

**Table 1. Plant Ser/Thr protein phosphatases from *Arabidopsis thaliana***

No.	Class	Deposition Numbers		Type / Isoform	UniProt KB / Swiss- Prot status	The closest human homolog	Indicators of sequence similarity		
		GenBANK	Uniprot KB				Ident. (%)	Simil. (%)	Gap (%)
<b>Ser/Thr Protein Phosphatases of the PPP family</b>									
1.	<b>PP1</b>	At2g29400	P30366	isoz-1	+	P62140_PP1B	80.8	92.3	0.4
2.		At5g59160	P48482	isoz-2	+	P62136_PP1A	83.8	92.3	0.0
3.		At1g64040	P48483	isoz-3	+	P62136_PP1A	78.6	91.1	0.0
4.		At2g39840	P48484	isoz-4	+	P62136_PP1A	80.8	90.8	0.0
5.		At3g46820	P48485	isoz-5	+	P62136_PP1A	83.0	91.5	0.0
6.		At4g11240	P48486	isoz-6	+	P62136_PP1A	79.7	93.4	0.0
7.		At5g43380	O82733	isoz-7	+	P62140_PP1B	79.3	90.4	0.0
8.		At5g27840	O82734	isoz-8	+	P62136_PP1A	75.3	89.3	0.0
9.		At3g05580	Q9M9W3	isoz-9	+	P62136_PP1A	76.4	89.7	0.0
10.		At2g29400	Q8LBH8	AAM64756.1	-	P62136_PP1A	83.0	91.5	0.0
11.		At5g59160	A8I799	ABV91338.1	-	P62140_PP1B	45.6	62.1	4.9
12.		At1g08420	B9DFZ9	Putative 2A	-	P62140_PP1B	46	62.5	4.9
13.	<b>PP2A</b>	At1g59830	Q07099	isof-1	+	P67775_PP2AA	81.9	93.4	0.0
14.		At1g10430	Q07098	isof-2	+	P67775_PP2AA	81.5	94.1	0.0
15.		At3g58500	P48578	isof-3	+	P62714_PP2AB	82.3	90.8	0.0
16.		At2g42500	Q07100	isof-4	+	P62714_PP2AB	82.3	90.8	0.0
17.		At1g69960	O04951	isof-5	+	P67775_PP2AA	82.3	93.4	0.0
18.		At3g58500	Q8LAT9	AAM65153.1	-	P67775_PP2AA	81.2	89.7	0.0
19.		At2g42500	Q8LAW8	AAM65099.1	-	P67775_PP2AA	81.9	93.4	0.0
20.	<b>PP4/PPX</b>	At4g26720	P48529	PPX1	+	P60510_PP4C	81.3	90.4	0.4
21.		At5g55260	P48528	PPX2	+	P60510_PP4C	83.8	91.9	0.4
22.		At4g26720	Q8LPF9	AAM20731.1	-	P60510_PP4C	39.0	45.2	48.2
23.	<b>PP5</b>	At2g42810	Q84XU2	PAPP5	+	P53041_PPP5	62.8	78.7	0.0
24.		At2g42810	O22662	AAB84178.1	-	P53041_PPP5	38.6	48.7	36.1
25.	<b>PP6</b>	At1g50370	Q9SX52	FYPP1	+	O00743_PPP6	73.5	86.0	0.4
26.		At3g19980	Q9LHE7	FYPP3	+	O00743_PPP6	73.5	86.0	0.4
27.	<b>PP7</b>	At5g10900	Q9LEV0	inac hom	+	O14829-2_PPE1	21.1	40.8	11.5
28.		At1g48120	Q9LNG5	long f-m	+	O14829-2_PPE1	28.7	43.6	6.7
29.		At5g63870	Q9FN02	PP7	+	O14829-3_PPE1	30.9	46.0	10.4
30.	<b>BSL</b>	At4g03080	Q8L7U5	BSL1	+	P62140_PP1B	47.0	64.2	4.9
31.		At1g08420	Q9SJF0	BSL2	+	P62140_PP1B	46.0	62.5	4.9
32.		At2g27210	Q9SHS7	BSL3	+	P62136_PP1A	46.3	63.2	4.9
33.	<b>BSU</b>	At1g03445 At1g03450	Q9LR78	BSU1	+	P62140_PP1B	44.4	64.0	5.9

**Note:** The percent indicators (Ident. (%) - identity, Simil. (%) - similarity, Gap. (%) - gaps) of sequence similarity are given based on the results of pairwise alignment of catalytic domain of human protein phosphatase and appropriate region of the plant homologue.

