

# Phyre2

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Description	RVBD0153c_ptbB_181153_181983
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Detailed template information

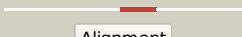

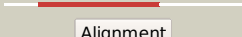
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2oz5A_</a>	Alignment		100.0	95	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> phosphotyrosine protein phosphatase ptpb; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis protein tyrosine2 phosphatase ptpb in complex with the specific inhibitor omts
2	<a href="#">d1ywfa1</a>	Alignment		100.0	100	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Mycobacterial PtpB-like
3	<a href="#">d1xria_</a>	Alignment		99.9	24	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
4	<a href="#">c6byfl_</a>	Alignment		99.8	22	<b>PDB header:</b> transferase <b>Chain:</b> I; <b>PDB Molecule:</b> tyrosine-protein phosphatase siw14; <b>PDBTitle:</b> crystal structure of the core catalytic domain of pp-ii phosphatase2 siw14 from s. cerevisiae in complex with citrate
5	<a href="#">c2m3vA_</a>	Alignment		99.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of tyrosine phosphatase related to biofilm2 formation a (tpba) from pseudomonas aeruginosa
6	<a href="#">c2f46A_</a>	Alignment		99.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative phosphatase (nma1982) from neisseria2 meningitidis z2491 at 1.41 a resolution
7	<a href="#">c3gxgA_</a>	Alignment		99.3	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative phosphatase (duf442); <b>PDBTitle:</b> crystal structure of putative phosphatase (duf442) (yp_001181608.1)2 from shewanella putrefaciens cn-32 at 1.60 a resolution
8	<a href="#">c2imgA_</a>	Alignment		99.3	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dual specificity protein phosphatase 23; <b>PDBTitle:</b> crystal structure of dual specificity protein phosphatase 23 from homo sapiens in complex with ligand malate ion
9	<a href="#">d1fpza_</a>	Alignment		99.2	22	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
10	<a href="#">c2i6oA_</a>	Alignment		99.2	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> sulfolobus solfataricus protein tyrosine <b>PDBTitle:</b> crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g-(p)y-k-n
11	<a href="#">c4r30C_</a>	Alignment		99.1	26	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> laforin; <b>PDBTitle:</b> structure of human laforin dual specificity phosphatase domain

12	<a href="#">c1yz4A_</a>	Alignment		99.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity phosphatase-like 15 isoform a; <b>PDBTitle:</b> crystal structure of dusp15
13	<a href="#">c2g6zB_</a>	Alignment		99.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dual specificity protein phosphatase 5; <b>PDBTitle:</b> crystal structure of human dusp5
14	<a href="#">c1fpzF_</a>	Alignment		99.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> cyclin-dependent kinase inhibitor 3; <b>PDBTitle:</b> crystal structure analysis of kinase associated phosphatase (kap) with2 a substitution of the catalytic site cysteine (cys140) to a serine
15	<a href="#">c1wrmA_</a>	Alignment		99.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity phosphatase 22; <b>PDBTitle:</b> crystal structure of jsp-1
16	<a href="#">d1mkpa_</a>	Alignment		99.0	15	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
17	<a href="#">c2r0bA_</a>	Alignment		99.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine/tyrosine-interacting protein; <b>PDBTitle:</b> crystal structure of human tyrosine phosphatase-like2 serine/threonine/tyrosine-interacting protein
18	<a href="#">c2e0tA_</a>	Alignment		99.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity phosphatase 26; <b>PDBTitle:</b> crystal structure of catalytic domain of dual specificity phosphatase2 26, ms0830 from homo sapiens
19	<a href="#">d1m3ga_</a>	Alignment		99.0	23	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
20	<a href="#">c2oudA_</a>	Alignment		99.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity protein phosphatase 10; <b>PDBTitle:</b> crystal structure of the catalytic domain of human mkp5
