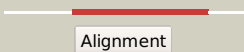

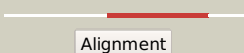
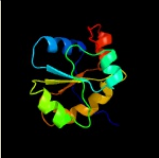


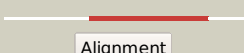
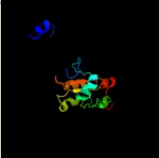





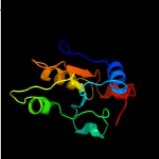



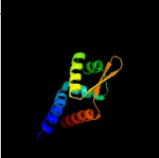






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1674c_(-) _1899267_1899923
Date	Fri Aug 2 13:30:27 BST 2019
Unique Job ID	4aade0c44ab63387

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3tp9B_</a>	 Alignment		99.9	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase and rhodanese domain protein; <b>PDBTitle:</b> crystal structure of alicyclobacillus acidocaldarius protein with2 beta-lactamase and rhodanese domains
2	<a href="#">c1yt8A_</a>	 Alignment		99.9	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiosulfate sulfurtransferase; <b>PDBTitle:</b> crystal structure of thiosulfate sulfurtransferase from pseudomonas2 aeruginosa
3	<a href="#">d1yt8a1</a>	 Alignment		99.9	23	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
4	<a href="#">c5ve5C_</a>	 Alignment		99.9	27	<b>PDB header:</b> oxidoreductase, transferase <b>Chain:</b> C: <b>PDB Molecule:</b> bpprf; <b>PDBTitle:</b> crystal structure of persulfide dioxygenase rhodanese fusion protein2 with rhodanese domain inactivating mutation (c314s) from burkholderia3 phytotfirmans in complex with glutathione
5	<a href="#">d1yt8a3</a>	 Alignment		99.9	27	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
6	<a href="#">c3nhvE_</a>	 Alignment		99.9	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> bh2092 protein; <b>PDBTitle:</b> crystal structure of bh2092 protein from bacillus halodurans,2 northeast structural genomics consortium target bhr228f
7	<a href="#">c2hhgA_</a>	 Alignment		99.9	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein rpa3614; <b>PDBTitle:</b> structure of protein of unknown function rpa3614, possible tyrosine2 phosphatase, from rhodopseudomonas palustris cga009
8	<a href="#">c3emeA_</a>	 Alignment		99.9	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> rhodanese-like domain protein; <b>PDBTitle:</b> crystal structure of rhodanese-like domain protein from2 staphylococcus aureus
9	<a href="#">c2kkoB_</a>	 Alignment		99.9	42	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> possible transcriptional regulatory protein <b>PDBTitle:</b> solution nmr structure of the homodimeric winged helix-turn-2 helix dna-binding domain (fragment 1-100) mb0332 from3 mycobacterium bovis, a possible arsr-family transcriptional4 regulator. northeast structural genomics consortium target5 mbr242e.
10	<a href="#">c3gk5A_</a>	 Alignment		99.9	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized rhodanese-related protein tvg0868615; <b>PDBTitle:</b> crystal structure of rhodanese-related protein (tvg0868615) from2 thermoplasma volcanium, northeast structural genomics consortium3 target tvr109a
11	<a href="#">c3ilmD_</a>	 Alignment		99.9	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> alr3790 protein; <b>PDBTitle:</b> crystal structure of the alr3790 protein from anabaena sp. northeast2 structural genomics consortium target nsr437h

