

Table S1 Weel homologs found in different species and their BLAST results

Species	Pairwise BLAST with <i>S. pombe</i> Weel							E-value	
	Database	Protein ID	Length	Name	Positives	Identities	Gaps		Score
Animalia									
<i>Aedes aegypti</i>	NCBI	XP_001661625.1	528	Weel	145/272 (53 %)	100/272 (37 %)	36/272 (13 %)	159 bit (403)	2·10 ⁻⁴⁵
	NCBI	XP_001657528.1	553	MytI	135/307 (43 %)	93/307 (30 %)	63/307 (20 %)	137 bit (346)	2·10 ⁻³⁸
<i>Anopheles gambiae</i>	NCBI	XP_317709.4	551	Weel	151/273 (55 %)	104/273 (38 %)	31/273 (11 %)	161 bit (407)	7·10 ⁻⁴⁶
	NCBI	XP_550868.4	578	MytI	132/312 (42 %)	88/312 (28 %)	68/312 (21 %)	132 bit (331)	2·10 ⁻³⁶
<i>Caenorhabditis elegans</i>	NCBI	NP_496058.1	468	Wee-1.1	123/278 (44 %)	73/278 (26 %)	42/278 (15 %)	91.7 bit (226)	1·10 ⁻²³
	NCBI	NP_496095.1	677	Wee-1.3	117/220 (53 %)	73/220 (33 %)	12/220 (5 %)	128 bit (321)	1·10 ⁻³⁴
<i>Danio rerio</i>	Uniprot	Q6DR10	612	WeelA	144/308 (46 %)	85/308 (28 %)	49/308 (15 %)	124 bit (310)	1·10 ⁻³³
	Uniprot	Q1LX51	532	Wee1B	152/329 (46 %)	97/329 (29 %)	60/329 (18 %)	135 bit (340)	1·10 ⁻³⁷
<i>Drosophila melanogaster</i>	NCBI	XP_005156179.1	554	MytI	139/286 (48 %)	99/286 (35 %)	41/286 (14 %)	155 bit (391)	6·10 ⁻⁴⁴
	NCBI	NP_477035.1	609	Weel	131/309 (42 %)	96/309 (31 %)	64/309 (20 %)	130 bit (326)	1·10 ⁻³⁵
<i>Gallus gallus</i>	Uniprot	Q9NI63	533	MytI	190/366 (51 %)	125/366 (34 %)	44/366 (12 %)	172 bit (436)	7·10 ⁻⁵⁰
	NCBI	NP_001026352.2	641	WeelA	160/356 (44 %)	102/356 (29 %)	51/356 (14 %)	128 bit (322)	7·10 ⁻³⁵
<i>Homo sapiens</i>	NCBI	E1BTE1.1	565	Wee1B	146/324 (45 %)	90/324 (28 %)	52/324 (16 %)	109 bit (272)	6·10 ⁻²⁹
	Uniprot	P30291	646	WeelA	124/256 (48 %)	82/256 (32 %)	24/256 (9 %)	128 bit (321)	1·10 ⁻³⁴
<i>Mus musculus</i>	Uniprot	P0C1S8	567	Wee1B	128/279 (45 %)	80/279 (29 %)	28/279 (10 %)	123 bit (308)	2·10 ⁻³³
	Uniprot	Q99640	499	MytI	143/272 (52 %)	103/272 (38 %)	27/272 (9 %)	168 bit (426)	9·10 ⁻⁴⁹
<i>Xenopus laevis</i>	Uniprot	P47810	646	WeelA	139/301 (46 %)	88/301 (29 %)	46/301 (15 %)	130 bit (328)	1·10 ⁻³⁵
	Uniprot	Q661T0	555	Wee1B	132/303 (43 %)	87/303 (29 %)	54/303 (17 %)	113 bit (283)	2·10 ⁻³⁰
<i>Plantae</i>	Uniprot	Q9ESG9	490	MytI	145/272 (53 %)	104/272 (38 %)	27/272 (9 %)	174 bit (440)	1·10 ⁻⁵⁰
	Uniprot	Q8AYK6	571	WeelA	124/256 (48 %)	81/256 (32 %)	24/256 (9 %)	122 bit (306)	3·10 ⁻³³
<i>Arabidopsis thaliana</i>	Uniprot	Q8QGV2	595	Wee1B	138/296 (46 %)	86/296 (29 %)	46/296 (15 %)	128 bit (322)	4·10 ⁻³⁵
	Uniprot	Q91618	548	MytI	147/273 (53 %)	99/273 (36 %)	28/273 (10 %)	168 bit (426)	2·10 ⁻⁴⁸
<i>Medicago truncatula</i>	NCBI	NP_171796.1	500	Weel	137/278 (49 %)	90/278 (32 %)	32/278 (11 %)	117 bit (293)	7·10 ⁻³²
	NCBI	XP_003625897.1	490	Weel	134/274 (48 %)	89/274 (32 %)	35/274 (12 %)	125 bit (315)	9·10 ⁻³⁵
<i>Oryza sativa</i>	NCBI	Q6Z829.1	520	Weel	142/292 (48 %)	91/292 (31 %)	39/292 (13 %)	127 bit (318)	7·10 ⁻³⁵
	NCBI	XP_002320354.2	473	Weel_1	113/219 (51 %)	78/219 (36 %)	11/219 (5 %)	120 bit (300)	7·10 ⁻³³
<i>Populus trichocarpa</i>	NCBI	XP_006386759.1	486	Weel_2	107/216 (49 %)	75/216 (35 %)	9/216 (4 %)	119 bit (298)	1·10 ⁻³²
	NCBI	XP_002453270.1	539	Weel	139/280 (49 %)	87/280 (31 %)	39/280 (13 %)	120 bit (301)	1·10 ⁻³²
<i>Zea mays</i>	Uniprot	B6U918	532	Weel	139/280 (49 %)	88/280 (31 %)	39/280 (13 %)	124 bit (311)	5·10 ⁻³⁴

