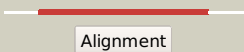

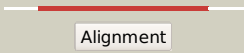



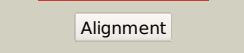



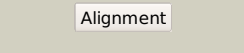

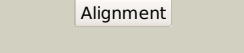
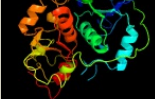


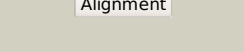

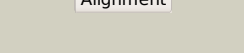

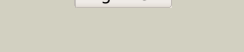



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0815c_(cysA2)_908488_909321
Date	Fri Jul 26 01:50:40 BST 2019
Unique Job ID	58c063650aa8524e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3aaxB_	 Alignment		100.0	99	PDB header: transferase Chain: B: PDB Molecule: putative thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
2	c3hzuA_	 Alignment		100.0	50	PDB header: transferase Chain: A: PDB Molecule: thiosulfate sulfurtransferase ssea; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
3	c1uarA_	 Alignment		100.0	51	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: crystal structure of rhodanese from thermus thermophilus hb8
4	c6h98A_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: native crystal structure of anaerobic ergothioneine biosynthesis2 enzyme from chlorobium limicola.
5	c3ippA_	 Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase ynje; PDBTitle: crystal structure of sulfur-free ynje
6	c1boiA_	 Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: n-terminally truncated rhodanese
7	c1e0cA_	 Alignment		100.0	27	PDB header: sulfurtransferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: sulfurtransferase from azotobacter vinelandii
8	c1okgA_	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: possible 3-mercaptopyruvate sulfurtransferase; PDBTitle: 3-mercaptopyruvate sulfurtransferase from leishmania major
9	c3utnX_	 Alignment		100.0	25	PDB header: transferase Chain: X: PDB Molecule: thiosulfate sulfurtransferase tum1; PDBTitle: crystal structure of tum1 protein from saccharomyces cerevisiae
10	c3o1hA_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: human 3-mercaptopyruvate sulfurtransferase
11	c1urhA_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: the "rhodanese" fold and catalytic mechanism of 2 3-mercaptopyruvate sulfotransferases: crystal structure3 of ssea from escherichia coli

12	c6mxvA_	Alignment		100.0	19	PDB header: unknown function Chain: A: PDB Molecule: rhodanese-like family protein; PDBTitle: the crystal structure of a rhodanese-like family protein from2 francisella tularensis subsp. tularensis schu s4
13	c2eg4B_	Alignment		100.0	28	PDB header: transferase Chain: B: PDB Molecule: probable thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase
14	c1yt8A_	Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: thiosulfate sulfurtransferase; PDBTitle: crystal structure of thiosulfate sulfurtransferase from pseudomonas2 aeruginosa
15	c3tp9B_	Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase and rhodanese domain protein; PDBTitle: crystal structure of alicyclobacillus acidocaldarius protein with2 beta-lactamase and rhodanese domains
16	d1uara1	Alignment		100.0	50	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
17	d1urha1	Alignment		100.0	27	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
18	d1rha1	Alignment		99.9	27	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
19	d1e0ca1	Alignment		99.9	23	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
20	d1okga1	Alignment		99.9	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
21	d1uara2	Alignment	not modelled	99.9	54	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
22	d1okga2	Alignment	not modelled	99.9	27	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
23	d1rha2	Alignment	not modelled	99.9	27	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
24	d1e0ca2	Alignment	not modelled	99.9	30	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
25	d1urha2	Alignment	not modelled	99.8	33	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
26	d1yt8a3	Alignment	not modelled	99.8	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
27	c3ilmD_	Alignment	not modelled	99.8	25	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr3790 protein; PDBTitle: crystal structure of the alr3790 protein from anabaena sp. northeast2 structural genomics consortium target nsr437h
28	d1yt8a1	Alignment	not modelled	99.8	19	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
						PDB header: oxidoreductase, transferase Chain: C: PDB Molecule: bpprf;