12	<a href="#">dlr1ua_</a>	Alignment		99.8	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
13	<a href="#">dlqxnA_</a>	Alignment		99.8	22	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Single-domain sulfurtransferase
14	<a href="#">c6mxvA_</a>	Alignment		99.8	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> rhodanese-like family protein; <b>PDBTitle:</b> the crystal structure of a rhodanese-like family protein from2 francisella tularensis subsp. tularensis schu s4
15	<a href="#">digmxA_</a>	Alignment		99.8	21	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Single-domain sulfurtransferase
16	<a href="#">dlr1ta_</a>	Alignment		99.8	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
17	<a href="#">c2oqgA_</a>	Alignment		99.8	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family protein; <b>PDBTitle:</b> arsr-like transcriptional regulator from rhodococcus sp. rha1
18	<a href="#">c1r22B_</a>	Alignment		99.8	29	<b>PDB header:</b> transcription repressor <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor smtb; <b>PDBTitle:</b> crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
19	<a href="#">c4omzG_</a>	Alignment		99.8	35	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> nolr; <b>PDBTitle:</b> crystal structure of nolr from sinorhizobium fredii
20	<a href="#">c3fojA_</a>	Alignment		99.8	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of ssp1007 from staphylococcus2 saprophyticus subsp. saprophyticus. northeast structural3 genomics target syr101a.
21	<a href="#">c2lkpB_</a>	Alignment	not modelled	99.8	32	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, arsr family; <b>PDBTitle:</b> solution structure of apo-nmr
22	<a href="#">c3k9rA_</a>	Alignment	not modelled	99.8	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> alr3790 protein; <b>PDBTitle:</b> x-ray structure of the rhodanese-like domain of the alr3790 protein2 from anabaena sp. northeast structural genomics consortium target3 nsr437c.
23	<a href="#">d1yt8a4</a>	Alignment	not modelled	99.8	25	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
24	<a href="#">c4f67A_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0176 protein lpg2838; <b>PDBTitle:</b> three dimensional structure of the double mutant of upf0176 protein2 lpg2838 from legionella pneumophila at the resolution 1.8a, northeast3 structural genomics consortium (nesg) target lgr82
25	<a href="#">c3pqkD_</a>	Alignment	not modelled	99.8	32	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> biofilm growth-associated repressor; <b>PDBTitle:</b> crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
26	<a href="#">c2moiA_</a>	Alignment	not modelled	99.8	25	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> inner membrane protein ygap; <b>PDBTitle:</b> 3d nmr structure of the cytoplasmic rhodanese domain of the inner2 membrane protein ygap from escherichia coli
27	<a href="#">d1tq1a_</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Single-domain sulfurtransferase
28	<a href="#">c3ithA_</a>	Alignment	not modelled	99.8	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription activator hlyu;

