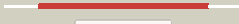



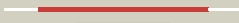



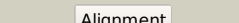

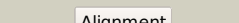

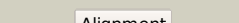











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3283_(sseA)_3664925_3665818
Date	Thu Aug 8 16:20:49 BST 2019
Unique Job ID	5fbab361e050b66f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hzuA_	 Alignment		100.0	100	PDB header: transferase Chain: A; PDB Molecule: thiosulfate sulfurtransferase ssea; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
2	c3aaxB_	 Alignment		100.0	50	PDB header: transferase Chain: B; PDB Molecule: putative thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
3	c1uarA_	 Alignment		100.0	52	PDB header: transferase Chain: A; PDB Molecule: rhodanese; PDBTitle: crystal structure of rhodanese from thermus thermophilus hb8
4	c6h98A_	 Alignment		100.0	27	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	27	PDB header: transferase Chain: A; PDB Molecule: putative thiosulfate sulfurtransferase ynje; PDBTitle: crystal structure of sulfur-free ynje
6	c1boiA_	 Alignment		100.0	28	PDB header: transferase Chain: A; PDB Molecule: rhodanese; PDBTitle: n-terminally truncated rhodanese
7	c1e0cA_	 Alignment		100.0	29	PDB header: sulfurtransferase Chain: A; PDB Molecule: sulfurtransferase; PDBTitle: sulfurtransferase from azotobacter vinelandii
8	c1okgA_	 Alignment		100.0	21	PDB header: transferase Chain: A; PDB Molecule: possible 3-mercaptopyruvate sulfurtransferase; PDBTitle: 3-mercaptopyruvate sulfurtransferase from leishmania major
9	c3utnX_	 Alignment		100.0	21	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	25	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	c2eg4B_	Alignment		100.0	26	PDB header: transferase Chain: B: PDB Molecule: probable thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase
13	c1yt8A_	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: thiosulfate sulfurtransferase; PDBTitle: crystal structure of thiosulfate sulfurtransferase from pseudomonas2 aeruginosa
14	c6mxvA_	Alignment		100.0	16	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
15	c3tp9B_	Alignment		100.0	23	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	55	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		100.0	30	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
19	d1e0ca1	Alignment		100.0	28	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
20	d1okga1	Alignment		100.0	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
21	d1uara2	Alignment	not modelled	99.9	52	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
22	d1okga2	Alignment	not modelled	99.9	25	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
23	d1rha2	Alignment	not modelled	99.9	24	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
24	d1e0ca2	Alignment	not modelled	99.9	35	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
25	d1yt8a3	Alignment	not modelled	99.9	21	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
26	c6bevB_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: B: PDB Molecule: thiosulfate sulfurtransferase/rhodanese-like domain- PDBTitle: human single domain sulfurtransferase tstd1
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	c3d1pA_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase yor285w; PDBTitle: atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae

29	d1yt8a1	Alignment	not modelled	99.8	15	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
30	c5ve5C	Alignment	not modelled	99.8	24	PDB header: oxidoreductase, transferase Chain: C: PDB Molecule: bpprf; PDBTitle: crystal structure of persulfide dioxygenase rhodanese fusion protein2 with rhodanese domain inactivating mutation (c314s) from burkholderia3 phytotfirmans in complex with glutathione
31	c2moiA	Alignment	not modelled	99.8	15	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
32	d1urha2	Alignment	not modelled	99.8	23	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
33	c3nhvE	Alignment	not modelled	99.8	24	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	d1yt8a4	Alignment	not modelled	99.8	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
35	c2hhgA	Alignment	not modelled	99.8	18	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
36	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
37	d1tq1a	Alignment	not modelled	99.8	14	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
38	c3emeA	Alignment	not modelled	99.8	20	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
39	d1qxna	Alignment	not modelled	99.8	16	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
40	c3gk5A	Alignment	not modelled	99.8	18	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
41	c3f4aA	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ygr203w; PDBTitle: structure of ygr203w, a yeast protein tyrosine phosphatase of the2 rhodanese family
42	c3g5jA	Alignment	not modelled	99.8	14	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
43	d1yt8a2	Alignment	not modelled	99.8	21	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
44	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
45	c3k9rA	Alignment	not modelled	99.8	25	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 anabaena sp. northeast structural genomics consortium target3 nsr437c.
46	c4f67A	Alignment	not modelled	99.8	10	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	c3fojA	Alignment	not modelled	99.8	22	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.
48	c2fsxA	Alignment	not modelled	99.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cog0607: rhodanese-related sulfurtransferase; PDBTitle: crystal structure of rv0390 from m. tuberculosis
49	c2dcqA	Alignment	not modelled	99.7	9	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
50	d1gmxA	Alignment	not modelled	99.7	15	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
51	d1whba	Alignment	not modelled	99.7	14	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
52	c2j6pF	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: F: PDB Molecule: sb(v)-as(v) reductase; PDBTitle: structure of as-sb reductase from leishmania major