**Table 2. Arabidopsis homologues of Mg<sup>2+</sup>/Mn<sup>2+</sup> dependent protein phosphatases**

No.	Class	Deposition Numbers		Type / Isoform	UniProt KB / Swiss-Prot status	The closest human homolog	Indicators of sequence similarity		
		GenBANK	Uniprot KB				Ident. (%)	Simil. (%)	Gap (%)
<b>PPP family: Mg<sup>2+</sup>/Mn<sup>2+</sup> dependent protein phosphatases</b>									
1.	<b>PP2C</b>	At1g03590	Q9LR65	Probable 2C 1	+	Q5SGD2_PPM1L	21.4	37.7	20.1
2.		At1g07160	Q8RX37	Probable 2C 2	+	Q5SGD2_PPM1L	35.4	53.1	12.5
3.		At1g07430	Q9LNW3	2C 3	+	O75688-4_PPM1B	32.9	42.9	21.3
4.		At1g07630	Q9LQN6	Probable 2 C4	+	Q9P2J9_PDP2	19.3	33.5	22.2
5.		At1g09160	O80492	Probable 2C 5	+	Q8NI37_PPTC7	13.9	29.1	5.6
6.		At1g16220	Q9SA22	Probable 2C 6	+	Q8N3J5_PPM1K	24.4	39.5	22.5
7.		At1g17550	Q9LNP9	2C 7	+	O75688-5_PPM1B	29.7	44.8	15.5
8.		At1g18030	Q9LMT1	Probable 2C 8	+	Q9H0C8_ILKAP	32.6	54.1	13.3
9.		At1g22280	Q9LME4	Probable 2C 9	+	P49593_PPM1F	31.4	47.3	4.1
10.		At1g34750	Q9S9Z7	Probable 2C10	+	P49593_PPM1F	32.2	48.6	4.1
11.		At1g43900	Q8VZN9	Probable 2C11	+	Q5SGD2_PPM1L	41.0	59.0	5.6
12.		At1g47380	Q9FX08	Probable 2C12	+	Q8N3J5_PPM1K	25.8	43.6	9.8
13.		At1g48040	Q9LNF4	Probable 2C13	+	Q8WY54-2_PPM1E	33.2	48.5	9.2
14.		At1g67820	Q9FXE4	Probable 2C14	+	Q5SGD2_PPM1L	30.0	45.2	28.2
15.		At1g68410	Q9M9C6	Probable 2C15	+	Q8N3J5_PPM1K	27.0	43.3	9.5
16.		At1g72770	Q9CAJ0	2C 16	+	O75688-5-PPM1B	33.6	46.9	17.1
17.		At1g78200	Q8L7I4	Probable 2C17	+	Q8N3J5_PPM1K	29.9	50.4	7.5
18.		At1g79630	Q8RXZ4	Probable 2C18	+	Q5SGD2_PPM1L	21.3	34.5	27.8
19.		At2g20050	Q9SL76	Probable 2C19	+	Q8N3J5_PPM1K	25.3	41.4	15.1
20.		At2g20630	Q9SIU8	Probable 2C20	+	P35813-2_PPPM1A	26.2	43.5	10.4
21.		At2g25070	O81716	Probable 2C21	+	O15355_PPM1G	31.4	42.9	37.9
22.		At2g25620	Q9SLA1	Probable 2C22	+	Q5SGD2_PPM1L	32.1	50.4	12.7
23.		At2g28890	Q9ZV25	Probable 2C23	+	Q9H0C8_ILKAP	16.9	32.1	33.8
