

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1yt8a1	 Alignment		99.9	22	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
2	c3tp9B_	 Alignment		99.9	20	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
3	d1yt8a3	 Alignment		99.9	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
4	c2hhgA_	 Alignment		99.9	19	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
5	c1yt8A_	 Alignment		99.9	21	PDB header: transferase Chain: A: PDB Molecule: thiosulfate sulfurtransferase; PDBTitle: crystal structure of thiosulfate sulfurtransferase from pseudomonas2 aeruginosa
6	d1qxna_	 Alignment		99.9	18	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
7	c3ilmD_	 Alignment		99.9	22	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
8	c2fsxA_	 Alignment		99.9	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cog0607: rhodanese-related sulfurtransferase; PDBTitle: crystal structure of rv0390 from m. tuberculosis
9	c3aaxB_	 Alignment		99.9	19	PDB header: transferase Chain: B: PDB Molecule: putative thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
10	c3gk5A_	 Alignment		99.9	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized rhodanese-related protein PDBTitle: crystal structure of rhodanese-related protein (tv0868615)2 from thermoplasma volcanium, northeast structural genomics3 consortium target tvr109a
11	c3emeA_	 Alignment		99.9	21	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

12	cle0cA	Alignment		99.9	24	PDB header: sulfurtransferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: sulfurtransferase from azotobacter vinelandii
13	clurhA	Alignment		99.9	28	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: the "rhodanese" fold and catalytic mechanism of 3-mercaptopyruvate sulfotransferases: crystal structure of ssea from escherichia coli
14	c3nhvE	Alignment		99.9	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
15	dle0ca1	Alignment		99.9	21	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
16	c3k9rA	Alignment		99.9	23	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.
17	d1tqla	Alignment		99.9	24	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
18	d1gmxa	Alignment		99.9	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
19	d1t3ka	Alignment		99.9	23	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
20	c3hzuA	Alignment		99.9	18	PDB header: transferase Chain: A: PDB Molecule: thiosulfate sulfurtransferase ssea; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
21	c1boiA	Alignment	not modelled	99.9	24	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: n-terminally truncated rhodanese
22	c1uarA	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: crystal structure of rhodanese from thermophilus hb8
23	c3d1pA	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase yor285w; PDBTitle: atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae
24	d1rha1	Alignment	not modelled	99.9	25	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
25	c3fojA	Alignment	not modelled	99.9	19	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.
26	d1urha1	Alignment	not modelled	99.9	26	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
27	d1uara2	Alignment	not modelled	99.9	21	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
28	c2dcqA	Alignment	not modelled	99.9	18	PDB header: unknown function Chain: A: PDB Molecule: putative protein at4g01050; PDBTitle: fully automated nmr structure determination of the2 rhodanese homology domain at4q01050(175-295) from3

					arabidopsis thaliana
29	c3ippA_	Alignment	not modelled	99.8	22 PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase ynje; PDBTitle: crystal structure of sulfur-free ynje
30	c3olhA_	Alignment	not modelled	99.8	21 PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: human 3-mercaptopyruvate sulfurtransferase
31	d1yt8a2	Alignment	not modelled	99.8	22 Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
32	c3i2vA_	Alignment	not modelled	99.8	18 PDB header: transferase Chain: A: PDB Molecule: adenyllyltransferase and sulfurtransferase mocs3; PDBTitle: crystal structure of human mocs3 rhodanese-like domain
33	d1yt8a4	Alignment	not modelled	99.8	18 Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
34	c2k0zA_	Alignment	not modelled	99.8	22 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
35	d1uara1	Alignment	not modelled	99.8	17 Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
36	d1okga1	Alignment	not modelled	99.8	19 Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
37	c3icrA_	Alignment	not modelled	99.8	19 PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a-disulfide reductase; PDBTitle: crystal structure of oxidized bacillus anthracis coadr-rhd
38	d1e0ca2	Alignment	not modelled	99.8	16 Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
39	c3g5jA_	Alignment	not modelled	99.8	22 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	d1c25a_	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
41	c3f4aA_	Alignment	not modelled	99.8	25 PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ygr203w; PDBTitle: structure of ygr203w, a yeast protein tyrosine phosphatase2 of the rhodanese family
42	d1rhsa2	Alignment	not modelled	99.8	20 Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
43	c2jtqA_	Alignment	not modelled	99.8	24 PDB header: transferase Chain: A: PDB Molecule: phage shock protein e; PDBTitle: rhodanese from e.coli
44	d1okga2	Alignment	not modelled	99.8	22 Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
45	c1okgA_	Alignment	not modelled	99.8	21 PDB header: transferase Chain: A: PDB Molecule: possible 3-mercaptopyruvate sulfurtransferase; PDBTitle: 3-mercaptopyruvate sulfurtransferase from leishmania major
46	d1ymka1	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
47	c3ntaA_	Alignment	not modelled	99.8	18 PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
48	c2j6pF_	Alignment	not modelled	99.8	23 PDB header: oxidoreductase Chain: F: PDB Molecule: sb(v)-as(v) reductase; PDBTitle: structure of as-sb reductase from leishmania major
49	c2uzqE_	Alignment	not modelled	99.7	20 PDB header: hydrolase Chain: E: PDB Molecule: m-phase inducer phosphatase 2; PDBTitle: protein phosphatase, new crystal form
50	c2eg4B_	Alignment	not modelled	99.7	23 PDB header: transferase Chain: B: PDB Molecule: probable thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase
51	c3op3A_	Alignment	not modelled	99.7	22 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
52	d1whba_	Alignment	not modelled	99.6	17 Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
53	c2vswB_	Alignment	not modelled	99.6	21 PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 16; PDBTitle: the structure of the rhodanese domain of the human dual2 specificity phosphatase 16
54	c2vswB_	Alignment	not modelled	99.6	21 PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 10;