29	c5ve5C	Alignment	not modelled	99.8	21	PDBTitle: crystal structure of persulfide dioxygenase rhodanese fusion protein2 with rhodanese domain inactivating mutation (c314s) from burkholderia3 phytotfirmans in complex with glutathione
30	c2moiA	Alignment	not modelled	99.8	16	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the cytoplasmic rhodanese domain of the inner2 membrane protein ygap from escherichia coli
31	c6bevB	Alignment	not modelled	99.8	14	PDB header: transferase Chain: B: PDB Molecule: thiosulfate sulfurtransferase/rhodanese-like domain- PDBTitle: human single domain sulfurtransferase tstd1
32	c3d1pA	Alignment	not modelled	99.8	22	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase yor285w; PDBTitle: atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae
33	c3nhvE	Alignment	not modelled	99.8	22	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: bh2092 protein; PDBTitle: crystal structure of bh2092 protein from bacillus halodurans,2 northeast structural genomics consortium target bhr228f
34	d1t3ka	Alignment	not modelled	99.8	17	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
35	d1yt8a4	Alignment	not modelled	99.8	12	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
36	d1qxna	Alignment	not modelled	99.8	21	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
37	c2hhgA	Alignment	not modelled	99.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rpa3614; PDBTitle: structure of protein of unknown function rpa3614, possible tyrosine2 phosphatase, from rhodopseudomonas palustris cga009
38	d1tq1a	Alignment	not modelled	99.8	18	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
39	c3g5jA	Alignment	not modelled	99.8	23	PDB header: nucleotide binding protein Chain: A: PDB Molecule: putative atp/gtp binding protein; PDBTitle: crystal structure of n-terminal domain of putative atp/gtp binding2 protein from clostridium difficile 630
40	c3emeA	Alignment	not modelled	99.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: rhodanese-like domain protein; PDBTitle: crystal structure of rhodanese-like domain protein from2 staphylococcus aureus
41	c3gk5A	Alignment	not modelled	99.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized rhodanese-related protein tvg0868615; PDBTitle: crystal structure of rhodanese-related protein (tvg0868615) from2 thermoplasma volcanium, northeast structural genomics consortium3 target tvr109a
42	d1yt8a2	Alignment	not modelled	99.8	19	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
43	c3i2vA	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: adenylyltransferase and sulfurtransferase mocs3; PDBTitle: crystal structure of human mocs3 rhodanese-like domain
44	c3k9rA	Alignment	not modelled	99.7	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: alr3790 protein; PDBTitle: x-ray structure of the rhodanese-like domain of the alr3790 protein2 from anaerobaculum sp. northeast structural genomics consortium target3 nsr437c.
45	c3f4aA	Alignment	not modelled	99.7	12	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ygr203w; PDBTitle: structure of ygr203w, a yeast protein tyrosine phosphatase of the2 rhodanese family
46	c4f67A	Alignment	not modelled	99.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0176 protein lpg2838; PDBTitle: three dimensional structure of the double mutant of upf0176 protein2 lpg2838 from legionella pneumophila at the resolution 1.8a, northeast3 structural genomics consortium (nsg) target lgr82
47	c2fsxA	Alignment	not modelled	99.7	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cog0607: rhodanese-related sulfurtransferase; PDBTitle: crystal structure of rv0390 from m. tuberculosis
48	c3fojA	Alignment	not modelled	99.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of ssp1007 from staphylococcus2 saprophyticus subsp. saprophyticus. northeast structural3 genomics target syr101a.
49	d1gmxA	Alignment	not modelled	99.7	23	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
50	c2dcqA	Alignment	not modelled	99.7	11	PDB header: unknown function Chain: A: PDB Molecule: putative protein at4g01050; PDBTitle: fully automated nmr structure determination of the2 rhodanese homology domain at4g01050(175-295) from3 arabidopsis thaliana
51	c2j6pF	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: F: PDB Molecule: sb(v)-as(v) reductase; PDBTitle: structure of as-sb reductase from leishmania major
52	c2k0zA	Alignment	not modelled	99.7	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein hp1203; PDBTitle: solution nmr structure of protein hp1203 from helicobacter pylori2 26695. northeast structural genomics