21	<a href="#">c4ki9A_</a>	Alignment	not modelled	99.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity protein phosphatase 12; <b>PDBTitle:</b> crystal structure of the catalytic domain of human dusp12 at 2.0 a2 resolution
22	<a href="#">c2nt2C_</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> protein phosphatase slingshot homolog 2; <b>PDBTitle:</b> crystal structure of slingshot phosphatase 2
23	<a href="#">c1zzwA_</a>	Alignment	not modelled	99.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity protein phosphatase 10; <b>PDBTitle:</b> crystal structure of catalytic domain of human map kinase2 phosphatase 5
24	<a href="#">c3rggA_</a>	Alignment	not modelled	99.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-tyrosine phosphatase mitochondrial 1; <b>PDBTitle:</b> crystal structure of ptpmt1 in complex with pi(5)p
25	<a href="#">d1vhra_</a>	Alignment	not modelled	99.0	19	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
26	<a href="#">c2gwoC_</a>	Alignment	not modelled	99.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dual specificity protein phosphatase 13; <b>PDBTitle:</b> crystal structure of tmdp
27	<a href="#">c5xjvA_</a>	Alignment	not modelled	98.9	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity protein phosphatase 13 isoform a; <b>PDBTitle:</b> two intermediate states of conformation switch in dual specificity2 phosphatase 13a
28	<a href="#">c2y96A_</a>	Alignment	not modelled	98.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity phosphatase dupd1; <b>PDBTitle:</b> structure of human dual-specificity phosphatase 27

29	<a href="#">c4kyrA</a>	Alignment	not modelled	98.9	18	<b>PDB header:</b> hydrolase, sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglucan phosphatase Isf2, chloroplatic; <b>PDBTitle:</b> structure of a product bound plant phosphatase
30	<a href="#">d1ohea2</a>	Alignment	not modelled	98.9	22	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
31	<a href="#">c3nmeA</a>	Alignment	not modelled	98.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sex4 glucan phosphatase; <b>PDBTitle:</b> structure of a plant phosphatase
32	<a href="#">c5z5bA</a>	Alignment	not modelled	98.9	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-tyrosine phosphatase; <b>PDBTitle:</b> crystal structure of tk-ptp in the g95a mutant form
33	<a href="#">c2wgpA</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity protein phosphatase 14; <b>PDBTitle:</b> crystal structure of human dual specificity phosphatase 14
34	<a href="#">c4nyhB</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> rna/rnp complex-1-interacting phosphatase; <b>PDBTitle:</b> orthorhombic crystal form of pir1 dual specificity phosphatase core
35	<a href="#">c3emuA</a>	Alignment	not modelled	98.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine rich repeat and phosphatase domain containing <b>PDBTitle:</b> crystal structure of a leucine rich repeat and phosphatase domain2 containing protein from entamoeba histolytica
36	<a href="#">d1v3aa</a>	Alignment	not modelled	98.8	28	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
37	<a href="#">c2hcmA</a>	Alignment	not modelled	98.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity protein phosphatase; <b>PDBTitle:</b> crystal structure of mouse putative dual specificity phosphatase2 complexed with zinc tungstate, new york structural genomics3 consortium
38	<a href="#">c4rkkA</a>	Alignment	not modelled	98.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> laforin; <b>PDBTitle:</b> structure of a product bound phosphatase
39	<a href="#">c2esbA</a>	Alignment	not modelled	98.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity protein phosphatase 18; <b>PDBTitle:</b> crystal structure of human dusp18
40	<a href="#">c3rz2B</a>	Alignment	not modelled	98.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein tyrosine phosphatase type iva 1; <b>PDBTitle:</b> crystal of prl-1 complexed with peptide
41	<a href="#">c4jmkA</a>	Alignment	not modelled	98.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity protein phosphatase 8; <b>PDBTitle:</b> structure of dusp8
42	<a href="#">c1oheA</a>	Alignment	not modelled	98.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cdc14b2 phosphatase; <b>PDBTitle:</b> structure of cdc14b phosphatase with a peptide ligand