24.		At2g29380	Q9ZW21	Probable 2C24	+	P35813-3_PPPM1A	30.2	40.2	13.9
25.		At2g30020	O80871	Probable 2C25	+	Q5SGD2_PPM1L	34.4	51.9	12.2
26.		At2g30170	O64730	Probable 2C26	+	Q8NI37_PPTC7	28.9	47.8	18.5
27.		At2g33700	P93006	Probable 2C27	+	O75688-4_PP2CB	31.3	49.1	10.9
28.		At2g34740	O64583	Probable 2C28	+	Q8N3J5_PPM1K	30.2	50.6	9.0
29.		At2g35350	O82302	Probable 2C29	+	Q9P2J9_PPM1G	16.1	31.7	9.3
30.		At2g40180	Q9XEE8	Probable 2C30	+	Q5SGD2_PPM1L	30.1	48.5	12.1
31.		At2g40860 At2g40870	Q940A2	Probable 2C31	+	Q8WY54-2_PPM1E	33.9	51.6	9.1
32.		At2g46920	Q8RWN7	2C 32	+	Q9ULR3_PPM1H	17.3	30.8	17.5
33.		At3g02750	Q9M8R7	Probable 2C33	+	Q5SGD2_PPM1L	21.9	35.9	26.0
34.		At3g05640	Q9M9W9	Probable 2C34	+	Q5SGD2_PPM1L	24.8	41.4	14.8
35.		At3g06270	Q7XJ53	Probable 2C35	+	Q8N3J5_PPM1K	24.9	40.8	17.0
36.		At3g09400	Q9SR24	Probable 2C36	+	Q9P2J9_PDP2	20.7	38.3	21.8
37.		At3g11410	P49598	2C 37	+	O75688-5_PP2CB	32.2	46.3	13.1
38.		At3g12620	Q9LHJ9	Probable 2C38	+	Q9H0C8_ILKAP	24.3	43.0	12.3
39.		At3g15260	Q9LDA7	Probable 2C39	+	Q5SGD2_PPM1L	33.1	50.2	7.2
40.		At3g16560	Q9LUS8	Probable 2C40	+	Q9P2J9_PDP2	20.5	37.4	20.8
41.		At3g16800	Q9LRZ4	Probable 2C41	+	Q5SGD2_PPM1L	12.3	26.7	9.9
42.		At3g17090	Q0V7V2	Probable 2C42	+	P49593_PPM1F	24.3	39.2	20.3
43.		At3g17250	Q9LUU7	Probable 2C43	+	O75688-5_PPM1B	27.1	47.0	6.0
44.		At3g23360	Q9LW60	Probable 2C44	+	P49593_PPM1F	26.0	48.3	9.0
45.		At3g27140	Q3EAZ3	2C45-like	+	Q8N819_PPM1N	26.3	39.0	29.0
46.		At3g51370	Q9SD12	Probable 2C46	+	Q9H0C8_ILKAP	23.7	43.7	12.7
47.		At3g51470	Q9SD02	Probable 2C47	+	O75688-5_PPM1B	31.9	51.5	9.2
48.		At3g55050	Q94CL8	Probable 2C48	+	Q9H0C8_ILKAP	23.0	41.7	12.7
49.		At3g62260	Q3EAF9	Probable 2C49	+	P35813-2_PPM1A	33.0	53.8	6.4
50.		At3g63320	Q9M1V8	Putative 2C50	+	Q9H0C8_ILKAP	25.0	37.1	28.6
51.		At3g63340	Q93YS2	Probable 2C51	+	Q8N3J5_PPM1K	25.1	38.3	35.2
52.		At4g03415	Q8GY60	Probable 2C52	+	Q5SGD2_PPM1L	21.3	36.1	20.3