53	c2k0zA_	Alignment	not modelled	99.7	17	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
54	c2vswB_	Alignment	not modelled	99.7	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
55	d1c25a_	Alignment	not modelled	99.7	17	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
56	d1ymka1	Alignment	not modelled	99.6	14	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
57	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
58	d2qwfa1	Alignment	not modelled	99.6	15	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
59	d1hzma_	Alignment	not modelled	99.6	19	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
60	c3icrA_	Alignment	not modelled	99.6	32	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a-disulfide reductase; PDBTitle: crystal structure of oxidized bacillus anthracis coadr-rhd
61	c2jtqA_	Alignment	not modelled	99.6	19	PDB header: transferase Chain: A: PDB Molecule: phage shock protein e; PDBTitle: rhodanese from e.coli
62	c2oucB_	Alignment	not modelled	99.6	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	c3op3A_	Alignment	not modelled	99.6	16	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
64	c2uzqE_	Alignment	not modelled	99.6	14	PDB header: hydrolase Chain: E: PDB Molecule: m-phase inducer phosphatase 2; PDBTitle: protein phosphatase, new crystal form
65	c3r2uC_	Alignment	not modelled	99.3	17	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	17	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	96.0	17	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	95.1	16	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Mycobacterial PtpB-like
69	c2oz5A_	Alignment	not modelled	94.6	18	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
70	c6byfl_	Alignment	not modelled	93.4	10	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	c3gxgA_	Alignment	not modelled	92.8	18	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
72	c3flhC_	Alignment	not modelled	91.9	19	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
73	d1npya1	Alignment	not modelled	91.8	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
74	d1xria_	Alignment	not modelled	91.4	13	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
75	c1u24A_	Alignment	not modelled	91.0	19	PDB header: hydrolase Chain: A: PDB Molecule: myo-inositol hexaphosphate phosphohydrolase; PDBTitle: crystal structure of selenomonas ruminantium phytase
76	c5cd1B_	Alignment	not modelled	90.9	17	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
77	c2imnA_	Alignment	not modelled	90.6	17	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 23;

