

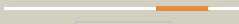


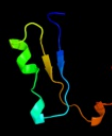























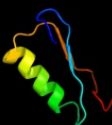



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ohgA_	 Alignment		100.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein from duf2233 family; PDBTitle: crystal structure of a protein with unknown function from duf22332 family (bacova_00430) from bacteroides ovatus at 1.80 a resolution
2	c2fsxA_	 Alignment		82.0	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cog0607: rhodanese-related sulfurtransferase; PDBTitle: crystal structure of rv0390 from m. tuberculosis
3	dlyt8a4	 Alignment		74.7	21	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
4	dlqxA_	 Alignment		68.0	7	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
5	clurhA_	 Alignment		64.7	10	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: the "rhodanese" fold and catalytic mechanism of 2 3-mercaptopyruvate sulfurtransferases: crystal structure of ssea from escherichia coli
6	clwv9B_	 Alignment		62.8	16	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
7	c3icrA_	 Alignment		62.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a-disulfide reductase; PDBTitle: crystal structure of oxidized bacillus anthracis coadr-rhd
8	c2dcqA_	 Alignment		61.0	5	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
9	c3d1pA_	 Alignment		59.0	9	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase yor285w; PDBTitle: atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae
10	c3ilmD_	 Alignment		58.3	10	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
11	c3ntaA_	 Alignment		54.3	8	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase

12	d1yt8a2	Alignment		51.7	17	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multi domain sulfurtransferase (rhodanese)
13	d1e0ca1	Alignment		48.7	12	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multi domain sulfurtransferase (rhodanese)
14	c1e0ca_	Alignment		48.4	15	PDB header: sulfurtransferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: sulfurtransferase from azotobacter vinelandii
15	d1aqt2	Alignment		47.6	18	Fold: Epsilon subunit of F1F0-ATP synthase N-terminal domain Superfamily: Epsilon subunit of F1F0-ATP synthase N-terminal domain Family: Epsilon subunit of F1F0-ATP synthase N-terminal domain
16	d1yt8a1	Alignment		42.2	8	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multi domain sulfurtransferase (rhodanese)
17	c1h8eH_	Alignment		41.1	18	PDB header: hydrolase Chain: H: PDB Molecule: bovine mitochondrial f1-atpase; PDBTitle: (adp.alf4)2(adp.so4) bovine f1-atpase2 (all three catalytic sites occupied)
18	c2hhgA_	Alignment		37.6	13	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
19	c3aaxB_	Alignment		37.6	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
20	d1yt8a3	Alignment		37.4	15	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multi domain sulfurtransferase (rhodanese)
21	c2qe7H_	Alignment	not modelled	37.4	21	PDB header: hydrolase Chain: H: PDB Molecule: atp synthase subunit epsilon; PDBTitle: crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
22	c2e5yA_	Alignment	not modelled	36.3	27	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase epsilon chain; PDBTitle: epsilon subunit and atp complex of f1f0-atp synthase from2 the thermophilic bacillus ps3
23	c3k9rA_	Alignment	not modelled	36.0	10	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.
24	c3g5jA_	Alignment	not modelled	34.5	16	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
25	d1urha1	Alignment	not modelled	31.2	15	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multi domain sulfurtransferase (rhodanese)
26	c2hldH_	Alignment	not modelled	29.9	18	PDB header: hydrolase Chain: H: PDB Molecule: atp synthase delta chain, mitochondrial; PDBTitle: crystal structure of yeast mitochondrial f1-atpase
27	d1okga2	Alignment	not modelled	29.8	8	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multi domain sulfurtransferase (rhodanese)
28	c2rq7A_	Alignment	not modelled	29.6	18	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase epsilon chain; PDBTitle: solution structure of the epsilon subunit chimera combining2 the n-terminal beta-sandwich domain from t. elongatus