53.	At4g08260	Q9SUF4	Probable 2C53	+	Q5SGD2_PPM1L	29.1	43.7	20.9
54.	At4g11040	Q9T010	Probable 2C54	+	P35813_PPM1A	16.3	33.1	19.8
55.	At4g16580	Q9SUK9	Probable 2C55	+	Q8NI37_PPTC7	38.2	50.8	9.8
56.	At4g26080	P49597	Probable 2C56	+	O75688-5_PP2CB	31.8	46.3	19.3
57.	At4g27800	P49599	Probable 2C57	+	O75688-5_PP2CB	27.0	46.3	11.0
58.	At4g28400	Q93YW5	Probable 2C58	+	Q5SGD2_PPM1L	34.8	51.4	7.9
59.	At4g31750	Q8RXV3	Probable 2C59	+	Q5SGD2_PPM1L	44.2	58.6	5.2
60.	At4g31860	Q9SZ53	Probable 2C60	+	P35813-2_PPM1A	29.7	47.1	18.3
61.	At4g32950	O82637	Probable 2C61	+	P35813-2_PPM1A	25.7	39.9	12.7
62.	At4g33500	Q93V88	Probable 2C62	+	Q8NI37_PPTC7	30.6	48.6	13.7
63.	At4g33920	O81760	Probable 2C63	+	P49593_PPM1F	22.6	38.2	19.3
64.	At4g38520	Q5PNS9	Probable 2C64	+	Q9P0J1_PDP1	23.6	38.5	19.4
65.	At5g01700	Q6NKS1	Probable 2C65	+	O75688-5_PPM1B	24.2	37.5	13.7
66.	At5g02400	Q9LZ86	Probable 2C66	+	Q9P0J1_PDP1	18.6	32.5	37.8
67.	At5g02760	Q501F9	Probable 2C67	+	Q9H0C8_ILKAP	25.2	42.6	11.4
68.	At5g06750	Q84JD5	Probable 2C68	+	Q9H0C8_ILKAP	24.7	41.8	12.8
69.	At5g10740	Q8LAY8	Probable 2C69	+	Q5SGD2_PPM1L	44.6	57.8	5.2
70.	At5g19280	P46014	Probable 2C70	+	Q8N819-2_PPM1N	27.5	39.4	9.7
71.	At5g24940	Q4PSE8	Probable 2C71	+	Q5SGD2_PPM1L	44.6	58.2	5.2
72.	At5g26010	Q9XGZ9	Probable 2C72	+	Q8N3J5_PPM1K	25.1	41.0	15.9
73.	At5g27930	Q0WRB2	Probable 2C73	+	O75688-5_PPM1B	29.4	39.9	15.7
74.	At5g36250	Q9FG61	Probable 2C74	+	Q5SGD2_PPM1L	22.4	38.0	23.1
75.	At5g51760	Q9FLI3	Probable 2C75	+	O75688-5_PPM1B	29.2	44.6	17.4
76.	At5g53140	Q94AT1	Probable 2C76	+	Q5SGD2_PPM1L	37.4	50.0	13.3
77.	At5g57050	O04719	Probable 2C77	+	P35813-2_PPM1A	33.3	46.8	16.3
78.	At5g59220	Q9FIF5	Probable 2C78	+	O75688-5_PPM1B	33.1	44.4	17.4
79.	At5g66080	Q9FKX4	Probable 2C79	+	Q9P2J9_PDP2	21.1	36.1	28.2
80.	At5g66720	Q9LVQ8	Probable 2C80	+	Q8NI37_PPTC7	34.2	47.9	12.5

