	CS (154-243); p23_NUDC_like (159-243)	root, shoot, leaf, stigma and ovary, grain, endosperm, embryo			
<i>Triticum aestivum</i>	<i>TraesCS7B02G094500</i>	<i>TraesCS7B02G094500</i>	A0A3B6SDZ9	6	320	CS (158-247); p23_NUDC_like (163-247)	root, shoot, leaf, stigma and ovary, embryo	cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Triticum aestivum</i>	<i>TraesCS7D02G190700</i>	<i>TraesCS7D02G190700</i>	A0A3B6TMJ0	6	314	CS (152-241); p23_NUDC_like (157-241)	root, shoot, leaf, stigma and ovary, grain, endosperm, embryo			
<i>Oryza sativa</i>	<i>Os01g0668000</i>	<i>Os01g0668000</i>	B9EYI7	6	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm, nucleus	response to stress	
<i>Oryza sativa</i>	<i>Os02g0743800</i>	<i>Os02g0743800</i>	A0A0P0VPG4, Q6Z2U6	1	196					

<i>Oryza sativa</i>	Os06g0231300	Os06g0231300	A3B9X9	6	308	CS (146-235); p23_NUDC_like (151-235)				
<i>Setaria italica</i>	SETIT_011893mg	SETIT_011893mg	K3YCE7	5	301	CS (159-247); p23_NUDC_like (164-247)		cytoplasm	unfolded protein binding, protein folding	
<i>Setaria italica</i>	SETIT_006940mg	101764727	K3XYN4	6	285	CS (120-212); p23_NUDC_like (147-212)				
<i>Sorghum bicolor</i>	SORBI_3001G301800	SORBI_3001G301800	C5WSG2	5	158	CS (16-104); p23_NUDC_like (21-104)		cytoplasm	unfolded protein binding, protein folding	
<i>Sorghum bicolor</i>	SORBI_3002G400200	SORBI_3002G400200	C5X444	5	159	CS (16-105); p23_NUDC_like (21-105)		cytoplasm	unfolded protein binding, protein folding	
<i>Sorghum bicolor</i>	SORBI_3001G520500	SORBI_3001G520500	C5WZY5	6	181	CS (19-108); p23_NUDC_like (24-108)		cytoplasm	unfolded protein binding, protein folding	
<i>Sorghum bicolor</i>	SORBI_3010G094500	SORBI_3010G094500	A0A194YI58	7	264	CS (102-191); p23_NUDC_like (107-191)				
<i>Zea mays</i>	Zm00001d015423	100283235	B6T1R3	2	158	CS (16-104)	root, tassel, cob, internode tissue, seed	cytoplasm	unfolded protein binding, protein folding	
<i>Zea mays</i>	Zm00001d007069	ZEAMMB73_Zm00001d007069	A0A1D6F2Q5	7	162	p23_NUDC_like (1-73)	root, internode tissue, seed	cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Zea mays</i>	Zm00001d044815	100282404	B4G0G4	6	302	CS (140-229); p23_NUDC_like (145-229)	root, shoot, leaf, tassel, cob, seed, embryo		response to stress	
<i>Zea mays</i>	Zm00001d037236	100273219	B4FTP9	6	308	CS (146-235); p23_NUDC_like (151-235)	root, shoot, leaf, tassel, cob, seed, embryo	cytoplasm	unfolded protein binding, protein folding, response to stress	
<i>Zostera marina</i>	ZOSMA_112G00430	ZOSMA_112G00430	A0A0K9Q555	5	157	CS (16-104)		cytoplasm	unfolded protein binding, protein folding	
<i>Zostera marina</i>	ZOSMA_191G00110	ZOSMA_191G00110	A0A0K9PPK1	4	111			cytoplasm	unfolded protein binding, protein folding	
<i>Zostera marina</i>	ZOSMA_325G00030	ZOSMA_325G00030	A0A0K9PAX6	6	205	CS (77-166)		cytoplasm	unfolded protein binding, protein folding	