						bp-13 f1 and the c-terminal alpha-helical domain from spinach4 chloroplast f1
29	c3hzuA_	Alignment	not modelled	28.9	10	PDB header: transferase Chain: A: PDB Molecule: thiosulfate sulfurtransferase ssea; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
30	c3fojA_	Alignment	not modelled	28.7	8	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	c3olhA_	Alignment	not modelled	28.4	13	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: human 3-mercaptopyruvate sulfurtransferase
32	d1okga1	Alignment	not modelled	28.4	6	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
33	d1tq1a_	Alignment	not modelled	27.0	8	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
34	d1uara1	Alignment	not modelled	26.9	12	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
35	c2w7vB_	Alignment	not modelled	26.7	15	PDB header: transport protein Chain: B: PDB Molecule: general secretion pathway protein I; PDBTitle: periplasmic domain of epsI from vibrio parahaemolyticus
36	d1rhsa2	Alignment	not modelled	25.3	11	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
37	c2k0zA_	Alignment	not modelled	25.2	19	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
38	c2jtgA_	Alignment	not modelled	25.2	5	PDB header: transferase Chain: A: PDB Molecule: phage shock protein e; PDBTitle: rhodanese from e.coli
39	c1uarA_	Alignment	not modelled	24.1	12	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: crystal structure of rhodanese from thermus thermophilus hb8
40	d1rhsa1	Alignment	not modelled	23.0	10	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
41	d1uara2	Alignment	not modelled	22.8	8	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
42	c1yt8A_	Alignment	not modelled	22.4	15	PDB header: transferase Chain: A: PDB Molecule: thiosulfate sulfurtransferase; PDBTitle: crystal structure of thiosulfate sulfurtransferase from pseudomonas2 aeruginosa
43	d2hgsa1	Alignment	not modelled	22.1	30	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Eukaryotic glutathione synthetase, substrate-binding domain
44	c3ippA_	Alignment	not modelled	21.3	18	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase ynj6; PDBTitle: crystal structure of sulfur-free ynj6
45	c3tp9B_	Alignment	not modelled	20.2	11	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
46	c3i2vA_	Alignment	not modelled	19.5	8	PDB header: transferase Chain: A: PDB Molecule: adenylyltransferase and sulfurtransferase mocs3; PDBTitle: crystal structure of human mocs3 rhodanese-like domain
47	c1boiA_	Alignment	not modelled	18.5	11	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: n-terminally truncated rhodanese
48	c3gk5A_	Alignment	not modelled	17.8	6	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized rhodanese-related protein PDBTitle: crystal structure of rhodanese-related protein (tvg0868615)2 from thermoplasma volcanium, northeast structural genomics3 consortium target tvr109a
49	c1fs0E_	Alignment	not modelled	17.1	18	PDB header: hydrolase Chain: E: PDB Molecule: atp synthase epsilon subunit; PDBTitle: complex of gamma/epsilon atp synthase from e.coli
50	d1lm8v_	Alignment	not modelled	16.3	24	Fold: Prealbumin-like Superfamily: VHL Family: VHL
51	d1urha2	Alignment	not modelled	15.7	17	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
52	d1gmxa_	Alignment	not modelled	14.9	12	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
						Fold: Glycosyl hydrolase domain