43	<a href="#">c5xw4A</a>	Alignment	not modelled	98.7	22	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase cdc14; <b>PDBTitle:</b> crystal structure of budding yeast cdc14p (wild type) in the apo state
44	<a href="#">d1rxda</a>	Alignment	not modelled	98.7	22	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
45	<a href="#">c3s4oB</a>	Alignment	not modelled	98.7	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein tyrosine phosphatase-like protein; <b>PDBTitle:</b> protein tyrosine phosphatase (putative) from leishmania major
46	<a href="#">c3s4eA</a>	Alignment	not modelled	98.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity protein phosphatase 19; <b>PDBTitle:</b> crystal structure of a novel mitogen-activated protein kinase2 phosphatase, skrp1
47	<a href="#">c6i28A</a>	Alignment	not modelled	98.6	22	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> orf98 ptp-2; <b>PDBTitle:</b> crystal structure of cydia pomonella ptp-2 phosphatase
48	<a href="#">c2c46B</a>	Alignment	not modelled	98.6	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> mrna capping enzyme; <b>PDBTitle:</b> crystal structure of the human rna guanylyltransferase and 5'-2 phosphatase
49	<a href="#">c4tvvA</a>	Alignment	not modelled	98.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine phosphatase ii superfamily protein; <b>PDBTitle:</b> crystal structure of lppa from legionella pneumophila
50	<a href="#">c1yn9B</a>	Alignment	not modelled	98.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> polynucleotide 5'-phosphatase; <b>PDBTitle:</b> crystal structure of baculovirus rna 5'-phosphatase2 complexed with phosphate
51	<a href="#">c2j17A</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase yil113w; <b>PDBTitle:</b> ptyr bound form of sdp-1
52	<a href="#">d1i9sa</a>	Alignment	not modelled	98.3	23	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
53	<a href="#">c5m43A</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of yvh1 phosphatase domain from chaetomium2 thermophilum
54	<a href="#">c4nx8A</a>	Alignment	not modelled	98.2	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-tyrosine phosphatase 2; <b>PDBTitle:</b> structure of a ptp-like phytase from bdellovibrio bacteriovorus

55	<a href="#">c2p4dA_</a>	Alignment	not modelled	98.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity protein phosphatase; <b>PDBTitle:</b> structure-assisted discovery of variola major h1 phosphatase2 inhibitors
56	<a href="#">c6apxA_</a>	Alignment	not modelled	98.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,dual specificity <b>PDBTitle:</b> crystal structure of human dual specificity phosphatase 1 catalytic2 domain (c258s) as a maltose binding protein fusion in complex with3 the monobody ysx1
57	<a href="#">c1u24A_</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> myo-inositol hexaphosphate phosphohydrolase; <b>PDBTitle:</b> crystal structure of selenomonas ruminantium phytase
58	<a href="#">c5ncrA_</a>	Alignment	not modelled	97.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine phosphatase; <b>PDBTitle:</b> oh1 from the orf virus: a tyrosine phosphatase that displays distinct2 structural features and triple substrate specificity
59	<a href="#">c4y7iB_</a>	Alignment	not modelled	97.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> myotubularin-related protein 8; <b>PDBTitle:</b> crystal structure of mtmr8
60	<a href="#">c1g4wR_</a>	Alignment	not modelled	97.7	24	<b>PDB header:</b> signaling protein <b>Chain:</b> R: <b>PDB Molecule:</b> protein tyrosine phosphatase sptp; <b>PDBTitle:</b> crystal structure of the salmonella tyrosine phosphatase and gtpase2 activating protein sptp
61	<a href="#">c3awfC_</a>	Alignment	not modelled	97.7	21	<b>PDB header:</b> hydrolase, membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> voltage-sensor containing phosphatase; <b>PDBTitle:</b> crystal structure of pten-like domain of ci-vsp (236-576)
62	<a href="#">c3f41B_</a>	Alignment	not modelled	97.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phytase; <b>PDBTitle:</b> structure of the tandemly repeated protein tyrosine2 phosphatase like phytase from mitsuokella multacida