28	<a href="#">c3jrhA</a>	Alignment	not modelled	99.8	29	<b>PDBTitle:</b> crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
29	<a href="#">d1t3ka</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Cell cycle control phosphatase, catalytic domain
30	<a href="#">d1e0ca1</a>	Alignment	not modelled	99.8	29	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
31	<a href="#">d1yt8a2</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
32	<a href="#">c2zkzC</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional repressor pagr; <b>PDBTitle:</b> crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
33	<a href="#">c3f6vA</a>	Alignment	not modelled	99.8	26	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family protein; <b>PDBTitle:</b> crystal structure of possible transcriptional regulator for arsenical2 resistance
34	<a href="#">c3d1pA</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thiosulfate sulfurtransferase yor285w; <b>PDBTitle:</b> atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae
35	<a href="#">c2k0zA</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein hp1203; <b>PDBTitle:</b> solution nmr structure of protein hp1203 from helicobacter pylori2 26695. northeast structural genomics consortium (nesg) target3 pt1/ontario center for structural proteomics target hp1203
36	<a href="#">c1e0cA</a>	Alignment	not modelled	99.8	32	<b>PDB header:</b> sulfurtransferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfurtransferase; <b>PDBTitle:</b> sulfurtransferase from azotobacter vinelandii
37	<a href="#">c5xpbB</a>	Alignment	not modelled	99.8	37	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator rv0081; <b>PDBTitle:</b> crystal structure of m.tuberculosis rv0081
38	<a href="#">c3icrA</a>	Alignment	not modelled	99.8	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme a-disulfide reductase; <b>PDBTitle:</b> crystal structure of oxidized bacillus anthracis coadr-rhd
39	<a href="#">c2fsxA</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cog0607: rhodanese-related sulfurtransferase; <b>PDBTitle:</b> crystal structure of rv0390 from m. tuberculosis
40	<a href="#">c1urhA</a>	Alignment	not modelled	99.8	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-mercaptopyruvate sulfurtransferase; <b>PDBTitle:</b> the "rhodanese" fold and catalytic mechanism of2 3-mercaptopyruvate sulfotransferases: crystal structure3 of ssea from escherichia coli
41	<a href="#">c3aaxB</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative thiosulfate sulfurtransferase; <b>PDBTitle:</b> crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
42	<a href="#">c3cuoB</a>	Alignment	not modelled	99.8	33	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator ygav; <b>PDBTitle:</b> crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
43	<a href="#">c3i2vA</a>	Alignment	not modelled	99.8	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylyltransferase and sulfurtransferase mocs3; <b>PDBTitle:</b> crystal structure of human mocs3 rhodanese-like domain
44	<a href="#">c6j05B</a>	Alignment	not modelled	99.8	34	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator arsr; <b>PDBTitle:</b> structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
45	<a href="#">c3hzuA</a>	Alignment	not modelled	99.8	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiosulfate sulfurtransferase ssea; <b>PDBTitle:</b> crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
46	<a href="#">c6bevB</a>	Alignment	not modelled	99.8	35	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thiosulfate sulfurtransferase/rhodanese-like domain- <b>PDBTitle:</b> human single domain sulfurtransferase tstd1
47	<a href="#">c3ntaA</a>	Alignment	not modelled	99.8	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fad-dependent pyridine nucleotide-disulphide <b>PDBTitle:</b> structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
48	<a href="#">c6h98A</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfurtransferase; <b>PDBTitle:</b> native crystal structure of anaerobic ergothioneine biosynthesis2 enzyme from chlorobium limicola.
49	<a href="#">c6j0eB</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> arsenic responsive repressor arsr; <b>PDBTitle:</b> structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
50	<a href="#">c2jscB</a>	Alignment	not modelled	99.8	33	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator rv1994c/mt2050; <b>PDBTitle:</b> nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
51	<a href="#">c3g5jA</a>	Alignment	not modelled	99.8	25	<b>PDB header:</b> nucleotide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative atp/gtp binding protein; <b>PDBTitle:</b> crystal structure of n-terminal domain of putative atp/gtp binding2 protein from clostridium difficile 630
						<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulator, arsr

52	<a href="#">c3f6oB_</a>	Alignment	not modelled	99.8	22	family <b>PDBTitle:</b> crystal structure of arsr family transcriptional regulator,2 rha00566
53	<a href="#">c1boiA_</a>	Alignment	not modelled	99.8	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rhodanese; <b>PDBTitle:</b> n-terminally truncated rhodanese
54	<a href="#">d1uara2</a>	Alignment	not modelled	99.8	30	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
55	<a href="#">d1rhsa1</a>	Alignment	not modelled	99.8	31	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
56	<a href="#">c1uarA_</a>	Alignment	not modelled	99.7	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rhodanese; <b>PDBTitle:</b> crystal structure of rhodanese from thermus thermophilus hb8
57	<a href="#">d1u2wa1</a>	Alignment	not modelled	99.7	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
58	<a href="#">c2dcqA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative protein at4g01050; <b>PDBTitle:</b> fully automated nmr structure determination of the2 rhodanese homology domain at4g01050(175-295) from3 arabidopsis thaliana
59	<a href="#">d1urha1</a>	Alignment	not modelled	99.7	30	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
60	<a href="#">d1e0ca2</a>	Alignment	not modelled	99.7	29	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
61	<a href="#">d1okga1</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
62	<a href="#">d1uara1</a>	Alignment	not modelled	99.7	25	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
63	<a href="#">c3ippA_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thiosulfate sulfurtransferase ynje; <b>PDBTitle:</b> crystal structure of sulfur-free ynje
64	<a href="#">c2jtqA_</a>	Alignment	not modelled	99.7	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phage shock protein e; <b>PDBTitle:</b> rhodanese from e.coli
65	<a href="#">d1c25a_</a>	Alignment	not modelled	99.7	22	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Cell cycle control phosphatase, catalytic domain
66	<a href="#">c3f4aA_</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ygr203w; <b>PDBTitle:</b> structure of ygr203w, a yeast protein tyrosine phosphatase of the2 rhodanese family
67	<a href="#">c3utnX_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> thiosulfate sulfurtransferase tum1; <b>PDBTitle:</b> crystal structure of tum1 protein from saccharomyces cerevisiae
68	<a href="#">c3olhA_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-mercaptopyruvate sulfurtransferase; <b>PDBTitle:</b> human 3-mercaptopyruvate sulfurtransferase
69	<a href="#">d1ymka1</a>	Alignment	not modelled	99.7	22	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Cell cycle control phosphatase, catalytic domain
70	<a href="#">c1okgA_</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> possible 3-mercaptopyruvate sulfurtransferase; <b>PDBTitle:</b> 3-mercaptopyruvate sulfurtransferase from leishmania major
71	<a href="#">c2eg4B_</a>	Alignment	not modelled	99.6	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable thiosulfate sulfurtransferase; <b>PDBTitle:</b> crystal structure of probable thiosulfate sulfurtransferase
72	<a href="#">d2p4wa1</a>	Alignment	not modelled	99.6	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF1790-like
73	<a href="#">c2uzqE_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> m-phase inducer phosphatase 2; <b>PDBTitle:</b> protein phosphatase, new crystal form
74	<a href="#">c2j6pF_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> sb(v)-as(v) reductase; <b>PDBTitle:</b> structure of as-sb reductase from leishmania major
75	<a href="#">d1rhsa2</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
76	<a href="#">c3op3A_</a>	Alignment	not modelled	99.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> m-phase inducer phosphatase 3; <b>PDBTitle:</b> crystal structure of cell division cycle 25c protein isoform a from2 homo sapiens
77	<a href="#">d1okga2</a>	Alignment	not modelled	99.6	26	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
78	<a href="#">d1ulya_</a>	Alignment	not modelled	99.5	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Hypothetical protein PH1932