**Note:** The percent indicators (Ident. (%) - identity, Simil. (%) - similarity, Gap. (%) - gaps) of sequence similarity are given based on the results of pairwise alignment of catalytic domain of human protein phosphatase and appropriate region of the plant homologue.

**Table 3. Arabidopsis homologues of tyrosine-specific protein phosphatases**

No.	Class	Deposition Numbers		Type / Isoform	UniProt KB / Swiss- Prot status	The closest human homolog	Indicators of sequence similarity			
		GenBANK	UniprotKB				Ident. (%)	Simil. (%)	Gap (%)	
<b>Protein tyrosine phosphatase superfamily (CX<sub>1</sub>R)</b>										
1.	<b>PTPs I (classic)</b>	At1g71860	O82656	PTP1	+	P29350-2_PTPN6	37.4	51.6	5.3	
2.		At1g05000	Q9ZVN4	Probable PTP	+	P60484_PTEN	17.3	31.5	20.4	
3.	<b>DSPs I (DSPs)</b>	At5g10480	Q8VZB2	PASTICCINO2 HACD	+	Q6Y1H2_PTPLB	44.2	65.5	0.6	
4.		At3g55270	Q9C5S1 (Q9M3C4, Q940K2)	PTP MKP1	+	Q8WTR2_DUSP19	34.3	56.4	0.6	
5.		At3g06110	Q9M8K7	DSPTP1B / MKP2	+	Q9HIR2_DUS15	37.1	57.9	2.1	
6.		At2g04550	Q84JU4	PTP IBR5	+	P28562_DUSP1	34.3	55.7	5	
7.		At3g01510	F4J117 (Q8LCU3)	LIKE SEX4 1	+	O95278-8_EPM2A	23.5	35.9	13.1	
8.		At3g10940	Q9SRK5	LIKE SEX4 2	+	P51452_DUS3	22.1	42.9	13.6	
9.		At3g52180	Q9FEB5	PTPKIS1/DSP4	+	O95278-8_EPM2A	16.3	33.3	13.1	
10.		At2g35680	Q9ZQP1	Putative DSP8	+	Q8WUK0_PTPMT1	37.4	55.4	2.9	
11.		At5g56610	Q6NKR2	DSP PTP	-	Q8WUK0_PTPMT1	36.7	52.5	2.5	
12.		<b>PTEN</b>	At5g39400	Q9FLZ5	CaLB/PTEN-like	-	P60484_PTEN	43.8	60.8	16.2
13.			At3g50110	Q8H106	PTP/TEN3	-	P60484_PTEN	33.6	45	31.3
14.	At3g19420		Q9LT75	PTP-like	-	P60484_PTEN	43.4	62.8	7.8	
15.			Q8GZT8	AAO13749.1	-	P60484_PTEN	43.4	62.8	7.8	
16.			Q9SN07	CAB62119.1	-	P60484_PTEN	33.6	45	31.3	
17.	At3g23610		Q9ZR37	DSPTP1	+	Q8WYL5_SSH1	43.9	58.3	0.0	
18.	At5g23720		Q75QN6	DSPTP PHS1	+	Q6B8I1_DUSP13	40.7	51.7	2.1	
19.			Q8L613	AAM20532.1	-	Q6B8I1_DUSP13	39.3	52	4.7	
20.			Q9FJU7	BAB09879.1	-	Q8WUK0_PTPMT1	30.7	43.6	4.3	
21.	At2g40570		Q7Y230	AAP37680.1	-	Q16690_DUSP5	19.0	29.6	28.2	
22.	<b>Myotub-PP</b>		At5g04540	Q9LZ70	CAB85561.1	-	Q13615_MTMR3	35.3	44.9	28.9
23.		Q0WP53		Myotubularin- like protein	-	Q13615_MTMR3	36.4	45.5	28.3	
24.	<b>mRNA capping</b>	At5g01290	Q9SS77	AAD56326.1	-	O75319_DUS11	35	52.6	8.8	
25.			Q8GSD7	AAN17417.1	-	O75319_DUS11	33.3	51.4	9.4	
26.			Q9LFA7	CAB69857.1	-	O75319_DUS11	32.4	51.5	8.1	
27.	<b>PTPs II Cdc25</b>	At5g03455	Q8GY31	DSP Cdc25	+	P30307-4_CDC25C	22.2	37.6	8.5	
28.	<b>PTPs III LMWPTP</b>	At3g44620	Q67YE7	PTP	-	P24666_LMW-PTP	39.2	51.9	5.1	
29.			F4J355	PTP	-	P24666_LMW-PTP	33.7	45.3	17.7	
30.			B7U881	ACJ64855.1	-	P24666_LMW-PTP	38	50.6	9.5	
31.			B7U884	ACJ64858.1	-	P24666_LMW-PTP	22.8	31	36.1	
32.			B7U885	ACJ64859.1	-	P24666_LMW-PTP	13.3	21.3	51.3	
33.			B7U886	ACJ64860.1	-	P24666_LMW-PTP	12	19.3	64.7	
34.			B7U887	ACJ64861.1	-	P24666_LMW-PTP	21.2	31.1	36.4	
35.			Q9M283	CAB86920.1	-	P24666_LMW-PTP	8	12	73.3	
36.			Q9M1P2	PTP-like	-	P24666_LMW-PTP	39.2	51.9	5.1	

**Note:** The percent indicators (Ident. (%) - identity, Simil. (%) - similarity, Gap. (%) - gaps) of sequence similarity are given based on the results of pairwise alignment of catalytic domain of human protein phosphatase and appropriate region of the plant homologue.