63	<a href="#">d1zsqA2</a>	Alignment	not modelled	97.6	15	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Myotubularin-like phosphatases
64	<a href="#">c1zsqA_</a>	Alignment	not modelled	97.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> myotubularin-related protein 2; <b>PDBTitle:</b> crystal structure of mtmr2 in complex with2 phosphatidylinositol 3-phosphate
65	<a href="#">d2pt0a1</a>	Alignment	not modelled	97.5	15	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Myo-inositol hexaphosphate phosphohydrolase (phytase) PhyA
66	<a href="#">c1d5rA_</a>	Alignment	not modelled	97.3	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoinositide phosphatase pten; <b>PDBTitle:</b> crystal structure of the pten tumor suppressor
67	<a href="#">c3n0aA_</a>	Alignment	not modelled	97.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase auxilin; <b>PDBTitle:</b> crystal structure of auxilin (40-400)
68	<a href="#">d1d5ra2</a>	Alignment	not modelled	97.2	24	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
69	<a href="#">c3ps5A_</a>	Alignment	not modelled	97.1	21	<b>PDB header:</b> hydrolase, signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase non-receptor type 6; <b>PDBTitle:</b> crystal structure of the full-length human protein tyrosine2 phosphatase shp-1
70	<a href="#">d1g4us2</a>	Alignment	not modelled	97.0	19	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Higher-molecular-weight phosphotyrosine protein phosphatases
71	<a href="#">d1wcha_</a>	Alignment	not modelled	97.0	20	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Higher-molecular-weight phosphotyrosine protein phosphatases
72	<a href="#">c2b3oA_</a>	Alignment	not modelled	97.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase, non-receptor type <b>PDBTitle:</b> crystal structure of human tyrosine phosphatase shp-1
73	<a href="#">c1larB_</a>	Alignment	not modelled	97.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (lar); <b>PDBTitle:</b> crystal structure of the tandem phosphatase domains of rtp lar
74	<a href="#">c3m4uB_</a>	Alignment	not modelled	96.8	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine specific protein phosphatase, putative; <b>PDBTitle:</b> crystal structure of trypanosoma brucei protein tyrosine phosphatase2 tbptp1
75	<a href="#">c2shpA_</a>	Alignment	not modelled	96.8	26	<b>PDB header:</b> tyrosine phosphatase <b>Chain:</b> A: <b>PDB Molecule:</b> shp-2; <b>PDBTitle:</b> tyrosine phosphatase shp-2
76	<a href="#">d1lyva_</a>	Alignment	not modelled	96.8	19	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Higher-molecular-weight phosphotyrosine protein phosphatases
77	<a href="#">c3sr9A_</a>	Alignment	not modelled	96.7	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor-type tyrosine-protein phosphatase s; <b>PDBTitle:</b> crystal structure of mouse ptpsigma
78	<a href="#">c4az1B_</a>	Alignment	not modelled	96.7	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine specific protein phosphatase; <b>PDBTitle:</b> crystal structure of the trypanosoma cruzi protein tyrosine2 phosphatase tcptp1, a potential therapeutic target for chagas'3 disease
79	<a href="#">d1jlna_</a>	Alignment	not modelled	96.7	26	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Higher-molecular-weight phosphotyrosine protein phosphatases

80	<a href="#">d1fp<sub>ra</sub></a>	Alignment	not modelled	96.6	21	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Higher-molecular-weight phosphotyrosine protein phosphatases
81	<a href="#">c3s3f<sub>A</sub></a>	Alignment	not modelled	96.6	35	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase 10d; <b>PDBTitle:</b> crystal structure of the catalytic domain of ptp10d from drosophila2 melanogaster with a small molecule inhibitor vanadate
82	<a href="#">c3i36<sub>A</sub></a>	Alignment	not modelled	96.6	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> vascular protein tyrosine phosphatase 1; <b>PDBTitle:</b> crystal structure of rat protein tyrosine phosphatase eta catalytic2 domain
83	<a href="#">c2qdm<sub>A</sub></a>	Alignment	not modelled	96.6	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase non-receptor type 7; <b>PDBTitle:</b> crystal structure of the hept catalytic domain c270s/d236a/q314a2 mutant