						consortium (nesg) target3 pt1/ontario center for structural proteomics target hp1203
53	d1whba_	Alignment	not modelled	99.7	9	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
54	c2jtqA_	Alignment	not modelled	99.6	31	PDB header: transferase Chain: A: PDB Molecule: phage shock protein e; PDBTitle: rhodanese from e.coli
55	d1c25a_	Alignment	not modelled	99.6	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
56	c2vswB_	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 16; PDBTitle: the structure of the rhodanese domain of the human dual specificity2 phosphatase 16
57	d2gwfa1	Alignment	not modelled	99.6	10	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
58	d1ymka1	Alignment	not modelled	99.6	24	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
59	c3ntaA_	Alignment	not modelled	99.6	31	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
60	c2uzqE_	Alignment	not modelled	99.5	19	PDB header: hydrolase Chain: E: PDB Molecule: m-phase inducer phosphatase 2; PDBTitle: protein phosphatase, new crystal form
61	c3icrA_	Alignment	not modelled	99.5	39	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a-disulfide reductase; PDBTitle: crystal structure of oxidized bacillus anthracis coadr-rhd
62	c2oucB_	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the map kinase binding domain of mkp5
63	d1hzma_	Alignment	not modelled	99.5	21	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
64	c3op3A_	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: A: PDB Molecule: m-phase inducer phosphatase 3; PDBTitle: crystal structure of cell division cycle 25c protein isoform a from2 homo sapiens
65	c3r2uC_	Alignment	not modelled	99.2	25	PDB header: hydrolase Chain: C: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: 2.1 angstrom resolution crystal structure of metallo-beta-lactamase2 from staphylococcus aureus subsp. aureus col
66	c1wv9B_	Alignment	not modelled	99.1	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: rhodanese homolog tt1651; PDBTitle: crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
67	c2f46A_	Alignment	not modelled	96.2	19	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative phosphatase (nma1982) from neisseria2 meningitidis z2491 at 1.41 a resolution
68	d1ywfa1	Alignment	not modelled	95.5	22	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Mycobacterial PtpB-like
69	c3gxqA_	Alignment	not modelled	95.2	13	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphatase (duf442); PDBTitle: crystal structure of putative phosphatase (duf442) (yp_001181608.1)2 from shewanella putrefaciens cn-32 at 1.60 a resolution
70	c6byfl_	Alignment	not modelled	94.3	9	PDB header: transferase Chain: I: PDB Molecule: tyrosine-protein phosphatase siw14; PDBTitle: crystal structure of the core catalytic domain of pp-ip phosphatase2 siw14 from s. cerevisiae in complex with citrate
71	c3flhC_	Alignment	not modelled	93.7	20	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein lp_1913; PDBTitle: crystal structure of lp_1913 protein from lactobacillus plantarum,2 northeast structural genomics consortium target lpr140b
72	d1xria_	Alignment	not modelled	91.0	14	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
73	c2oz5A_	Alignment	not modelled	90.3	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phosphotyrosine protein phosphatase ptpb; PDBTitle: crystal structure of mycobacterium tuberculosis protein tyrosine2 phosphatase ptpb in complex with the specific inhibitor omts
74	c2i6oA_	Alignment	not modelled	90.1	16	PDB header: hydrolase Chain: A: PDB Molecule: sulfolobus solfataricus protein tyrosine PDBTitle: crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g-(p)y-k-n
75	c5cd1B_	Alignment	not modelled	88.2	19	PDB header: transferase/rna Chain: B: PDB Molecule: trna (adenine(58)-n(1))-methyltransferase non-catalytic PDBTitle: structure of an asymmetric tetramer of human trna m1a582 methyltransferase in a complex with sah and trna3lys
76	c2imgA_	Alignment	not modelled	87.1	11	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 23; PDBTitle: crystal structure of dual specificity protein phosphatase2 23 from homo sapiens in complex with ligand malate ion
77	c3rqaA_	Alignment	not modelled	86.9	9	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase

77	c1gqa	Alignment	not modelled	88.9	9	mitochondrial 1; PDBTitle: crystal structure of ptpmt1 in complex with pi(5)p PDB header: hydrolase
78	c1u24A	Alignment	not modelled	86.8	18	Chain: A; PDB Molecule: myo-inositol hexaphosphate phosphohydrolase; PDBTitle: crystal structure of selenomonas ruminantium phytase PDB header: hydrolase
79	c4nx8A	Alignment	not modelled	86.8	21	Chain: A; PDB Molecule: protein-tyrosine phosphatase 2; PDBTitle: structure of a ptp-like phytase from bdellovibrio bacteriovorus PDB header: hydrolase
80	d1npya1	Alignment	not modelled	86.1	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
81	c2m3vA	Alignment	not modelled	84.0	15	PDB header: hydrolase Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of tyrosine phosphatase related to biofilm2 formation a (tpba) from pseudomonas aeruginosa PDB header: hydrolase
82	c4tvvA	Alignment	not modelled	81.6	21	Chain: A; PDB Molecule: tyrosine phosphatase ii superfamily protein; PDBTitle: crystal structure of lppa from legionella pneumophila Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
83	d1tyza	Alignment	not modelled	80.8	16	PDB header: hydrolase Chain: F; PDB Molecule: cyclin-dependent kinase inhibitor 3; PDBTitle: crystal structure analysis of kinase associated phosphatase (kap) with2 a substitution of the catalytic site cysteine (cys140) to a serine
84	c1fpzF	Alignment	not modelled	79.6	18	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
85	d1p15a	Alignment	not modelled	77.2	15	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
86	d1rxda	Alignment	not modelled	74.5	8	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
87	c2nz6A	Alignment	not modelled	74.4	9	PDB header: hydrolase Chain: A; PDB Molecule: receptor-type tyrosine-protein phosphatase eta; PDBTitle: crystal structure of the ptptr inactivating mutant c1239s
88	d1fpza	Alignment	not modelled	73.2	18	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
89	d1ohea2	Alignment	not modelled	72.5	7	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
90	d1lara1	Alignment	not modelled	72.4	11	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
91	d1g4us2	Alignment	not modelled	72.2	15	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
92	c2shpA	Alignment	not modelled	71.9	19	PDB header: tyrosine phosphatase Chain: A; PDB Molecule: shp-2; PDBTitle: tyrosine phosphatase shp-2
93	c5ncrA	Alignment	not modelled	71.1	17	PDB header: hydrolase Chain: A; PDB Molecule: tyrosine phosphatase; PDBTitle: oh1 from the orf virus: a tyrosine phosphatase that displays distinct2 structural features and triple substrate specificity PDB header: ribosome
94	c5m43A	Alignment	not modelled	70.6	16	Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of yvh1 phosphatase domain from chaetomium2 thermophilum PDB header: hydrolase
95	c3rz2B	Alignment	not modelled	70.4	12	Chain: B; PDB Molecule: protein tyrosine phosphatase type iva 1; PDBTitle: crystal of prl-1 complexed with peptide
96	c4rkka	Alignment	not modelled	70.0	17	PDB header: hydrolase Chain: A; PDB Molecule: laforin; PDBTitle: structure of a product bound phosphatase
97	c2c7sA	Alignment	not modelled	69.9	11	PDB header: hydrolase Chain: A; PDB Molecule: receptor-type tyrosine-protein phosphatase kappa; PDBTitle: crystal structure of human protein tyrosine phosphatase kappa at 1.95a2 resolution
98	c3s3fA	Alignment	not modelled	69.9	18	PDB header: hydrolase/hydrolase inhibitor Chain: A; PDB Molecule: tyrosine-protein phosphatase 10d; PDBTitle: crystal structure of the catalytic domain of ptp10d from drosophila2 melanogaster with a small molecule inhibitor vanadate
99	c2b9yA	Alignment	not modelled	69.7	14	PDB header: isomerase Chain: A; PDB Molecule: putative aminooxidase; PDBTitle: crystal structure of cla-producing fatty acid isomerase2 from p. acnes
100	c3vs9F	Alignment	not modelled	69.7	9	PDB header: transferase Chain: F; PDB Molecule: type iii polyketide synthase; PDBTitle: crystal structure of type iii pks arsc mutant
101	c5j8rC	Alignment	not modelled	69.2	10	PDB header: hydrolase Chain: C; PDB Molecule: tyrosine-protein phosphatase non-receptor type 12; PDBTitle: crystal structure of the catalytic domain of human protein tyrosine2 phosphatase non-receptor type 12 - k61r mutant
102	c2b3oA	Alignment	not modelled	68.2	19	PDB header: hydrolase Chain: A; PDB Molecule: tyrosine-protein phosphatase, non-receptor type