**Table 4. *Arabidopsis* homologues of aspartate-based protein phosphatases**

No.	Class	Deposition Numbers		Type / Isoform	UniProt KB / Swiss- Prot status	The closest human homolog	Indicators of sequence similarity		
		GenBANK	Uniprot KB				Ident. (%)	Simil. (%)	Gap (%)
<b>Asp-based protein phosphatases with a DXDXT/V catalytic signature</b>									
1.	<b>FCP / FCP-like</b>	At4g21670	Q5YDB6	CTDP-like 1	+	Q9Y5B0_CTDP1	23.2	37.3	16.9
2.		At5g01270	Q5YDB5	CTDP-like 2	+	Q9Y5B0_CTDP1	23.2	37.3	16.9
3.		At2g33540	Q8LL04	CTDP-like 3	+	Q9Y5B0_CTDP1	31.5	53.3	10.9
4.		At5g58003	Q00IB6	CTDP-like 4	+	Q9Y5B0_CTDP1	27.8	50.6	11.1
5.		At1g43600	Q3E7I8	NLI protein	-	Q9Y5B0_CTDP1	31.4	50.6	9.0
6.		At1g43610	Q3ECX9	NLI protein	-	Q9Y5B0_CTDP1	30.8	50.6	9.0
7.		At3g17550	Q9LUP3	MKP6	-	Q9Y5B0_CTDP1	32.0	50.8	6.0
8.		At5g54210	Q9FL74	HDH-like protein	-	Q9Y5B0_CTDP1	31.2	48.4	9.6
9.		At1g20320	Q9LN24	HDH-like protein	-	Q9Y5B0_CTDP1	33.3	52.3	7.2
10.		At2g04930	Q9SI33	HDH-like protein	-	Q9Y5B0_CTDP1	32.5	53.1	11.3
11.		BAB02162	Q9LJR5	K7L4	-	Q9Y5B0_CTDP1	26.6	44.8	7.8
12.		At3g19600	F4JCB2	RNAPII CTD	-	Q9Y5B0_CTDP1	29.9	50.6	13.4
13.		At3g19600	Q9LJN6	MMB12	-	Q9Y5B0_CTDP1	29.9	50.6	13.4
14.		At2g02290	Q9ZVR2	HDH-like protein	-	Q9Y5B0_CTDP1	26.8	45.2	9.6
15.		At5g23470	Q9FHL1	HDH-like protein	-	Q9Y5B0_CTDP1	28.7	45.9	9.6
16.		At1g29770	Q9FXF4	HDH-like protein	-	O15194_CTDSL	42.9	65.3	2.0
17.		At1g29780	Q9FXF5	HDH-like protein	-	O15194_CTDSL	45.2	69.2	1.4
18.		At3g55960	Q9LY49	HDH-like protein	-	O15194_CTDSL	30.5	48.2	12.2
19.		At5g45700	Q9FK73	HDH-like protein	-	O95476_DLRD	42.5	59.5	4.6
20.		At5g46410	Q8VY28	SCP1-like4	-	Q05D32_CTSL2	46.2	64.8	0.0
21.		At4g18140	F4JQR6	SCP1-like 4b	-	Q05D32_CTSL2	45.5	64.8	0.0
22.		At5g11860	Q9LYI7	SCP1-like 5	-	Q05D32_CTSL2	58.6	79.3	0.0
23.		At1g55900	Q8VYE2	TIM50	+	Q3ZCQ8_TIM50	38.8	60.5	0.0
24.	<b>HAD (chronophins)3</b>	At5g36700	Q9LTH1	PGLP1B	-	Q96GD0_PLPP	35.2	52.9	13.8
25.		At5g36790	Q8GY27	PGLP1A	-	Q96GD0_PLPP	33.2	50.0	17.9
26.		At5g47760	Q8GWU0	PGLP2	-	Q96GD0_PLPP	33.0	49.6	18.1

**Note:** The percent indicators (Ident. (%) - identity, Simil. (%) - similarity, Gap. (%) - gaps) of sequence similarity are given based on the results of pairwise alignment of catalytic domain of human protein phosphatase and appropriate region of the plant homologue.

