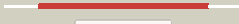



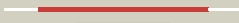





















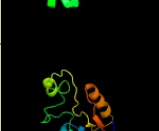
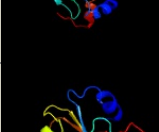





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0390 (-) _469594_470016
Date	Tue Jul 23 14:50:46 BST 2019
Unique Job ID	794fd568ab009368

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fsxA_	 Alignment		100.0	98	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cog0607: rhodanese-related sulfurtransferase; PDBTitle: crystal structure of rv0390 from m. tuberculosis
2	c2dcqA_	 Alignment		99.9	28	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
3	d1yt8a1	 Alignment		99.9	28	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
4	c1yt8A_	 Alignment		99.9	28	PDB header: transferase Chain: A: PDB Molecule: thiosulfate sulfurtransferase; PDBTitle: crystal structure of thiosulfate sulfurtransferase from pseudomonas2 aeruginosa
5	d1qxna_	 Alignment		99.9	30	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
6	c2hhgA_	 Alignment		99.9	29	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
7	c3tp9B_	 Alignment		99.9	28	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
8	c1e0cA_	 Alignment		99.9	15	PDB header: sulfurtransferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: sulfurtransferase from azotobacter vinelandii
9	c1urhA_	 Alignment		99.9	16	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
10	c3d1pA_	 Alignment		99.9	23	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase yor285w; PDBTitle: atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae
11	d1e0ca1	 Alignment		99.9	16	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)

12	c3aaxB	Alignment		99.9	15	PDB header: transferase Chain: B: PDB Molecule: putative thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
13	c1boiA	Alignment		99.9	16	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: n-terminally truncated rhodanese
14	c3ilmD	Alignment		99.9	19	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
15	c6mxvA	Alignment		99.9	20	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
16	d1tq1a	Alignment		99.9	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
17	c3hzuA	Alignment		99.9	12	PDB header: transferase Chain: A: PDB Molecule: thiosulfate sulfurtransferase ssea; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
18	d1rha1	Alignment		99.9	15	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
19	c5ve5C	Alignment		99.9	31	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 phytofirmans in complex with glutathione
20	c3i2vA	Alignment		99.9	18	PDB header: transferase Chain: A: PDB Molecule: adenylyltransferase and sulfurtransferase mocs3; PDBTitle: crystal structure of human mocs3 rhodanese-like domain
21	c1uarA	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: crystal structure of rhodanese from thermus thermophilus hb8
22	c3ippA	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase ynje; PDBTitle: crystal structure of sulfur-free ynje
23	d1yt8a3	Alignment	not modelled	99.8	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
24	d1yt8a4	Alignment	not modelled	99.8	17	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
25	d1uara2	Alignment	not modelled	99.8	21	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
26	c3emeA	Alignment	not modelled	99.8	26	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
27	c6h98A	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: native crystal structure of anaerobic ergothioneine biosynthesis2 enzyme from chlorobium limicola.
28	d1urha1	Alignment	not modelled	99.8	16	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
29	c4f67A	Alignment	not modelled	99.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0176 protein lpg2838; PDBTitle: three dimensional structure of the double mutant of

29	c4t07A	Alignment	not modelled	99.8	17	upf0176 protein2 lpg2838 from legionella pneumophila at the resolution 1.8a, northeast3 structural genomics consortium (nesg) target lgr82
30	c3fojA	Alignment	not modelled	99.8	25	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.
31	c3utnX	Alignment	not modelled	99.8	14	PDB header: transferase Chain: X: PDB Molecule: thiosulfate sulfurtransferase tum1; PDBTitle: crystal structure of tum1 protein from saccharomyces cerevisiae
32	c3olhA	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: human 3-mercaptopyruvate sulfurtransferase
33	d1yt8a2	Alignment	not modelled	99.8	22	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
34	c6bevB	Alignment	not modelled	99.8	20	PDB header: transferase Chain: B: PDB Molecule: thiosulfate sulfurtransferase/rhodanese-like domain- PDBTitle: human single domain sulfurtransferase tstd1
35	d1okga1	Alignment	not modelled	99.8	19	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
36	d1uara1	Alignment	not modelled	99.8	11	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
37	c3k9rA	Alignment	not modelled	99.8	19	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.
38	c3nhvE	Alignment	not modelled	99.8	21	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
39	c3gk5A	Alignment	not modelled	99.8	21	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
40	c2moiA	Alignment	not modelled	99.8	25	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
41	c1okgA	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: possible 3-mercaptopyruvate sulfurtransferase; PDBTitle: 3-mercaptopyruvate sulfurtransferase from leishmania major
42	d1t3ka	Alignment	not modelled	99.8	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
43	d1e0ca2	Alignment	not modelled	99.8	14	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
44	c3g5jA	Alignment	not modelled	99.8	21	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
45	d1gmxa	Alignment	not modelled	99.8	26	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
46	c2k0zA	Alignment	not modelled	99.8	24	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
47	c3icrA	Alignment	not modelled	99.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a-disulfide reductase; PDBTitle: crystal structure of oxidized bacillus anthracis coad-rhd
48	d1okga2	Alignment	not modelled	99.7	13	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
49	c2jtqA	Alignment	not modelled	99.7	25	PDB header: transferase Chain: A: PDB Molecule: phage shock protein e; PDBTitle: rhodanese from e.coli
50	c3f4aA	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ygr203w; PDBTitle: structure of ygr203w, a yeast protein tyrosine phosphatase of the2 rhodanese family
51	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
52	d1rhsa2	Alignment	not modelled	99.7	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
53	d1c25a	Alignment	not modelled	99.7	19	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain

54	c3ntaA	Alignment	not modelled	99.7	30	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
55	d1ymka1	Alignment	not modelled	99.7	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
56	c2eg4B	Alignment	not modelled	99.6	14	PDB header: transferase Chain: B: PDB Molecule: probable thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase
57	d1urha2	Alignment	not modelled	99.6	11	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
58	c3op3A	Alignment	not modelled	99.6	19	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
59	c2uzqE	Alignment	not modelled	99.6	22	PDB header: hydrolase Chain: E: PDB Molecule: m-phase inducer phosphatase 2; PDBTitle: protein phosphatase, new crystal form
60	c2vswB	Alignment	not modelled	99.6	13	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
61	c1wv9B	Alignment	not modelled	99.5	21	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
62	d1hzma	Alignment	not modelled	99.5	14	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
63	d1whba	Alignment	not modelled	99.5	14	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
64	c2oucB	Alignment	not modelled	99.5	11	PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the map kinase binding domain of mkp5
65	d2gwfa1	Alignment	not modelled	99.5	16	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
66	c3r2uC	Alignment	not modelled	99.4	8	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
67	c3gxqA	Alignment	not modelled	94.3	9	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
68	c3flhC	Alignment	not modelled	94.2	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
69	c2f46A	Alignment	not modelled	91.5	14	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
70	c5ghaC	Alignment	not modelled	88.5	17	PDB header: transferase/transport protein Chain: C: PDB Molecule: sulfur transferase ttua; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
71	c3vrhA	Alignment	not modelled	87.7	14	PDB header: rna binding protein Chain: A: PDB Molecule: putative uncharacterized protein ph0300; PDBTitle: crystal structure of ph0300
72	c3rgqA	Alignment	not modelled	83.4	15	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase mitochondrial 1; PDBTitle: crystal structure of ptpmt1 in complex with pi(5)p
73	d1xria	Alignment	not modelled	83.2	13	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
74	d1ywfa1	Alignment	not modelled	80.0	19	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Mycobacterial PtpB-like
75	c3ohqA	Alignment	not modelled	77.7	18	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
76	d1npya1	Alignment	not modelled	75.0	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
77	c2i6oA	Alignment	not modelled	72.6	10	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
78	c3bicA	Alignment	not modelled	71.8	10	PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase, mitochondrial precursor; PDBTitle: crystal structure of human methylmalonyl-coa mutase
						PDB header: isomerase