53	d1hl9a1	Alignment	not modelled	14.9	13	Superfamily: Glycosyl hydrolase domain Family: Putative alpha-L-fucosidase C-terminal domain
54	c3a0cA_	Alignment	not modelled	14.6	6	PDB header: sugar binding protein Chain: A: PDB Molecule: mannose/sialic acid-binding lectin; PDBTitle: crystal structure of an anti-hiv mannose-binding lectin from2 polygonatum cyrtonea hua
55	d1jofa_	Alignment	not modelled	12.3	14	Fold: 7-bladed beta-propeller Superfamily: 3-carboxy-cis,cis-mucoante lactonizing enzyme Family: 3-carboxy-cis,cis-mucoante lactonizing enzyme
56	d3coxa2	Alignment	not modelled	12.1	22	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: GMC oxidoreductases
57	d2fb5a1	Alignment	not modelled	11.7	23	Fold: Yojj-like Superfamily: Yojj-like Family: Yojj-like
58	d1npla_	Alignment	not modelled	11.6	17	Fold: beta-Prism II Superfamily: alpha-D-mannose-specific plant lectins Family: alpha-D-mannose-specific plant lectins
59	c2dpfB_	Alignment	not modelled	10.6	11	PDB header: plant protein Chain: B: PDB Molecule: curculin; PDBTitle: crystal structure of curculin1 homodimer
60	c2fsdB_	Alignment	not modelled	9.1	41	PDB header: viral protein Chain: B: PDB Molecule: putative baseplate protein; PDBTitle: a common fold for the receptor binding domains of2 lactococcal phages? the crystal structure of the head3 domain of phage bil170
61	d1udxa3	Alignment	not modelled	9.0	15	Fold: Obg GTP-binding protein C-terminal domain Superfamily: Obg GTP-binding protein C-terminal domain Family: Obg GTP-binding protein C-terminal domain
62	d1b2pa_	Alignment	not modelled	8.9	11	Fold: beta-Prism II Superfamily: alpha-D-mannose-specific plant lectins Family: alpha-D-mannose-specific plant lectins
63	d2co5a1	Alignment	not modelled	8.7	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: F93-like
64	c3hv1A_	Alignment	not modelled	8.4	10	PDB header: transport protein Chain: A: PDB Molecule: polar amino acid abc uptake transporter substrate PDBTitle: crystal structure of a polar amino acid abc uptake2 transporter substrate binding protein from streptococcus3 thermophilus
65	c2x34A_	Alignment	not modelled	8.1	14	PDB header: carbohydrate-binding protein Chain: A: PDB Molecule: cellulose-binding protein, x158; PDBTitle: structure of a polyisoprenoid binding domain from2 saccharophagus degradans implicated in plant cell wall3 breakdown
66	c3n5bB_	Alignment	not modelled	8.0	14	PDB header: transcription regulator Chain: B: PDB Molecule: asr0485 protein; PDBTitle: the complex of pii and pipx from anabaena
67	d1bwua_	Alignment	not modelled	7.8	13	Fold: beta-Prism II Superfamily: alpha-D-mannose-specific plant lectins Family: alpha-D-mannose-specific plant lectins
68	c2xg8D_	Alignment	not modelled	7.5	21	PDB header: transcription Chain: D: PDB Molecule: pipx; PDBTitle: structural basis of gene regulation by protein pii: the2 crystal complex of pii and pipx from synechococcus3 elongatus pcc 7942
69	c2o6pA_	Alignment	not modelled	7.4	17	PDB header: transport protein Chain: A: PDB Molecule: iron-regulated surface determinant protein c; PDBTitle: crystal structure of the heme-iscd complex
70	c2vzkD_	Alignment	not modelled	7.3	8	PDB header: transferase Chain: D: PDB Molecule: glutamate n-acetyltransferase 2 beta chain; PDBTitle: structure of the acyl-enzyme complex of an n-terminal2 nucleophile (ntn) hydrolase, oat2
71	d2o6pa1	Alignment	not modelled	7.1	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: NEAT domain-like Family: NEAT domain
72	c3emeA_	Alignment	not modelled	6.8	13	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
73	d1vpba_	Alignment	not modelled	6.7	24	Fold: Putative modulator of DNA gyrase, PmbA/TldD Superfamily: Putative modulator of DNA gyrase, PmbA/TldD Family: Putative modulator of DNA gyrase, PmbA/TldD
74	c3gn3B_	Alignment	not modelled	6.5	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative protein-disulfide isomerase; PDBTitle: crystal structure of a putative protein-disulfide isomerase from2 pseudomonas syringae to 2.5a resolution.
75	d1xd6a_	Alignment	not modelled	6.4	12	Fold: beta-Prism II Superfamily: alpha-D-mannose-specific plant lectins Family: alpha-D-mannose-specific plant lectins
76	d1xd5a_	Alignment	not modelled	6.4	11	Fold: beta-Prism II Superfamily: alpha-D-mannose-specific plant lectins Family: alpha-D-mannose-specific plant lectins
77	c3hi0B_	Alignment	not modelled	6.3	13	PDB header: hydrolase Chain: B: PDB Molecule: putative exopolyphosphatase; PDBTitle: crystal structure of putative exopolyphosphatase (17739545) from2 agrobacterium tumefaciens str. c58 (dupont) at 2.30 a resolution
						Fold: Galactose-binding domain-like

78	d1o59a1	Alignment	not modelled	6.3	33	Superfamily: Galactose-binding domain-like Family: Allantoicase repeat
79	c3it4B_	Alignment	not modelled	6.2	19	PDB header: transferase Chain: B: PDB Molecule: arginine biosynthesis bifunctional protein argj PDBTitle: the crystal structure of ornithine acetyltransferase from2 mycobacterium tuberculosis (rv1653) at 1.7 a
80	c1gkpD_	Alignment	not modelled	6.1	23	PDB header: hydrolase Chain: D: PDB Molecule: hydantoinase; PDBTitle: d-hydantoinase (dihydropyrimidinase) from thermus sp. in2 space group c2221
81	c3kihC_	Alignment	not modelled	6.1	18	PDB header: sugar binding protein Chain: C: PDB Molecule: 5-bladed -propeller lectin; PDBTitle: the crystal structures of two fragments truncated from 5-bladed -2 propeller lectin, tachylectin-2 (lib2-d2-15)
82	c1okgA_	Alignment	not modelled	5.8	8	PDB header: transferase Chain: A: PDB Molecule: possible 3-mercaptopyruvate sulfurtransferase; PDBTitle: 3-mercaptopyruvate sulfurtransferase from leishmania major
83	d1kwga1	Alignment	not modelled	5.5	25	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
84	c1vraB_	Alignment	not modelled	5.5	14	PDB header: transferase Chain: B: PDB Molecule: arginine biosynthesis bifunctional protein argj; PDBTitle: crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
85	d2vera1	Alignment	not modelled	5.1	23	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Dr-family adhesin