**Table 5. Plant Ser/Thr protein phosphatase homologues from moss (*P. patens*)**

No.	Deposition Numbers		Type / Isoform	UniProtKB / Swiss-Prot status	The closest human homologue	Indicators of sequence similarity		
	GenBANK	UniprotKB				Ident. (%)	Simil. (%)	Gap (%)
<b>Ser/Thr Protein Phosphatases of the PPP family</b>								
1.	PHYPADRAFT_95594	A9TPW7	Predicted	-	P62140_PP1B	82.0	91.0	0.0
2.	PHYPADRAFT_226377	A9TXC9	Predicted	-	P67775_PP2AA	85.6	95.2	0.0
3.	PHYPADRAFT_169532	A9TE32	Predicted	-	P60510_PP4C	75.7	81.6	10.9
4.	PHYPADRAFT_106477	A9SHX7	Predicted	-	P53041_PPP5	61.7	76.9	0.0
5.	PHYPADRAFT_206051	A9RVI2	Predicted	-	O00743_PPP6	72.4	86.4	0.4
6.	PHYPADRAFT_152342	A9RMR0	Predicted	-	Q5SGD2_PPM1L	37.3	57.4	7.2
7.	PHYPADRAFT_141150	A9T6S2	Predicted	-	Q5SGD2_PPM1L	37.2	54.0	9.6
8.	PHYPADRAFT_92442	A9TGG3	Predicted	-	Q5SGD2_PPM1L	37.3	56.2	7.2
9.	PHYPADRAFT_184828	A9SGX4	Predicted	-	P35813_PPPM1A	30.2	49.3	8.6
10.	PHYPADRAFT_126453	A9S9Z7	Predicted	-	P35813_PPPM1A	33.9	52.5	5.4
11.	PHYPADRAFT_130877	A9SJD8	Predicted	-	P35813_PPPM1A	33.7	53.3	4.7
12.	PHYPADRAFT_225330	A9TTK6	Predicted	-	P35813_PPPM1A	30.4	46.8	16.7
13.	PHYPADRAFT_139554	A9T341	Predicted	-	O15355_PPM1G	29.2	40.9	39.4
14.	PHYPADRAFT_115305	A9RJT1	Predicted	-	O75688_PPM1B	32.3	50.2	14.8
15.	PHYPADRAFT_106079	A9SAC2	Predicted	-	Q5SGD2_PPM1L	33.3	49.6	3.6
16.	PHYPADRAFT_32342	A9TT55	Predicted	-	O75688_PPM1B	33.0	46.4	15.8
17.	PHYPADRAFT_13662	A9SHN9	Predicted	-	O75688_PPM1B	30.6	42.6	15.5
<b>Protein tyrosine phosphatase superfamily (CX<sub>r</sub>R)</b>								
1.	PHYPADRAFT_179159	A9RXK5	Predicted	-	A6NDG6_PGP	33.0	50.5	16.5
2.	PHYPADRAFT_174353	A9RFS6	Predicted	-	A6NDG6_PGP	33.6	51.4	16.8
3.	PHYPADRAFT_140952	A9T6C0	Predicted	-	P60484_PTEN	10.5	28.6	7.5
4.	PHYPADRAFT_131125	A9SJW3	Predicted	-	P13686_PPA5	30.3	48.9	7.7
5.	PHYPADRAFT_114693	A9RIT6	Predicted	-	P13686_PPA5	29.0	48.5	7.8
6.	PHYPADRAFT_114432	A9RHZ5	Predicted	-	Q6ZNF0_PAPL	29.0	41.6	14.0
7.	PHYPADRAFT_133613	A9SQV9	Predicted	-	Q6ZNF0_PAPL	25.4	40.3	25.4
8.	PHYPADRAFT_133228	A9SPK4	Predicted	-	Q9UK59_DBR1	58.8	74.2	1.7
<b>Asp-based protein phosphatases with a DXDXT/V catalytic signature</b>								
1.	PHYPADRAFT_86918	A9T1Q3	Predicted	-	Q9Y5B0_CTDP1	31.3	49.4	12.0
2.	PHYPADRAFT_74853	A9S5I0	Predicted	-	Q9Y5B0_CTDP1	30.1	49.4	12.0
3.	PHYPADRAFT_198166	A9TTN5	Predicted	-	Q9Y5B0_CTDP1	30.2	51.6	9.4
4.	PHYPADRAFT_152342	A9TXM9	Predicted	-	Q9Y5B0_CTDP1	23.3	46.0	6.0

**Note:** The percent indicators (Ident. (%) - identity, Simil. (%) - similarity, Gap. (%) - gaps) of sequence similarity are given based on the results of pairwise alignment of catalytic domain of human protein phosphatase and appropriate region of the plant homologue.