77	c2imgA	Alignment	not modelled	90.0	17	PDBTitle: crystal structure of dual specificity protein phosphatase2 23 from homo sapiens in complex with ligand malate ion PDB header: hydrolase
78	c4nx8A	Alignment	not modelled	90.1	16	Chain: A; PDB Molecule: protein-tyrosine phosphatase 2; PDBTitle: structure of a ptp-like phytase from bdellovibrio bacteriovorus
79	c2i6oA	Alignment	not modelled	89.4	12	PDB header: hydrolase Chain: A; PDB Molecule: sulfolobus solfataricus protein tyrosine phosphatase PDBTitle: crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g-(p)y-k-n
80	c4tvvA	Alignment	not modelled	88.1	20	PDB header: hydrolase Chain: A; PDB Molecule: tyrosine phosphatase ii superfamily protein; PDBTitle: crystal structure of lppa from legionella pneumophila
81	c3rgqA	Alignment	not modelled	87.6	12	PDB header: hydrolase Chain: A; PDB Molecule: protein-tyrosine phosphatase mitochondrial 1; PDBTitle: crystal structure of ptptm1 in complex with pi(5)p
82	c4rkkA	Alignment	not modelled	87.3	16	PDB header: hydrolase Chain: A; PDB Molecule: laforin; PDBTitle: structure of a product bound phosphatase
83	c1yn9B	Alignment	not modelled	87.2	15	PDB header: hydrolase Chain: B; PDB Molecule: polynucleotide 5'-phosphatase; PDBTitle: crystal structure of baculovirus rna 5'-phosphatase2 complexed with phosphate
84	c5ergA	Alignment	not modelled	87.2	11	PDB header: transferase Chain: A; PDB Molecule: trna (adenine(58)-n(1))-methyltransferase non-catalytic PDBTitle: crystal structure of the two-subunit trna m1a58 methyltransferase2 trm6-trm61 in complex with sam
85	d1vi2a1	Alignment	not modelled	85.6	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
86	c1fpzF	Alignment	not modelled	84.5	13	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
87	d1ohea2	Alignment	not modelled	81.4	9	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
88	c4r30C	Alignment	not modelled	81.1	17	PDB header: hydrolase Chain: C; PDB Molecule: laforin; PDBTitle: structure of human laforin dual specificity phosphatase domain
89	d1fpza	Alignment	not modelled	81.0	13	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
90	c3f41B	Alignment	not modelled	80.4	11	PDB header: hydrolase Chain: B; PDB Molecule: phytase; PDBTitle: structure of the tandemly repeated protein tyrosine2 phosphatase like phytase from mitsuokella multacida
91	c3rz2B	Alignment	not modelled	80.2	17	PDB header: hydrolase Chain: B; PDB Molecule: protein tyrosine phosphatase type iva 1; PDBTitle: crystal of prl-1 complexed with peptide
92	c1npyA	Alignment	not modelled	79.7	13	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical shikimate 5-dehydrogenase-like protein hi0607; PDBTitle: structure of shikimate 5-dehydrogenase-like protein hi0607
93	c2m3vA	Alignment	not modelled	79.2	12	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
94	c1zzwA	Alignment	not modelled	79.2	17	PDB header: hydrolase Chain: A; PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of catalytic domain of human map kinase2 phosphatase 5
95	c2g6zB	Alignment	not modelled	78.8	15	PDB header: hydrolase Chain: B; PDB Molecule: dual specificity protein phosphatase 5; PDBTitle: crystal structure of human dusp5
96	c1oheA	Alignment	not modelled	78.5	8	PDB header: hydrolase Chain: A; PDB Molecule: cdc14b2 phosphatase; PDBTitle: structure of cdc14b phosphatase with a peptide ligand
97	c2oudA	Alignment	not modelled	77.7	17	PDB header: hydrolase Chain: A; PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the catalytic domain of human mkp5
98	c5ccbB	Alignment	not modelled	75.7	17	PDB header: transferase/rna Chain: B; PDB Molecule: trna (adenine(58)-n(1))-methyltransferase non-catalytic PDBTitle: crystal structure of human m1a58 methyltransferase in a complex with2 trna3lys and sah
99	c2hcmA	Alignment	not modelled	75.4	20	PDB header: hydrolase Chain: A; PDB Molecule: dual specificity protein phosphatase; PDBTitle: crystal structure of mouse putative dual specificity phosphatase2 complexed with zinc tungstate, new york structural genomics3 consortium
100	c2r0bA	Alignment	not modelled	74.7	15	PDB header: hydrolase Chain: A; PDB Molecule: serine/threonine/tyrosine-interacting protein; PDBTitle: crystal structure of human tyrosine phosphatase-like2 serine/threonine/tyrosine-interacting protein
101	c5z5bA	Alignment	not modelled	74.3	13	PDB header: hydrolase Chain: A; PDB Molecule: protein-tyrosine phosphatase; PDBTitle: crystal structure of tk-tp in the g95a mutant form
						PDB header: hydrolase Chain: B; PDB Molecule: rna/rnp complex-1-interacting