79	<a href="#">c1wv9B_</a>	Alignment	not modelled	99.5	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> rhodanese homolog tt1651; <b>PDBTitle:</b> crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
80	<a href="#">c2vswB_</a>	Alignment	not modelled	99.5	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dual specificity protein phosphatase 16; <b>PDBTitle:</b> the structure of the rhodanese domain of the human dual specificity2 phosphatase 16
81	<a href="#">c4g6qA_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the crystal structure of a functionally unknown protein kfla_6221 from2 kribbella flavida dsm 17836
82	<a href="#">d1whba_</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Ubiquitin carboxyl-terminal hydrolase 8, USP8
83	<a href="#">c2oucB_</a>	Alignment	not modelled	99.4	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dual specificity protein phosphatase 10; <b>PDBTitle:</b> crystal structure of the map kinase binding domain of mkp5
84	<a href="#">d1hzma_</a>	Alignment	not modelled	99.4	26	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Cell cycle control phosphatase, catalytic domain
85	<a href="#">d2gwfa1</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Ubiquitin carboxyl-terminal hydrolase 8, USP8
86	<a href="#">d2d1ha1</a>	Alignment	not modelled	99.4	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
87	<a href="#">d1urha2</a>	Alignment	not modelled	99.4	26	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
88	<a href="#">c2qufB_</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor pf0095; <b>PDBTitle:</b> crystal structure of transcription factor axxa-pf0095 from pyrococcus2 furiosus
89	<a href="#">c3r2uC_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> metallo-beta-lactamase family protein; <b>PDBTitle:</b> 2.1 angstrom resolution crystal structure of metallo-beta-lactamase2 from staphylococcus aureus subsp. aureus col
90	<a href="#">d1ub9a_</a>	Alignment	not modelled	99.2	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
91	<a href="#">c5dukA_</a>	Alignment	not modelled	99.1	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna binding protein; <b>PDBTitle:</b> n-terminal structure of putative dna binding transcription factor from2 thermoplasmatales archaeon scgc ab-539-n05
92	<a href="#">c4nb5D_</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> dna binding protein; <b>PDBTitle:</b> crystal structure of a transcriptional regulator
93	<a href="#">c4gcvD_</a>	Alignment	not modelled	98.7	19	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcription protein; <b>PDBTitle:</b> structure of a putative transcription factor (pa1374)from pseudomonas2 aeruginosa
94	<a href="#">c6cmvA_</a>	Alignment	not modelled	98.5	16	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator Irs14-like protein; <b>PDBTitle:</b> crystal structure of archaeal biofilm regulator (abfr2) from2 sulfolobus acidocaldarius
95	<a href="#">c3r0aB_</a>	Alignment	not modelled	98.5	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> possible transcriptional regulator from methanosarcina mazeri go1 (gi2 21227196)
96	<a href="#">c4a5mH_</a>	Alignment	not modelled	98.5	16	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator yybr; <b>PDBTitle:</b> redox regulator hypr in its oxidized form
97	<a href="#">d1z7ua1</a>	Alignment	not modelled	98.5	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> HxIR-like
98	<a href="#">d1ku9a_</a>	Alignment	not modelled	98.5	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DNA-binding protein Mj223
99	<a href="#">d1y0ua_</a>	Alignment	not modelled	98.5	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
100	<a href="#">d2fswa1</a>	Alignment	not modelled	98.4	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> HxIR-like
101	<a href="#">c5hs9A_</a>	Alignment	not modelled	98.4	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator yodb; <b>PDBTitle:</b> crystal structure of the quinone-bound yodb from b. subtilis
102	<a href="#">d2f2ea1</a>	Alignment	not modelled	98.4	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> HxIR-like
103	<a href="#">d1sfxa_</a>	Alignment	not modelled	98.4	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
104	<a href="#">c4hqeB_</a>	Alignment	not modelled	98.4	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator qssr; <b>PDBTitle:</b> the crystal structure of qssr-dna complex
105	<a href="#">c5jbrA_</a>	Alignment	not modelled	98.3	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein bcav_2135; <b>PDBTitle:</b> crystal structure of uncharacterized protein bcav_2135