84	<a href="#">c1ygu<sub>A</sub></a>	Alignment	not modelled	96.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> leukocyte common antigen; <b>PDBTitle:</b> crystal structure of the tandem phosphatase domains of rtp2 cd45 with a ptyr peptide
85	<a href="#">c1lw3<sub>A</sub></a>	Alignment	not modelled	96.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> myotubularin-related protein 2; <b>PDBTitle:</b> crystal structure of myotubularin-related protein 22 complexed with phosphate
86	<a href="#">c2nlk<sub>A</sub></a>	Alignment	not modelled	96.5	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein tyrosine phosphatase, receptor type, g variant <b>PDBTitle:</b> crystal structure of d1 and d2 catalytic domains of human protein2 tyrosine phosphatase gamma (d1+d2 ptprg)
87	<a href="#">c2jld<sub>A</sub></a>	Alignment	not modelled	96.5	37	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor-type tyrosine-protein phosphatase epsilon; <b>PDBTitle:</b> protein tyrosine phosphatase, receptor type, e isoform
88	<a href="#">d1lara1</a>	Alignment	not modelled	96.5	31	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Higher-molecular-weight phosphotyrosine protein phosphatases
89	<a href="#">d2shpa1</a>	Alignment	not modelled	96.4	26	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Higher-molecular-weight phosphotyrosine protein phosphatases
90	<a href="#">c2h04<sub>A</sub></a>	Alignment	not modelled	96.4	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein tyrosine phosphatase, receptor type, b, <b>PDBTitle:</b> structural studies of protein tyrosine phosphatase beta catalytic2 domain in complex with inhibitors
91	<a href="#">c2b49<sub>A</sub></a>	Alignment	not modelled	96.3	37	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein tyrosine phosphatase, non-receptor type 3; <b>PDBTitle:</b> crystal structure of the catalytic domain of protein tyrosine2 phosphatase, non-receptor type 3
92	<a href="#">c4ikc<sub>A</sub></a>	Alignment	not modelled	96.3	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol phosphatase ptpq; <b>PDBTitle:</b> crystal structure of catalytic domain of ptpq
93	<a href="#">c2c7s<sub>A</sub></a>	Alignment	not modelled	96.3	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor-type tyrosine-protein phosphatase kappa; <b>PDBTitle:</b> crystal structure of human protein tyrosine phosphatase kappa at 1.95a2 resolution
94	<a href="#">d1lara2</a>	Alignment	not modelled	96.3	26	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Higher-molecular-weight phosphotyrosine protein phosphatases
95	<a href="#">d1p15<sub>a</sub></a>	Alignment	not modelled	96.2	38	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Higher-molecular-weight phosphotyrosine protein phosphatases
96	<a href="#">c2yf0<sub>A</sub></a>	Alignment	not modelled	96.2	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> myotubularin-related protein 6; <b>PDBTitle:</b> human myotubularin related protein 6 (mtmr6)
97	<a href="#">c2bij<sub>A</sub></a>	Alignment	not modelled	96.2	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase, non-receptor type 5; <b>PDBTitle:</b> crystal structure of the human protein tyrosine phosphatase ptpn52 (step, striatum enriched enriched phosphatase)
98	<a href="#">d1rpma</a>	Alignment	not modelled	96.2	31	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Higher-molecular-weight phosphotyrosine protein phosphatases
99	<a href="#">c4qun<sub>B</sub></a>	Alignment	not modelled	96.2	34	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine-protein phosphatase non-receptor type 3; <b>PDBTitle:</b> crystal structure of the ptpn3 (ptph1) catalytic domain c842s mutant
100	<a href="#">d1larb1</a>	Alignment	not modelled	96.1	31	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Higher-molecular-weight phosphotyrosine protein phosphatases
101	<a href="#">c3jrl<sub>A</sub></a>	Alignment	not modelled	96.1	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oncogenic tyrosine phosphatase shp2; <b>PDBTitle:</b> crystal structure of the oncogenic tyrosine phosphatase shp2 complexed2 with a salicylic acid-based small molecule inhibitor
