




















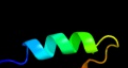


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1vhra_</a>	 Alignment		86.9	20	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
2	<a href="#">c2y96A_</a>	 Alignment		86.7	20	<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
3	<a href="#">c2r0bA_</a>	 Alignment		84.0	28	<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
4	<a href="#">c2esbA_</a>	 Alignment		83.5	28	<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
5	<a href="#">c1wrnA_</a>	 Alignment		83.3	20	<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
6	<a href="#">c2imgA_</a>	 Alignment		83.0	24	<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 phosphatase2 23 from homo sapiens in complex with ligand malate ion
7	<a href="#">d1xria_</a>	 Alignment		81.2	22	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
8	<a href="#">c3emuA_</a>	 Alignment		81.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine rich repeat and phosphatase domain <b>PDBTitle:</b> crystal structure of a leucine rich repeat and phosphatase2 domain containing protein from entamoeba histolytica
9	<a href="#">c2gwoC_</a>	 Alignment		80.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dual specificity protein phosphatase 13; <b>PDBTitle:</b> crystal structure of tmpd
10	<a href="#">c2g6zB_</a>	 Alignment		80.5	20	<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
11	<a href="#">d1m3ga_</a>	 Alignment		80.2	28	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like

12	<a href="#">c1zzwA_</a>	Alignment		79.9	24	<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
13	<a href="#">c3rggA_</a>	Alignment		79.8	28	<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
14	<a href="#">c3nmeA_</a>	Alignment		79.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sex4 glucan phosphatase; <b>PDBTitle:</b> structure of a plant phosphatase
15	<a href="#">c2oudA_</a>	Alignment		78.5	24	<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
16	<a href="#">c2nt2C_</a>	Alignment		78.2	28	<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
17	<a href="#">c1fpzF_</a>	Alignment		77.9	24	<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 phosphatase2 (kap) with a substitution of the catalytic site cysteine3 (cys140) to a serine
18	<a href="#">c1yz4A_</a>	Alignment		77.4	24	<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
19	<a href="#">c2e0tA_</a>	Alignment		77.2	20	<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
20	<a href="#">d1mkpa_</a>	Alignment		77.0	24	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
21	<a href="#">c2wgpA_</a>	Alignment	not modelled	76.4	24	<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
22	<a href="#">d1i9sa_</a>	Alignment	not modelled	75.5	36	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
23	<a href="#">d1ohea2</a>	Alignment	not modelled	75.4	16	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
24	<a href="#">c2hcmA_</a>	Alignment	not modelled	75.3	32	<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
25	<a href="#">c1yn9B_</a>	Alignment	not modelled	74.9	20	<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
26	<a href="#">c2j17A_</a>	Alignment	not modelled	72.4	24	<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
27	<a href="#">d1rxda_</a>	Alignment	not modelled	69.8	20	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
28	<a href="#">d1v3aa_</a>	Alignment	not modelled	68.6	20	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
						<b>PDB header:</b> transferase