54	c200cB	Alignment	not modelled	99.0	22	PDBTitle: crystal structure of the map kinase binding domain of mkip5
55	d2gwfa1	Alignment	not modelled	99.6	21	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
56	c1wv9B	Alignment	not modelled	99.6	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
57	d1urha2	Alignment	not modelled	99.6	23	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multi domain sulfurtransferase (rhodanese)
58	c3r2uC	Alignment	not modelled	99.5	16	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
59	d1hzma	Alignment	not modelled	99.5	18	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
60	c3flhC	Alignment	not modelled	94.7	24	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein lp_1913; PDBTitle: crystal structure of lp_1913 protein from lactobacillus2 plantarum,northeast structural genomics consortium target3 lpr140b
61	c3gxgA	Alignment	not modelled	80.6	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
62	c2f46A	Alignment	not modelled	77.2	10	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
63	d1ywfa1	Alignment	not modelled	57.1	18	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Mycobacterial PtpB-like
64	c3i32A	Alignment	not modelled	54.7	13	PDB header: rna binding protein,hydrolase Chain: A: PDB Molecule: heat resistant rna dependent atpase; PDBTitle: dimeric structure of a hera helicase fragment including the c-terminal2 reca domain, the dimerization domain, and the rna binding domain
65	c3ohgA	Alignment	not modelled	53.5	19	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
66	d1a1va2	Alignment	not modelled	51.6	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
67	c1h83A	Alignment	not modelled	36.5	23	PDB header: oxidoreductase Chain: A: PDB Molecule: polyamine oxidase; PDBTitle: structure of polyamine oxidase in complex with2 1,8-diaminooctane
68	c2b9yA	Alignment	not modelled	35.6	24	PDB header: isomerase Chain: A: PDB Molecule: putative aminooxidase; PDBTitle: crystal structure of cla-producing fatty acid isomerase2 from p. acnes
69	d1oywa3	Alignment	not modelled	34.0	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
70	d1d5ra2	Alignment	not modelled	32.3	12	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
71	d1nkt4	Alignment	not modelled	32.3	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
72	d2g0ta1	Alignment	not modelled	29.0	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
73	d1fuka	Alignment	not modelled	27.8	7	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
74	d1j9ia	Alignment	not modelled	27.3	29	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
75	d1pp7u	Alignment	not modelled	26.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: 39 kda initiator binding protein, IBP39, N-terminal domain
76	c2v1xB	Alignment	not modelled	24.6	9	PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent dna helicase q1; PDBTitle: crystal structure of human recq-like dna helicase
77	d1jf8a	Alignment	not modelled	23.4	14	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
78	c3rh0A	Alignment	not modelled	22.7	29	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase; PDBTitle: corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
79	d1b5qa1	Alignment	not modelled	21.8	32	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain

					Family: FAD-linked reductases, N-terminal domain
80	d1nw2a_	Alignment	not modelled	21.5	18 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
81	d1djqa2	Alignment	not modelled	20.8	19 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: C-terminal domain of adrenodoxin reductase-like
82	c3rggA_	Alignment	not modelled	20.3	13 PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase mitochondrial 1; PDBTitle: crystal structure of ptpmt1 in complex with pi(5)p
83	d1xria_	Alignment	not modelled	20.3	11 Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
84	d1zmaa1	Alignment	not modelled	20.3	11 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
85	c3nbmA_	Alignment	not modelled	20.1	25 PDB header: transferase Chain: A: PDB Molecule: pts system, lactose-specific iibc components; PDBTitle: the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
86	c2i6oA_	Alignment	not modelled	19.2	15 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
87	c2c46B_	Alignment	not modelled	18.9	20 PDB header: transferase Chain: B: PDB Molecule: mrna capping enzyme; PDBTitle: crystal structure of the human rna guanylyltransferase and2 5'-phosphatase
88	c3gnjD_	Alignment	not modelled	18.4	13 PDB header: structural genomics, unknown function Chain: D: PDB Molecule: thioredoxin domain protein; PDBTitle: the crystal structure of a thioredoxin-related protein from2 desulfitobacterium hafniense dcb
89	d1jl3a_	Alignment	not modelled	18.2	11 Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
90	d1p6qa_	Alignment	not modelled	18.0	24 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
91	c2hjbV_	Alignment	not modelled	17.8	11 PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent rna helicase dbpa; PDBTitle: structure of the second domain (residues 207-368) of the2 bacillus subtilis yxin protein
92	d1p5dx2	Alignment	not modelled	17.7	13 Fold: Phosphoglucosomutase, first 3 domains Superfamily: Phosphoglucosomutase, first 3 domains Family: Phosphoglucosomutase, first 3 domains
93	c2jgnB_	Alignment	not modelled	17.6	10 PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent rna helicase ddx3x; PDBTitle: ddx3 helicase domain
94	c1e1cA_	Alignment	not modelled	17.3	16 PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase alpha chain; PDBTitle: methylmalonyl-coa mutase h244a mutant
95	c3earA_	Alignment	not modelled	17.2	12 PDB header: hydrolase Chain: A: PDB Molecule: hera; PDBTitle: novel dimerization motif in the dead box rna helicase hera: form 1,2 partial dimer
96	d2g2ja1	Alignment	not modelled	16.5	10 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
97	d2b5ea4	Alignment	not modelled	16.2	14 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
98	d1hv8a2	Alignment	not modelled	15.7	19 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
99	c3bicA_	Alignment	not modelled	15.6	18 PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase, mitochondrial precursor; PDBTitle: crystal structure of human methylmalonyl-coa mutase