Species	Protein						Pairwise BLAST with <i>S. pombe</i> Weel					
	Database	Protein ID	Length	Name	Positives	Identities	Gaps	Score	E-value			
<i>Fungi</i>												
<i>Aspergillus nidulans</i>	NCBI	XP_663426.1	1050	Weel	159/246 (64 %)	112/246 (46 %)	22/246 (8 %)	239 bit (611)	8·10 ⁻⁷⁰			
<i>Candida albicans</i>	NCBI	XP_723552.1	1178	Weel	159/246 (64 %)	112/246 (46 %)	22/246 (8 %)	239 bit (611)	8·10 ⁻⁷⁰			
<i>Cryptococcus neoformans</i>	NCBI	XP_572188.1	1167	Weel	160/324 (49 %)	109/324 (34 %)	52/324 (16 %)	158 bit (399)	2·10 ⁻⁴⁵			
	NCBI	XP_572122.1	1121	Mytl	139/269 (51 %)	100/269 (37 %)	50/269 (18 %)	162 bit (411)	6·10 ⁻⁴⁵			
<i>Mucor circinelloides</i>	NCBI	EPB91742.1	579	Weel	171/292 (58 %)	108/292 (37 %)	24/292 (8 %)	201 bit (512)	1·10 ⁻⁵⁹			
<i>Pneumocystis murina</i>	NCBI	XP_007872875.1	666	Weel	349/631 (55 %)	266/631 (42 %)	91/631 (14 %)	424 bit (1089)	5·10 ⁻¹⁴⁰			
<i>Saccharomyces cerevisiae</i>	NCBI	NP_012348.1	819	Weel	179/252 (71 %)	128/252 (51 %)	12/252 (4 %)	251 bit (641)	8·10 ⁻⁷⁵			
<i>Schizosaccharomyces cryophilus</i>	BROAD	SPOG_03328	856	Weel	611/906 (67 %)	507/906 (56 %)	102/906 (11 %)	820 bit (2119)	0*			
	NCBI	SPOG_01456	586	Mikl	187/299 (62 %)	133/299 (44 %)	7/299 (2 %)	255 bit (652)	4·10 ⁻⁷⁸			
<i>Schizosaccharomyces japonicus</i>	NCBI	XP_002175395.1	815	Weel	537/921 (58 %)	436/921 (47 %)	150/921 (16 %)	642 bit (1657)	0*			
	NCBI	XP_002174982.1	560	Mikl	259/509 (50 %)	174/509 (34 %)	75/509 (14 %)	242 bit (617)	1·10 ⁻⁷³			
<i>Schizosaccharomyces octosporus</i>	BROAD	SOCG_03907	858	Weel	600/908 (66 %)	492/908 (54 %)	101/908 (11 %)	712 bit (1839)	0*			
	NCBI	SOCG_02546	583	Mikl	255/486 (52 %)	178/486 (37 %)	55/486 (11 %)	257 bit (657)	7·10 ⁻⁷⁹			
<i>Schizosaccharomyces pombe</i>	PomBase	SPCC18B5.03	877	Weel	-	-	-	-	-			
	NCBI	NP_595093.1	581	Mikl	200/337 (59 %)	141/337 (42 %)	23/337 (6 %)	241 bit (614)	5·10 ⁻⁷³			
<i>Trichosporon asahii</i>	NCBI	EKD02425.1	1135	1135	170/347 (48 %)	120/347 (35 %)	59/347 (17 %)	186 bit (472)	2·10 ⁻⁵²			
	NCBI	EKD00750.1	959	959	136/241 (56 %)	95/241 (39 %)	26/241 (10 %)	174 bit (440)	1·10 ⁻⁴⁸			
<i>Protista</i>												
<i>Dictyostelium discoideum</i>	NCBI	XP_629953.1	352	Weel_1 (M)	172/309 (55 %)	108/309 (35 %)	31/309 (10 %)	182 bit (462)	8·10 ⁻⁵²			
	NCBI	XP_635350.1	778	Weel_2 (W)	149/314 (47 %)	100/314 (32 %)	53/314 (16 %)	161 bit (408)	2·10 ⁻⁴²			
<i>Ectocarpus siliculosus</i>	NCBI	CB133486.1	930	Weel	121/225 (53 %)	80/225 (36 %)	12/225 (5 %)	134 bit (336)	5·10 ⁻³⁶			
	NCBI	CB129530.1	1403	Mytl	140/276 (50 %)	93/276 (34 %)	31/276 (11 %)	159 bit (403)	8·10 ⁻⁴⁴			
<i>Nannochloropsis gaditania</i>	NCBI	XP_005854279.1	480	Weel	120/230 (52 %)	87/230 (38 %)	16/230 (6 %)	139 bit (350)	4·10 ⁻³⁹			
	NCBI	EW24042.1	484	Mytl	119/225 (52 %)	86/225 (38 %)	16/225 (7 %)	140 bit (352)	1·10 ⁻³⁹			
<i>Ostreococcus tauri</i>	NCBI	CEF99444.1	502	Weel	122/233 (52 %)	70/233 (30 %)	8/233 (3 %)	120 bit (300)	9·10 ⁻³³			
	NCBI	XP_003081501.1	517	Mytl	104/204 (50 %)	73/204 (36 %)	5/204 (2 %)	119 bit (299)	2·10 ⁻³²			
<i>Paramecium tetraurelia</i>	NCBI	XP_001440096.1	392	Weel	129/246 (52 %)	75/246 (30 %)	24/246 (9 %)	123 bit (309)	2·10 ⁻³⁴			
	NCBI	XP_001427977.1	461	Mytl	130/252 (51 %)	77/252 (31 %)	19/252 (7 %)	120 bit (302)	3·10 ⁻³³			