<i>Zostera marina</i>	ZOSMA_21G00700	ZOSMA_21G00700	A0A0K9PJT1	6	333	CS (171-260)		cytoplasm	unfolded protein binding, protein folding	
<i>Amborella trichopoda</i>	AMTR_s00029p00243890	AMTR_s00029p00243890	W1PIK0	4	139	CS (16-104); p23_NUDC_like (21-104)		cytoplasm, nucleus	unfolded protein binding, protein folding	
<i>Amborella trichopoda</i>	AMTR_s00017p00231540	AMTR_s00017p00231540	W1PM11	6	311	CS (148-237); p23_NUDC_like (21-104)		cytoplasm	unfolded protein binding, protein folding	
<i>Selaginella moellendorffii</i>	SELMODRAFT_121870	SELMODRAFT_121870	D8RGA0	5	157	CS (16-104); p23_NUDC_like (21-104)		cytoplasm	unfolded protein binding, protein folding	
<i>Selaginella moellendorffii</i>	SELMODRAFT_115773	SELMODRAFT_115773	D8SFG5	5	169	CS (6-96); p23_NUDC_like (11-96)		cytoplasm	unfolded protein binding, protein folding	
<i>Selaginella moellendorffii</i>	SELMODRAFT_85440	SELMODRAFT_85440	D8R5J0	5	169	CS (6-96); p23_NUDC_like (11-96)		cytoplasm	unfolded protein binding, protein folding	

<i>Physcomitrella patens</i>	Pp3c16_190	PHYPA_020249	A9SZ22	6	158	CS (17-105); p23_NUDC_like (22-105)		cytoplasm, nucleus	unfolded protein binding, protein folding	
<i>Physcomitrella patens</i>	Pp3c24_16270	PHYPA_029156	A0A2K1IH15	3	148	CS (8-103); p23_NUDC_like (13-103)		cytoplasm	unfolded protein binding, protein folding	
<i>Physcomitrella patens</i>	Pp3c11_14270	PHYPA_015017	A0A2K1JUQ1	6	392	CS (230-319); p23_NUDC_like (235-319)		cytoplasm	unfolded protein binding, protein folding	
<i>Physcomitrella patens</i>	Pp3c4_23090	PHYPA_006628	A0A2K1KPQ5	6	472	CS (284-373); p23_NUDC_like (289-373)		cytoplasm	unfolded protein binding, protein folding	
<i>Physcomitrella patens</i>	Pp3c2_28400	Pp3c2_28400	A0A2K1L3C1	2	278	CS (194-236); p23_NUDC_like (195-240)				
<i>Physcomitrella patens</i>	Pp3c1_7900	PHYPA_000356	A0A2K1L7F1	7	362	CS (199-289); p23_NUDC_like (204-289)		cytoplasm	unfolded protein binding, protein folding	
<i>Marchantia polymorpha</i>	MARPO_0037s0041	MARPO_0037s0041	A0A2R6X445	5	157	CS (16-104); p23_NUDC_like (21-104)		cytoplasm, nucleus	unfolded protein binding, protein folding	
<i>Marchantia polymorpha</i>	MARPO_0030s0062	MARPO_0030s0062	A0A2R6X894	6	348	CS (186-275); p23_NUDC_like (191-275)		cytoplasm	unfolded protein binding, protein folding	
<i>Klebsormidium nitens</i>	KFL_003070120	KFL_003070120	A0A1Y1I6Z6	5	158	CS (16-104)		cytoplasm	unfolded protein binding, protein folding	
<i>Klebsormidium nitens</i>	KFL_002820210	KFL_002820210	A0A1Y1I5U3	6	340	CS (178-267)		cytoplasm	unfolded protein binding, protein folding	
<i>Chlamydomonas reinhardtii</i>	CHLRE_08g369400v5	CHLRE_08g369400v5	A8J474	5	162	CS (16-104); p23_NUDC_like (21-104)		cytoplasm	unfolded protein binding, protein folding	
<i>Chlamydomonas reinhardtii</i>	CHLRE_13g590400v5	CHLRE_13g590400v5	A8IW64	7	317	CS (165-263); p23_NUDC_like (170-263)		cytoplasm	unfolded protein binding, protein folding	