29	<a href="#">c2c46B</a>	Alignment	not modelled	68.3	36	<b>Chain:</b> B: <b>PDB Molecule:</b> mrna capping enzyme; <b>PDBTitle:</b> crystal structure of the human rna guanylyltransferase and2 5'-phosphatase
30	<a href="#">c2i6oA</a>	Alignment	not modelled	67.9	24	<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
31	<a href="#">d1fpza</a>	Alignment	not modelled	65.4	28	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
32	<a href="#">c3rz2B</a>	Alignment	not modelled	65.1	20	<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
33	<a href="#">c3s4oB</a>	Alignment	not modelled	64.5	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
34	<a href="#">d1d5ra2</a>	Alignment	not modelled	46.1	32	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
35	<a href="#">c2p4dA</a>	Alignment	not modelled	45.6	32	<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 h12 phosphatase inhibitors
36	<a href="#">d1vdda</a>	Alignment	not modelled	30.2	18	<b>Fold:</b> Recombination protein RecR <b>Superfamily:</b> Recombination protein RecR <b>Family:</b> Recombination protein RecR
37	<a href="#">d1texa</a>	Alignment	not modelled	24.8	36	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
38	<a href="#">d1kcfa1</a>	Alignment	not modelled	24.5	40	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> SAP domain <b>Family:</b> SAP domain
39	<a href="#">c1vddC</a>	Alignment	not modelled	20.1	17	<b>PDB header:</b> recombination <b>Chain:</b> C: <b>PDB Molecule:</b> recombination protein recr; <b>PDBTitle:</b> crystal structure of recombinational repair protein recr
40	<a href="#">c1oheA</a>	Alignment	not modelled	19.5	16	<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
41	<a href="#">c3ap3A</a>	Alignment	not modelled	18.2	50	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-tyrosine sulfotransferase 2; <b>PDBTitle:</b> crystal structure of human tyrosylprotein sulfotransferase-2 complexed2 with pap
42	<a href="#">c1b9qA</a>	Alignment	not modelled	12.2	80	<b>PDB header:</b> collagen facit xiv <b>Chain:</b> A: <b>PDB Molecule:</b> protein (collagen alpha 1); <b>PDBTitle:</b> nmr structure of heparin binding site of non collagenous2 domain i (nc1) of collagen facit xiv
43	<a href="#">c1b9pA</a>	Alignment	not modelled	12.2	80	<b>PDB header:</b> collagen facit xiv <b>Chain:</b> A: <b>PDB Molecule:</b> protein (collagen alpha 1); <b>PDBTitle:</b> nmr structure of heparin binding site of non collagenous2 domain i (nc1) of collagen facit xiv
44	<a href="#">c2zq5A</a>	Alignment	not modelled	11.5	36	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of sulfotransferase stf1 from2 mycobacterium tuberculosis h37rv (type1 form)
45	<a href="#">c2ksdA</a>	Alignment	not modelled	10.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aerobic respiration control sensor protein arcb; <b>PDBTitle:</b> backbone structure of the membrane domain of e. coli2 histidine kinase receptor arcb, center for structures of3 membrane proteins (csm) target 4310c
46	<a href="#">c3u4gA</a>	Alignment	not modelled	10.4	50	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> namn:dmb phosphoribosyltransferase; <b>PDBTitle:</b> the structure of cobt from pyrococcus horikoshii
47	<a href="#">c2z6vA</a>	Alignment	not modelled	9.1	36	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of sulfotransferase stf9 from2 mycobacterium avium
48	<a href="#">c2jp3A</a>	Alignment	not modelled	9.0	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fxyd domain-containing ion transport regulator 4; <b>PDBTitle:</b> solution structure of the human fxyd4 (chif) protein in sds2 micelles
49	<a href="#">c2f46A</a>	Alignment	not modelled	7.6	13	<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
50	<a href="#">c1vkjA</a>	Alignment	not modelled	7.2	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> heparan sulfate (glucosamine) 3-o-sulfotransferase2 isoform 1 in the presence of pap
51	<a href="#">d1vkja</a>	Alignment	not modelled	7.2	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
52	<a href="#">c3awfC</a>	Alignment	not modelled	6.8	32	<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)
53	<a href="#">c3rn1A</a>	Alignment	not modelled	6.2	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfotransferase; <b>PDBTitle:</b> crystal structure of sulfotransferase from alicyclobacillus2 acidocaldarius
54	<a href="#">c3maiA</a>	Alignment	not modelled	6.1	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna processing chain a;

54	<a href="#">c3mgA_</a>	Alignment	not modelled	5.1	42	<b>PDBTitle:</b> crystal structure of putative dna processing protein dpra from2 rhodopseudomonas palustris cga009
55	<a href="#">d1cuka1</a>	Alignment	not modelled	5.7	18	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> DNA helicase RuvA subunit, C-terminal domain <b>Family:</b> DNA helicase RuvA subunit, C-terminal domain
56	<a href="#">c2pqnB_</a>	Alignment	not modelled	5.6	25	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> mitochondrial division protein 1; <b>PDBTitle:</b> crystal structure of yeast fis1 complexed with a fragment of yeast2 mdv1
57	<a href="#">d1jb0k_</a>	Alignment	not modelled	5.5	39	<b>Fold:</b> Photosystem I reaction center subunit X, PsaK <b>Superfamily:</b> Photosystem I reaction center subunit X, PsaK <b>Family:</b> Photosystem I reaction center subunit X, PsaK
58	<a href="#">c1jb0K_</a>	Alignment	not modelled	5.5	39	<b>PDB header:</b> photosynthesis <b>Chain:</b> K: <b>PDB Molecule:</b> photosystem 1 reaction centre subunit x; <b>PDBTitle:</b> crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
59	<a href="#">d1sdia_</a>	Alignment	not modelled	5.5	22	<b>Fold:</b> YcfC-like <b>Superfamily:</b> YcfC-like <b>Family:</b> YcfC-like
60	<a href="#">c3bd9A_</a>	Alignment	not modelled	5.3	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> heparan sulfate glucosamine 3-o-sulfotransferase <b>PDBTitle:</b> human 3-o-sulfotransferase isoform 5 with bound pap
61	<a href="#">c1q90G_</a>	Alignment	not modelled	5.2	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> G: <b>PDB Molecule:</b> cytochrome b6f complex subunit petg; <b>PDBTitle:</b> structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
62	<a href="#">d1q90g_</a>	Alignment	not modelled	5.2	31	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetG subunit of the cytochrome b6f complex <b>Family:</b> PetG subunit of the cytochrome b6f complex