* In some cases, the E-value is too small to be calculated; therefore 0 is given in those cells.

Table S2 Cdc25 homologs found in different species and their BLAST results

Species	Protein							E-value	
	Database	Protein ID	Length	Name	Positives	Identities	Gaps		Score
Pairwise BLAST with <i>S. pombe</i> Cdc25									
Animalia									
<i>Anopheles gambiae</i>	NCBI	XP_319526.5	705	Cdc25	85/155 (55 %)	65/155 (42 %)	12/155 (7 %)	134 bit (338)	2·10 ⁻³⁷
	NCBI	NP_491862.1	604	Cdc-25.1	83/147 (56 %)	58/147 (39 %)	10/147 (6 %)	103 bit (257)	2·10 ⁻²⁷
	NCBI	NP_503446.1	480	Cdc-25.2	81/167 (48 %)	58/167 (35 %)	9/167 (5 %)	95.9 bit (237)	3·10 ⁻²⁵
<i>Caenorhabditis elegans</i>	NCBI	NP_498972.1	316	Cdc-25.3	91/164 (55 %)	61/164 (37 %)	17/164 (10 %)	107 bit (268)	5·10 ⁻³⁰
	NCBI	NP_496197.2	278	Cdc-25.4	82/169 (48 %)	53/169 (31 %)	17/169 (10 %)	82.4 bit (202)	7·10 ⁻²²
<i>Danio rerio</i>	NCBI	NP_001108567.1	563	Cdc25B	134/267 (50 %)	90/267 (34 %)	46/267 (17 %)	142 bit (358)	1·10 ⁻⁴⁰
	NCBI	NP_001128154.1	387	Cdc25D	80/152 (52 %)	56/152 (37 %)	26/152 (17 %)	110 bit (275)	1·10 ⁻³⁰
<i>Drosophila melanogaster</i>	NCBI	NP_476633.1	426	Twine	90/154 (58 %)	67/154 (44 %)	7/154 (4 %)	130 bit (327)	4·10 ⁻³⁷
	NCBI	NP_524547.1	479	String	97/184 (52 %)	65/184 (35 %)	12/184 (6 %)	130 bit (328)	5·10 ⁻³⁷
<i>Gallus gallus</i>	NCBI	NP_001186501.1	526	Cdc25	94/169 (55 %)	67/169 (40 %)	17/169 (10 %)	135 bit (339)	3·10 ⁻³⁸
	UniProt	P30304	524	Cdc25A	99/171 (57 %)	69/171 (40 %)	17/171 (9 %)	138 bit (347)	3·10 ⁻³⁹
<i>Homo sapiens</i>	UniProt	P30305	580	Cdc25B	87/141 (61 %)	70/141 (50 %)	7/141 (4 %)	146 bit (369)	7·10 ⁻⁴²