79	cle1cA_	Alignment	not modelled	71.1	13	Chain: A: PDB Molecule: methylmalonyl-coa mutase alpha chain; PDBTitle: methylmalonyl-coa mutase h244a mutant
80	c6ozdB_	Alignment	not modelled	71.0	20	PDB header: structural genomics Chain: B: PDB Molecule: putative exported protein; PDBTitle: crystal structure of putative exported protein (bpps2145) from2 burkholderia pseudomallei k96243
81	d1ni5a1	Alignment	not modelled	70.3	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
82	c2y96A_	Alignment	not modelled	68.8	13	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase dupd1; PDBTitle: structure of human dual-specificity phosphatase 27
83	c4kyrA_	Alignment	not modelled	67.3	13	PDB header: hydrolase, sugar binding protein Chain: A: PDB Molecule: phosphoglucan phosphatase lsf2, chloroplastic; PDBTitle: structure of a product bound plant phosphatase
84	c4nyhB_	Alignment	not modelled	67.2	6	PDB header: hydrolase Chain: B: PDB Molecule: rna/rnp complex-1-interacting phosphatase; PDBTitle: orthorhombic crystal form of pir1 dual specificity phosphatase core
85	c5h3kA_	Alignment	not modelled	65.2	19	PDB header: unknown function Chain: A: PDB Molecule: slr0280 protein; PDBTitle: crystal structure of a hypothetical protein from synechocystis
86	d1j3a_	Alignment	not modelled	62.6	19	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
87	c3nmeA_	Alignment	not modelled	61.0	10	PDB header: hydrolase Chain: A: PDB Molecule: sex4 glucan phosphatase; PDBTitle: structure of a plant phosphatase
88	d1k92a1	Alignment	not modelled	60.6	11	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
89	d1vhra_	Alignment	not modelled	60.0	15	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
90	c1fpzF_	Alignment	not modelled	59.6	14	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
91	c2e0tA_	Alignment	not modelled	58.0	21	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
92	c2gwoC_	Alignment	not modelled	58.0	14	PDB header: hydrolase Chain: C: PDB Molecule: dual specificity protein phosphatase 13; PDBTitle: crystal structure of tmpd
93	c2oz5A_	Alignment	not modelled	57.9	15	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
94	c4kr7A_	Alignment	not modelled	57.8	31	PDB header: transferase/rna Chain: A: PDB Molecule: probable trna sulfurtransferase; PDBTitle: crystal structure of a 4-thiouridine synthetase - rna complex with2 bound atp
95	c5ergB_	Alignment	not modelled	57.5	14	PDB header: transferase Chain: B: PDB Molecule: trna (adenine(58)-n(1))-methyltransferase catalytic subunit PDBTitle: crystal structure of the two-subunit trna m1a58 methyltransferase2 trm6-trm61 in complex with sam
96	c2l18A_	Alignment	not modelled	57.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase; PDBTitle: an arsenate reductase in the phosphate binding state
97	c3t38B_	Alignment	not modelled	57.2	18	PDB header: oxidoreductase Chain: B: PDB Molecule: arsenate reductase; PDBTitle: corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1'
98	d1fpza_	Alignment	not modelled	55.8	14	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
99	c2b9yA_	Alignment	not modelled	54.6	11	PDB header: isomerase Chain: A: PDB Molecule: putative aminooxidase; PDBTitle: crystal structure of cla-producing fatty acid isomerase2 from p. acnes
100	c2vx0B_	Alignment	not modelled	54.4	19	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
101	c2wgpA_	Alignment	not modelled	53.8	17	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 14; PDBTitle: crystal structure of human dual specificity phosphatase 14
102	d1xnga1	Alignment	not modelled	53.3	12	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
103	c4cdgA_	Alignment	not modelled	52.5	17	PDB header: hydrolase Chain: A: PDB Molecule: bloom syndrome protein; PDBTitle: crystal structure of the bloom's syndrome helicase blm in complex with2 nanobody PDB header: rna binding protein,hydrolase Chain: A: PDB Molecule: heat resistant rna dependent atpase;

104	c3i32A_	Alignment	not modelled	51.3	12	PDBTitle: dimeric structure of a hera helicase fragment including the c-terminal2 reca domain, the dimerization domain, and the rna binding domain
105	d1wy5a1	Alignment	not modelled	51.3	9	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
106	d7reqa2	Alignment	not modelled	50.2	14	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
107	c5xjvA_	Alignment	not modelled	49.2	13	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
108	c3rh0A_	Alignment	not modelled	48.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase; PDBTitle: corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
109	d1oywa3	Alignment	not modelled	48.5	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
110	c2c5sA_	Alignment	not modelled	48.1	24	PDB header: rna-binding protein Chain: A: PDB Molecule: probable thiamine biosynthesis protein thii; PDBTitle: crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
111	d1jf8a_	Alignment	not modelled	47.9	16	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
112	c1k97A_	Alignment	not modelled	44.6	12	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
113	d1d5ra2	Alignment	not modelled	44.1	8	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
114	c1vbka_	Alignment	not modelled	44.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1313; PDBTitle: crystal structure of ph1313 from pyrococcus horikoshii ot3
115	d1a1va2	Alignment	not modelled	42.4	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
116	c6hcyA_	Alignment	not modelled	41.4	12	PDB header: membrane protein Chain: A: PDB Molecule: metalloreductase steap4; PDBTitle: human steap4 bound to nadp, fad, heme and fe(iii)-nta.
117	c2oudA_	Alignment	not modelled	41.0	15	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the catalytic domain of human mkp5
118	d1nka4	Alignment	not modelled	39.8	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
119	d1vl2a1	Alignment	not modelled	39.8	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
120	c5xavB_	Alignment	not modelled	39.5	21	PDB header: biosynthetic protein Chain: B: PDB Molecule: intracellular polyhydroxyalkanoate synthase; PDBTitle: structure of phac from chromobacterium sp. usm2