						PDBTitle: crystal structure of human tyrosine phosphatase shp-1 Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
103	d1larb1	Alignment	not modelled	67.8	11	PDB header: protein binding Chain: D; PDB Molecule: apolipoprotein a-i binding protein; PDBTitle: crystal structure of mouse apolipoprotein a-i binding protein
104	c2dg2D_	Alignment	not modelled	66.9	21	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
105	d1rpma_	Alignment	not modelled	66.1	11	PDB header: hydrolase Chain: A; PDB Molecule: phosphatidylinositol phosphatase ptpq; PDBTitle: crystal structure of catalytic domain of ptpq
106	c4ikcA_	Alignment	not modelled	65.5	16	PDB header: hydrolase, signaling protein Chain: A; PDB Molecule: tyrosine-protein phosphatase non-receptor type 6; PDBTitle: crystal structure of the full-length human protein tyrosine2 phosphatase shp-1
107	c3ps5A_	Alignment	not modelled	65.2	16	PDB header: hydrolase Chain: A; PDB Molecule: protein tyrosine phosphatase, receptor type, g variant PDBTitle: crystal structure of d1 and d2 catalytic domains of human protein2 tyrosine phosphatase gamma (d1+d2 ptpq)
108	c2nlkA_	Alignment	not modelled	65.0	21	PDB header: hydrolase Chain: A; PDB Molecule: receptor-type tyrosine-protein phosphatase s; PDBTitle: crystal structure of mouse ptpsigma
109	c3sr9A_	Alignment	not modelled	65.0	11	PDB header: hydrolase Chain: A; PDB Molecule: tyrosine-protein phosphatase yil113w; PDBTitle: ptyr bound form of sdp-1
110	c2j17A_	Alignment	not modelled	65.0	12	PDB header: hydrolase Chain: A; PDB Molecule: receptor-type tyrosine-protein phosphatase gamma; PDBTitle: crystal structure of the human tyrosine receptor phosphate gamma in2 complex with vanadate
111	c2hy3A_	Alignment	not modelled	64.4	16	PDB header: hydrolase Chain: C; PDB Molecule: dual specificity protein phosphatase 13; PDBTitle: crystal structure of tmdp
112	c2gwoC_	Alignment	not modelled	64.1	18	PDB header: hydrolase Chain: A; PDB Molecule: leukocyte common antigen; PDBTitle: crystal structure of the tandem phosphatase domains of rtp2 cd45 with a ptyr peptide
113	c1yguA_	Alignment	not modelled	64.0	16	PDB header: hydrolase Chain: B; PDB Molecule: tyrosine specific protein phosphatase, putative; PDBTitle: crystal structure of trypanosoma brucei protein tyrosine phosphatase2 tbptp1
114	c3m4uB_	Alignment	not modelled	63.8	11	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
115	d1vhra_	Alignment	not modelled	63.3	17	PDB header: hydrolase Chain: A; PDB Molecule: tyrosine-protein phosphatase non-receptor type 7; PDBTitle: crystal structure of the heptp catalytic domain c270s/d236a/q314a2 mutant
116	c2qdmA_	Alignment	not modelled	63.2	7	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
117	d1lara2	Alignment	not modelled	63.1	14	PDB header: hydrolase Chain: A; PDB Molecule: dual specificity phosphatase 26; PDBTitle: crystal structure of catalytic domain of dual specificity phosphatase2 26, ms0830 from homo sapiens
118	c2e0tA_	Alignment	not modelled	62.9	18	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
119	d1fpra_	Alignment	not modelled	62.9	15	PDB header: hydrolase Chain: A; PDB Molecule: protein tyrosine phosphatase, receptor type, b,; PDBTitle: structural studies of protein tyrosine phosphatase beta catalytic2 domain in complex with inhibitors
120	c2h04A_	Alignment	not modelled	62.6	16	