	UniProt	P30307	473	Cdc25C	94/152 (61 %)	65/152 (43 %)	7/152 (4 %)	145 bit (366)	5·10 ⁻⁴²
<i>Mus musculus</i>	UniProt	P48964	514	Cdc25A	96/169 (56 %)	67/169 (40 %)	17/169 (10 %)	134 bit (338)	3·10 ⁻³⁸
	UniProt	P30306	576	Cdc25B	86/141 (60 %)	67/141 (48 %)	7/141 (4 %)	143 bit (361)	6·10 ⁻⁴¹
	UniProt	P48967	447	Cdc25C	92/151 (60 %)	66/151 (44 %)	7/151 (4 %)	139 bit (351)	3·10 ⁻⁴⁰
	UniProt	P30308	550	Cdc25-1A	90/148 (60 %)	65/148 (44 %)	7/148 (4 %)	141 bit (356)	3·10 ⁻⁴⁰
	UniProt	P30309	550	Cdc25-1B	93/158 (58 %)	66/158 (42 %)	7/158 (4 %)	143 bit (361)	5·10 ⁻⁴¹
<i>Xenopus laevis</i>	UniProt	P30310	599	Cdc25-2	90/148 (60 %)	65/148 (44 %)	7/148 (4 %)	141 bit (355)	5·10 ⁻⁴⁰
	UniProt	P30311	572	Cdc25-3	89/148 (60 %)	65/148 (44 %)	7/148 (4 %)	140 bit (353)	7·10 ⁻⁴⁰
Plantae	UniProt	F5HR98	413	Cdc25D	90/158 (56 %)	72/158 (46 %)	6/158 (3 %)	130 bit (327)	3·10 ⁻³⁷
<i>Arabidopsis thaliana</i>	UniProt	Q8GY31	146	Cdc25	28/65 (43 %)	22/65 (34 %)	5/65 (7 %)	25.4 bit (54)	9·10 ⁻⁴
<i>Medicago truncatula</i>	NCBI	XP_003625699.1	168	Cdc25	29/65 (44 %)	21/65 (32 %)	5/65 (7 %)	25.8 bit (55)	9·10 ⁻⁴
<i>Oryza sativa</i>	NCBI	NP_001048698.1	130	Cdc25	25/63 (39 %)	17/63 (27 %)	11/63 (17 %)	22.3 bit (46)	7·10 ⁻³
<i>Populus trichocarpa</i>	NCBI	XP_006381390.1	87	Cdc25	27/60 (45 %)	17/60 (28 %)	11/60 (18 %)	21.2 bit (43)	9·10 ⁻³
	NCBI	NP_001048698.1	130	Cdc25_1	15/29 (51 %)	11/29 (38 %)	0/29 (0 %)	23.1 bit (48)	4·10 ⁻³
<i>Sorghum bicolor</i>	NCBI	XP_002466015.1	131	Cdc25_2	27/68 (39 %)	20/68 (29 %)	11/68 (16 %)	24.6 bit (52)	1·10 ⁻³
<i>Zea mays</i>	NCBI	NP_001144297.1	131	Cdc25	14/29 (48 %)	11/29 (38 %)	0/29 (0 %)	21.9 bit (45)	1·10 ⁻²