<i>Chlamydomonas reinhardtii</i>	CHLRE_07g329600v5	CHLRE_07g329600v5	A0A2K3DJS4	10	1102	CS (951-1033); p23_NUDC_like (951-1033)				
<i>Chlamydomonas reinhardtii</i>	CHLRE_17g711650v5	CHLRE_17g711650v5	A0A2K3CPM2	8	343	CS (182-270); p23_NUDC_like (187-270)		cytoplasm		

AtBOB1 homologs in other eukaryotic systems

Organism	Locus ID (NCBI)	Gene name	Uniprot ID	Number of exons	Protein length (aa)	Protein domain & position	Intracellular localization	Functions	References
<i>Homo sapiens</i>	30535	<i>NUDCD2</i>	Q8WVJ2	4	157	CS (14-104); p23_NUDC_like (12-104)	cytoplasm, cytosol, intercellular bridge, kinetochore, microtubule cytoskeleton, microtubule organizing center, mitotic spindle, spindle pole	unfolded protein binding, protein folding	Burkard et al. (2011); Scheuerle et al. (2023); Chen et al. (2020); Li et al. (2019)
<i>Homo sapiens</i>	22208	<i>NUDCD3</i>	Q8IVD9	6	361	CS (185-277); p23_NUDC_like (184-285)	cytoplasm, cytoplasm dynein complex	unfolded protein binding, cilium assembly, protein folding, protein localization to pericentriolar material	Rose et al. 2010; Cai et al. 2009; Zhou et al. 2006
<i>Homo sapiens</i>	8045	<i>NUDC</i>	Q9Y266	9	331	CS (167-258); p23_NUDC_like (172-258)	cytoplasm, cytosol, intercellular bridge, microtubule, midbody, mitotic spindle, nucleoplasm, spindle	cadherin binding, unfolded protein binding, cell division, mitotic metaphase chromosome alignment, mitotic spindle organization, nuclear migration, protein folding, response to peptide hormone	Miller et al. (1999); Matsumoto and Ledbetter (1999); Zhou et al. (2003); Aumais et al. (2003); Chen et al. (2015); Biebl et al. (2022); Islam et al. (2020); Bagci et al. (2020); Weiderhold et al. (2016); Zhou et al. (2016); Gladwyn-Ng et al. (2016); De Souza et al. (2014); Chuang et al. (2013); Zhu et al. (2010); Pang et al. (2009); Tang et al. (2008); Lin et al. (2004)
<i>Mus musculus</i>	<i>MGI</i> =1277103	<i>Nudcd2</i>	Q9CQ48	4	157	CS (19-91); p23_NUDC_like (12-104)	cytoplasm, cytosol, intercellular bridge, kinetochore, microtubule cytoskeleton, microtubule organizing center, mitotic spindle, spindle pole	unfolded protein binding, protein folding	Skarnes et al. (2011)
<i>Mus musculus</i>	<i>MGI</i> =2144158	<i>Nudcd3</i>	Q8R1N4	6	363	CS (187-279); p23_NUDC_like (186-287)	cytoplasm, cytoplasmic dynein complex	cilium assembly, protein folding, protein localization to pericentriolar material	Yang et al. (2022)
<i>Mus musculus</i>	<i>MGI</i> =106014	<i>Nudc</i>	Q35685	8	332	CS (168-259); p23_NUDC_like (173-259)	cytoplasm, cytosol, microtubule, midbody, mitotic spindle, nucleus	unfolded protein binding, cell division, mitotic metaphase chromosome alignment, mitotic spindle organization, nuclear migration, protein folding, response to peptide hormone	Aumais et al. (2001); Yamada et al. (2010)