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106	<a href="#">c3ctaA_</a>	Alignment	not modelled	98.3	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin kinase; <b>PDBTitle:</b> crystal structure of riboflavin kinase from thermoplasma acidophilum
107	<a href="#">d3ctaa1</a>	Alignment	not modelled	98.3	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
108	<a href="#">c3df8A_</a>	Alignment	not modelled	98.2	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> possible hxlr family transcriptional factor; <b>PDBTitle:</b> the crystal structure of a possible hxlr family transcriptional factor2 from thermoplasma volcanium gss1
109	<a href="#">c5jlsA_</a>	Alignment	not modelled	98.2	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> adhesin competence repressor; <b>PDBTitle:</b> crystal structure of adhesin competence repressor (adcr) from2 streptococcus pyogenes (c-terminally his tagged)
110	<a href="#">c4o6jA_</a>	Alignment	not modelled	98.2	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent transcription repressor related protein; <b>PDBTitle:</b> crystal structure of t. acidophilum ider
111	<a href="#">c3zmdD_</a>	Alignment	not modelled	98.2	21	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of absc, a marr family transcriptional2 regulator from streptomyces coelicolor
112	<a href="#">d1yyva1</a>	Alignment	not modelled	98.1	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> HxlR-like
113	<a href="#">c6jxbB_</a>	Alignment	not modelled	98.1	18	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid biosynthesis transcriptional regulator; <b>PDBTitle:</b> crystal structure of streptococcus pneumoniae fabt in complex with dna
114	<a href="#">c2gxqA_</a>	Alignment	not modelled	98.1	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> 146aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
115	<a href="#">d2a61a1</a>	Alignment	not modelled	98.1	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
116	<a href="#">d2etha1</a>	Alignment	not modelled	98.1	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
117	<a href="#">c2rdpA_</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator marr; <b>PDBTitle:</b> the structure of a marr family protein from bacillus2 stearothermophilus
118	<a href="#">c3k0lA_</a>	Alignment	not modelled	98.0	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> repressor protein; <b>PDBTitle:</b> crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
119	<a href="#">d1okra_</a>	Alignment	not modelled	98.0	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Penicillinase repressor
120	<a href="#">c3hruA_</a>	Alignment	not modelled	98.0	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> metalloregulator scar; <b>PDBTitle:</b> crystal structure of scar with bound zn2+