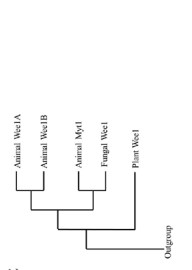
Species	Protein				Pairwise BLAST with <i>S. pombe</i> Cdc25				E-value
	Database	Protein ID	Length	Name	Positives	Identities	Gaps	Score	
Fungi	NCBI	XP_661545.1	556	Cdc25	160/300 (53 %)	108/300 (36 %)	24/300 (8 %)	184 bit (466)	1·10 ⁻⁵⁴
	NCBI	KHC80028.1	894	Cdc25	97/173 (56 %)	71/173 (41 %)	7/173 (4 %)	152 bit (384)	7·10 ⁻⁴³
	NCBI	NP_013750.1	554	Mth1	104/180 (57 %)	73/180 (41 %)	11/180 (6 %)	143 bit (360)	8·10 ⁻⁴¹
<i>Schizosaccharomyces</i>	NCBI	EPY49663.1	585	Cdc25	447/588 (76 %)	357/588 (61 %)	25/588 (4 %)	650 bit (1676)	0*
	NCBI	EPY50557.1	138	Ibpl	62/127 (48 %)	41/127 (32 %)	20/127 (15 %)	52.8 bit (125)	6·10 ⁻¹³
<i>Schizosaccharomyces japonicus</i>	NCBI	XP_002175445.1	592	Cdc25	389/611 (63 %)	291/611 (48 %)	34/611 (5 %)	480 bit (1235)	2·10 ⁻¹⁶⁶
	NCBI	XP_002175284.1	141	Ibpl	50/109 (45 %)	31/109 (28 %)	17/109 (15 %)	30.8 bit (68)	1·10 ⁻⁵
<i>Schizosaccharomyces octosporus</i>	NCBI	EPX74978.1	595	Cdc25	451/587 (76 %)	362/587 (62 %)	13/587 (2 %)	676 bit (1744)	0*
	NCBI	EPX75217.1	138	Ibpl	65/139 (46 %)	41/139 (29 %)	23/139 (16 %)	48.5 bit (114)	1·10 ⁻¹¹
<i>Schizosaccharomyces pombe</i>	PomBase	SPAC24H6.05	580	Cdc25	-	-	-	-	-
	NCBI	NP_595247.1	138	Ibpl	54/115 (46 %)	35/115 (30 %)	14/115 (12 %)	39.3 bit (90)	1·10 ⁻⁸
Protista									
<i>Chlorella variabilis</i>	NCBI	XP_005849973.1	1424	Cdc25	88/171 (51 %)	60/171 (35 %)	14/171 (8 %)	109 bit (273)	1·10 ⁻²⁸
	NCBI	XP_638997.1	1053	Cdc25	70/113 (61 %)	46/113 (41 %)	7/113 (6 %)	102 bit (255)	1·10 ⁻²⁶
<i>Entamoeba histolytica</i> **	NCBI	XP_649604.1	208	Cdc25	66/111 (59 %)	46/111 (41 %)	3/111 (2 %)	97.4 bit (241)	2·10 ⁻²⁷
	NCBI	XP_652126.2	256	Cdc25	67/115 (58 %)	46/115 (40 %)	6/115 (5 %)	82 bit (201)	8·10 ⁻²²
	NCBI	XP_649073.2	240	Cdc25	65/130 (50 %)	43/130 (33 %)	11/130 (8 %)	71.2 bit (173)	2·10 ⁻¹⁸
	NCBI	XP_650272.1	253	Cdc25	64/119 (53 %)	35/119 (29 %)	13/119 (10 %)	68.2 bit (165)	2·10 ⁻¹⁷
<i>Ostreococcus lucimarinus</i>	NCBI	XP_656775.1	263	Cdc25	54/89 (60 %)	33/89 (37 %)	5/89 (5 %)	65.1 bit (157)	3·10 ⁻¹⁶
	NCBI	XP_650308.2	292	Cdc25	72/145 (49 %)	45/145 (31 %)	15/145 (10 %)	60.5 bit (145)	1·10 ⁻¹⁴
<i>Ostreococcus tauri</i>	NCBI	XP_001416369.1	378	Cdc25	76/141 (53 %)	53/141 (38 %)	5/141 (3 %)	99.8 bit (247)	5·10 ⁻²⁷
<i>Ostreococcus tauri</i>	NCBI	XP_003075150.1	517	Cdc25	72/142 (50 %)	49/142 (35 %)	6/142 (4 %)	93.2 bit (230)	3·10 ⁻²⁴
<i>Paramecium tetraurelia</i>	NCBI	XP_001435144.1	253	Cdc25	76/139 (54 %)	47/139 (34 %)	9/139 (6 %)	81.6 bit (200)	8·10 ⁻²²