<i>Rattus norvegicus</i>	1307203	<i>Nudcd2</i>	Q5M823	5	157	CS (14-104); p23_NUDC_like (12-104)	cytoplasm, cytosol, intercellular bridge, kinetochore, microtubule organizing center, mitotic spindle, spindle pole	unfolded protein binding, protein folding	
<i>Rattus norvegicus</i>	6493297	<i>LOC100911422</i>	Q63525	8	332	CS (168-259); p23_NUDC_like (173-259)	cytoplasm, cytosol, microtubule, midbody, mitotic spindle, nucleus	unfolded protein binding, cell division, mitotic metaphase chromosome alignment, mitotic spindle organization, nuclear migration, protein folding	Morris et al. (1997); Morris and Yu-Lee (1998)
<i>Rattus norvegicus</i>	3215	<i>Nudc</i>	A0A0G2K0V8	8	316	CS (152-243); p23_NUDC_like (157-243)	microtubule, midbody, spindle	cell cycle, cell division	Morris et al. (1997); Morris and Yu-Lee (1998)
<i>Danio rerio</i>	<i>ZDB-GENE-040801-49</i>	<i>nudcd2</i>	Q6DC89	4	157	CS (14-104); p23_NUDC_like (12-104)	cytoplasm	unfolded protein binding, protein folding	
<i>Danio rerio</i>	<i>ZDB-GENE-040426-2255</i>	<i>nudcd3</i>	A0A0R4IY34	6	344	CS (168-260); p23_NUDC_like (167-268)			
<i>Danio rerio</i>	<i>ZDB-GENE-040426-899</i>	<i>nudc</i>	Q6NV13	9	333	CS (169-260); p23_NUDC_like (174-260)			
<i>Drosophila melanogaster</i>	<i>FBgn0051251</i>	<i>DmelCG31251</i>	Q8IN95		306	CS (133-223)	cytoplasm, Golgi apparatus	unfolded protein binding, nuclear migration, protein folding	Miller et al. (2023); Wei et al. (2020); Hosono et al. (2015); Erives (2015); Cugusi et al. (2015); Neely et al. (2010); Schnorrer et al. (2010)
<i>Drosophila melanogaster</i>	<i>FBgn0021768</i>	<i>nudC</i>	Q9VVA6	6	332	CS (168-259); p23_NUDC_like (173-259)	cytoplasm, cytosol	unfolded protein binding, mRNA transport, nuclear migration, nucleus localization, positive regulation of dendrite morphogenesis, protein folding	Cunniff et al. (1997); Örkenby et al. (2023); Wainman et al. (2009)
<i>Caenorhabditis elegans</i>	<i>WBGene00003829</i>	<i>nud-1</i>	G5EE74	2	320	CS (156-247); p23_NUDC_like (161-247)	cytoplasm, synapse	identical protein binding, unfolded protein binding, chaperone-mediated protein folding, embryo development ending in birth or egg hatching, locomotion, pronuclear migration, protein folding, synaptic transmission, GABAergic, synaptic vesicle transport, vulval development	Faircloth et al. (2009); Dawe et al. (2001)
<i>Schizosaccharomyces pombe</i>	<i>SPBC19F8.02</i>	<i>nud3</i>	Q60166	1	166	CS (6-97); p23_NUDC_like (11-97)	cytoplasm, microtubule, nucleus	unfolded protein binding, cell division, mitotic sister chromatid segregation, protein folding, protein maturation	
<i>Dictyostelium discoideum</i>	<i>DDB_G0286159</i>	<i>nudc</i>	Q54M64	2	171	CS (8-98); p23_NUDC_like (13-98)	cytoplasm, microtubule	unfolded protein binding, cell cycle, cell division, karyogamy, protein folding	

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