102	c4nyhB_	Alignment	not modelled	74.2	14	phosphatase; PDBTitle: orthorhombic crystal form of pir1 dual specificity phosphatase core
103	c4jmkA_	Alignment	not modelled	74.0	17	PDB header: hydrolase Chain: A; PDB Molecule: dual specificity protein phosphatase 8; PDBTitle: structure of dusp8
104	c1yz4A_	Alignment	not modelled	73.8	15	PDB header: hydrolase Chain: A; PDB Molecule: dual specificity phosphatase-like 15 isoform a; PDBTitle: crystal structure of dusp15
105	c6i28A_	Alignment	not modelled	73.7	14	PDB header: viral protein Chain: A; PDB Molecule: orf98 ptp-2; PDBTitle: crystal structure of cydia pomonella ptp-2 phosphatase
106	c2wgpA_	Alignment	not modelled	73.7	16	PDB header: hydrolase Chain: A; PDB Molecule: dual specificity protein phosphatase 14; PDBTitle: crystal structure of human dual specificity phosphatase 14
107	d1mkpa_	Alignment	not modelled	73.7	17	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
108	c5xjvA_	Alignment	not modelled	72.8	19	PDB header: hydrolase Chain: A; PDB Molecule: dual specificity protein phosphatase 13 isoform a; PDBTitle: two intermediate states of conformation switch in dual specificity2 phosphatase 13a
109	d1rxda_	Alignment	not modelled	72.7	15	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
110	d1vhra_	Alignment	not modelled	72.3	23	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
111	d1g4us2	Alignment	not modelled	72.2	19	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
112	c2shpA_	Alignment	not modelled	71.9	27	PDB header: tyrosine phosphatase Chain: A; PDB Molecule: shp-2; PDBTitle: tyrosine phosphatase shp-2
113	c4ki9A_	Alignment	not modelled	71.1	7	PDB header: hydrolase Chain: A; PDB Molecule: dual specificity protein phosphatase 12; PDBTitle: crystal structure of the catalytic domain of human dusp12 at 2.0 a2 resolution
114	c3emuA_	Alignment	not modelled	70.8	7	PDB header: hydrolase Chain: A; PDB Molecule: leucine rich repeat and phosphatase domain containing PDBTitle: crystal structure of a leucine rich repeat and phosphatase domain2 containing protein from entamoeba histolytica
115	c3ohgA_	Alignment	not modelled	70.6	22	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein from duf2233 family; PDBTitle: crystal structure of a protein with unknown function from duf22332 family (bacova_00430) from bacteroides ovatus at 1.80 a resolution
116	d1fpra_	Alignment	not modelled	70.2	14	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
117	c3i36A_	Alignment	not modelled	69.9	19	PDB header: hydrolase Chain: A; PDB Molecule: vascular protein tyrosine phosphatase 1; PDBTitle: crystal structure of rat protein tyrosine phosphatase eta catalytic2 domain
118	c2b3oA_	Alignment	not modelled	69.5	16	PDB header: hydrolase Chain: A; PDB Molecule: tyrosine-protein phosphatase, non-receptor type PDBTitle: crystal structure of human tyrosine phosphatase shp-1
119	c2nt2C_	Alignment	not modelled	69.4	15	PDB header: hydrolase Chain: C; PDB Molecule: protein phosphatase slingshot homolog 2; PDBTitle: crystal structure of slingshot phosphatase 2
120	c3nmeA_	Alignment	not modelled	68.6	14	PDB header: hydrolase Chain: A; PDB Molecule: sex4 glucan phosphatase; PDBTitle: structure of a plant phosphatase