* In some cases, the E-value is too small to be calculated; therefore 0 is given in those cells.

** There were 6 hits in the *Entamoeba histolytica* genome, but only the best result was considered (see text for details).

Table S3 An analysis of the phylogenetic trees' topologies of Wee1-like proteins

	A	B	C	D	E	Σ
Outgroup	10	10	10	1	2	33
<i>D. discoideum</i> 352*	16	12	8	3	0	39
<i>D. discoideum</i> 778*	3	0	0	0	0	3
<i>S. pombe</i> Plk1	5	14	8	2	1	30
Prank	24	8	10	2	1	45
ClustalX	13	6	6	0	0	25
maximum likelihood	9	14	2	0	0	25
neighbor joining	7	2	10	4	2	25
maximum parsimony	7	2	2	1	0	12
1, full protein	0	2	4	0	0	6
1, domain	6	4	2	0	0	12
2, full protein	3	5	2	0	2	12
3, full protein	4	4	3	1	0	12
4, full protein	0	0	3	0	0	3
4, domain	5	4	1	2	0	12
5, full protein	1	1	1	0	0	3
6, full protein	3	0	0	0	0	3
7, full protein	29	22	18	4	2	75
Σ						



* The numbers refer to the lengths of two different proteins of the same species.

Table S4 Lists of different species and their Weel-like proteins, used for constructing phylogenetic trees