102	<a href="#">c2hy3<sub>A</sub></a>	Alignment	not modelled	96.1	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor-type tyrosine-protein phosphatase gamma; <b>PDBTitle:</b> crystal structure of the human tyrosine receptor phosphate gamma in2 complex with vanadate
103	<a href="#">c2nz6<sub>A</sub></a>	Alignment	not modelled	96.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor-type tyrosine-protein phosphatase eta; <b>PDBTitle:</b> crystal structure of the ptprij inactivating mutant c1239s

104	<a href="#">c2i75A</a>	 Alignment	not modelled	96.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase non-receptor type 4; <b>PDBTitle:</b> crystal structure of human protein tyrosine phosphatase n4 (ptpn4)
105	<a href="#">d1yfoa</a>	 Alignment	not modelled	95.9	23	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Higher-molecular-weight phosphotyrosine protein phosphatases
106	<a href="#">c2vexA</a>	 Alignment	not modelled	95.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase non-receptor type 1; <b>PDBTitle:</b> crystal structure of protein tyrosine phosphatase 1b in complex with2 an isothiazolidinone-containing inhibitor
107	<a href="#">c5j8rC</a>	 Alignment	not modelled	95.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> tyrosine-protein phosphatase non-receptor type 12; <b>PDBTitle:</b> crystal structure of the catalytic domain of human protein tyrosine2 phosphatase non-receptor type 12 - k61r mutant
108	<a href="#">c2bz1A</a>	 Alignment	not modelled	95.8	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase, non-receptor type 14; <b>PDBTitle:</b> crystal structure of the human protein tyrosine phosphatase n14 at 1.2 65 a resolution
109	<a href="#">c2pa5A</a>	 Alignment	not modelled	95.7	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase non-receptor type 9; <b>PDBTitle:</b> crystal structure of human protein tyrosine phosphatase ptpn9
110	<a href="#">c2qepA</a>	 Alignment	not modelled	95.6	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor-type tyrosine-protein phosphatase n2; <b>PDBTitle:</b> crystal structure of the d1 domain of ptpn2 (ia2beta)
111	<a href="#">c1l8kA</a>	 Alignment	not modelled	95.6	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> t-cell protein-tyrosine phosphatase; <b>PDBTitle:</b> t cell protein-tyrosine phosphatase structure
112	<a href="#">d1l8ka</a>	 Alignment	not modelled	95.6	26	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Higher-molecular-weight phosphotyrosine protein phosphatases
113	<a href="#">d2f71a1</a>	 Alignment	not modelled	95.3	31	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Higher-molecular-weight phosphotyrosine protein phosphatases
114	<a href="#">c2qcjB</a>	 Alignment	not modelled	95.3	36	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine-protein phosphatase non-receptor type <b>PDBTitle:</b> native structure of lyp
115	<a href="#">c2oc3A</a>	 Alignment	not modelled	95.2	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase non-receptor type 18; <b>PDBTitle:</b> crystal structure of the catalytic domain of human protein tyrosine2 phosphatase non-receptor type 18
116	<a href="#">c2g59B</a>	 Alignment	not modelled	95.1	38	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> receptor-type tyrosine-protein phosphatase o; <b>PDBTitle:</b> crystal structure of the catalytic domain of protein2 tyrosine phosphatase from homo sapiens
117	<a href="#">c1e0cA</a>	 Alignment	not modelled	93.4	19	<b>PDB header:</b> sulfurtransferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfurtransferase; <b>PDBTitle:</b> sulfurtransferase from azotobacter vinelandii
118	<a href="#">c3i2vA</a>	 Alignment	not modelled	93.4	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylyltransferase and sulfurtransferase mocs3; <b>PDBTitle:</b> crystal structure of human mocs3 rhodanese-like domain
119	<a href="#">c3f4aA</a>	 Alignment	not modelled	93.2	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ygr203w; <b>PDBTitle:</b> structure of ygr203w, a yeast protein tyrosine phosphatase of the2 rhodanese family
120	<a href="#">c3aaxB</a>	 Alignment	not modelled	93.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative thiosulfate sulfurtransferase; <b>PDBTitle:</b> crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form