	1	2	3	4	5	6	7
<i>Homo sapiens</i>	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl
<i>Mus musculus</i>	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl
<i>Gallus gallus</i>	WeelA, WeelB	WeelA, WeelB	WeelA, WeelB	WeelA, WeelB	WeelA, WeelB	WeelA, WeelB	WeelA, WeelB
<i>Xenopus laevis</i>	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl
<i>Danio rerio</i>	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl	WeelA, WeelB, Mytl
<i>Drosophila melanogaster</i>	Weel, Mytl	Weel, Mytl	Weel, Mytl	Weel, Mytl	Weel, Mytl	Weel, Mytl	Weel, Mytl
<i>Aedes aegypti</i>	-	-	-	-	-	Weel, Mytl	Weel, Mytl
<i>Anopheles gambiae</i>	-	-	-	-	-	Weel, Mytl	Weel, Mytl
<i>Caenorhabditis elegans</i>	Weel.1, Weel.3	Weel.1, Weel.3	Weel.1, Weel.3	Weel.1, Weel.3	Weel.1, Weel.3	Weel.1, Weel.3	Weel.1, Weel.3
<i>Arabidopsis thaliana</i>	Weel	Weel	Weel	Weel	Weel	Weel	Weel
<i>Zea mays</i>	Weel	Weel	Weel	Weel	Weel	Weel	Weel
<i>Oryza sativa</i>	-	-	-	Weel	Weel	Weel	Weel
<i>Sorghum bicolor</i>	-	-	-	Weel	Weel	Weel	Weel
<i>Populus trichocarpa</i>	-	-	-	Weel	Weel	Weel.1, Weel.2	Weel.1, Weel.2
<i>Medicago truncatula</i>	-	-	-	Weel	Weel	Weel	Weel
<i>Schizosaccharomyces pombe</i>	Weel, Mikl	Weel, Mikl	Weel, Mikl	Weel, Mikl	Weel, Mikl	Weel, Mikl	Weel, Mikl
<i>Schizosaccharomyces japonicus</i>	Weel, Mikl	Weel, Mikl	Weel, Mikl	Weel, Mikl	Weel, Mikl	Weel, Mikl	Weel, Mikl
<i>Schizosaccharomyces octosporus</i>	-	-	Weel, Mikl	-	Weel, Mikl	Weel, Mikl	Weel, Mikl
<i>Schizosaccharomyces cryophilus</i>	-	-	Weel, Mikl	-	Weel, Mikl	Weel, Mikl	Weel, Mikl
<i>Aspergillus nidulans</i>	Weel	-	-	Weel	Weel	Weel	Weel
<i>Candida albicans</i>	Weel	-	-	Weel	Weel	Weel	Weel
<i>Saccharomyces cerevisiae</i>	Weel	-	-	Weel	Weel	Weel	Weel
<i>Cryptococcus neoformans</i>	-	-	-	-	-	Weel, Mytl	Weel, Mytl
<i>Mucor circinelloides</i>	-	-	-	-	-	Weel	Weel
<i>Pneumocystis murina</i>	-	-	-	-	-	Weel	Weel
<i>Trichosporon asahii</i>	-	-	-	-	-	Weel(1135), Mytl(959)	Weel(1135), Mytl(959)
<i>Dictyostelium discoideum</i>	-	-	-	-	-	Weel_1 (352)	-
<i>Ectocarpus siliculosus</i>	-	-	-	-	-	Weel, Mytl	Weel
<i>Nannochloropsis gaditania</i>	-	-	-	-	-	Mytl	Weel
<i>Ostreococcus tauri</i>	-	-	-	-	-	-	Weel
<i>Paramecium tetraurelia</i>	-	-	-	-	-	-	Weel, Mytl
Outgroup	<i>D. discoideum</i> 352 / 778	<i>D. discoideum</i> 352 / 778	<i>D. discoideum</i> 352 / 778	<i>D. discoideum</i> 352 / 778	<i>D. discoideum</i> 352 / 778	<i>D. discoideum</i> 778	<i>S. pombe</i> Polo kinase

Numbers after protein or species names refer to protein length.

Table S5 Variations of the alignments of sequences

Species list	Outgroup	Full protein	Domain sequence
1	<i>D. discoideum</i> 352	ClustalX	ClustalX
	<i>D. discoideum</i> 778	Prank	ClustalX
2	<i>D. discoideum</i> 352	ClustalX	ClustalX
	<i>D. discoideum</i> 778	Prank	ClustalX
3	<i>D. discoideum</i> 352	ClustalX	ClustalX
	<i>D. discoideum</i> 778	Prank	ClustalX
4	<i>D. discoideum</i> 352	ClustalX	ClustalX
	<i>D. discoideum</i> 778	Prank	ClustalX
5	<i>D. discoideum</i> 352	ClustalX	ClustalX
	<i>D. discoideum</i> 778	Prank	ClustalX
6	<i>D. discoideum</i> 352	ClustalX	ClustalX
	<i>D. discoideum</i> 778	Prank	ClustalX
7	<i>D. discoideum</i> 778	ClustalX	ClustalX
	<i>S. pombe</i> Polo kinase	ClustalX	ClustalX

For the species lists (1-7), see Table S4.