










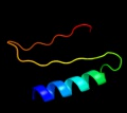

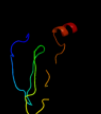










#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2j58G_	 Alignment		100.0	74	PDB header: membrane protein Chain: G: PDB Molecule: outer membrane lipoprotein wza; PDBTitle: the structure of wza
2	c2w8iG_	 Alignment		100.0	76	PDB header: membrane protein Chain: G: PDB Molecule: putative outer membrane lipoprotein wza; PDBTitle: crystal structure of wza24-345.
3	c3p42D_	 Alignment		99.9	21	PDB header: unknown function Chain: D: PDB Molecule: predicted protein; PDBTitle: structure of gfcc (ymcb), protein encoded by the e. coli group 42 capsule operon
4	d2fug13	 Alignment		88.8	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Nqo1 middle domain-like Family: Nqo1 middle domain-like
5	c2fugA_	 Alignment		84.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-quinone oxidoreductase chain 1; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
6	d1ghha_	 Alignment		77.2	18	Fold: DNA damage-inducible protein DinI Superfamily: DNA damage-inducible protein DinI Family: DNA damage-inducible protein DinI
7	c2xdvA_	 Alignment		62.9	16	PDB header: nuclear protein Chain: A: PDB Molecule: myc-induced nuclear antigen; PDBTitle: crystal structure of the catalytic domain of flj14393
8	c3uyiA_	 Alignment		56.8	36	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 8; PDBTitle: crystal structure of jmj5 catalytic core domain in complex with2 nickle and alpha-kg
9	d1vrba1	 Alignment		53.0	19	Fold: Double-stranded beta-helix Superfamily: Clavaminate synthase-like Family: Asparaginyl hydroxylase-like
10	d1lr5a_	 Alignment		47.0	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
11	c2zpmA_	 Alignment		45.9	29	PDB header: hydrolase Chain: A: PDB Molecule: regulator of sigma e protease; PDBTitle: crystal structure analysis of pdz domain b

12	dlrc6a_	Alignment		44.6	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
13	c3al6A_	Alignment		43.4	35	PDB header: unknown function Chain: A: PDB Molecule: jmc domain-containing protein c2orf60; PDBTitle: crystal structure of human tyw5
14	dlzofa1	Alignment		43.3	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
15	c3u7zA_	Alignment		41.0	11	PDB header: metal binding protein Chain: A: PDB Molecule: putative metal binding protein rumgna_00854; PDBTitle: crystal structure of a putative metal binding protein rumgna_008542 (zp_02040092.1) from ruminococcus gnavus atcc 29149 at 1.30 a3 resolution
16	dlx82a_	Alignment		39.8	8	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
17	c2xxzA_	Alignment		39.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 6b; PDBTitle: crystal structure of the human jmj3 jumonji domain
18	c3eytA_	Alignment		39.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein spoa0173; PDBTitle: crystal structure of thioredoxin-like superfamily protein spoa0173
19	c2opkC_	Alignment		38.1	16	PDB header: isomerase Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
20	c3k2oB_	Alignment		37.8	38	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional arginine demethylase and lysyl-hydroxylase PDBTitle: structure of an oxygenase
21	c3razA_	Alignment	not modelled	37.3	3	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-related protein; PDBTitle: the crystal structure of thioredoxin-related protein from neisseria2 meningitidis serogroup b
22	dlfe0a_	Alignment	not modelled	37.1	14	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
23	dlh2ka_	Alignment	not modelled	35.3	29	Fold: Double-stranded beta-helix Superfamily: Clavaminate synthase-like Family: Hypoxia-inducible factor HIF inhibitor (FIH1)
24	dlwp0a1	Alignment	not modelled	33.2	12	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
25	c3lorB_	Alignment	not modelled	32.5	16	PDB header: isomerase Chain: B: PDB Molecule: thiol-disulfide isomerase and thioredoxins; PDBTitle: the crystal structure of a thiol-disulfide isomerase from2 corynebacterium glutamicum to 2.2a
26	dlsfna_	Alignment	not modelled	32.4	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
27	dlrwua_	Alignment	not modelled	32.1	12	Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: YbeD-like
28	clrwuA_	Alignment	not modelled	32.1	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0250 protein ybed; PDBTitle: solution structure of conserved protein ybed from e. coli
				PDB header: structural genomics, unknown function		

29	c3cewA	Alignment	not modelled	31.9	21	Chain: A: PDB Molecule: uncharacterized cupin protein; PDBTitle: crystal structure of a cupin protein (bf4112) from bacteroides2 fragilis. northeast structural genomics consortium target bfr205
30	c2yztA	Alignment	not modelled	31.5	6	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ttha1756; PDBTitle: crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
31	dlzx5a1	Alignment	not modelled	31.1	24	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Type I phosphomannose isomerase
32	dlsq4a	Alignment	not modelled	31.0	9	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
33	clsefA	Alignment	not modelled	30.9	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
34	dlsefa	Alignment	not modelled	30.9	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbA-like
35	c2r37A	Alignment	not modelled	30.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione peroxidase 3; PDBTitle: crystal structure of human glutathione peroxidase 3 (selenocysteine to2 glycine mutant)
36	c2r32A	Alignment	not modelled	29.3	18	PDB header: immune system Chain: A: PDB Molecule: gcn4-pii/tumor necrosis factor ligand PDBTitle: crystal structure of human gitrl variant
37	dlz5ye1	Alignment	not modelled	27.7	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
38	dly7ma2	Alignment	not modelled	27.6	4	Fold: LysM domain Superfamily: LysM domain Family: LysM domain
39	c3ibmB	Alignment	not modelled	27.2	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: cupin 2, conserved barrel domain protein; PDBTitle: crystal structure of cupin 2 domain-containing protein hha1_0468 from2 halorhodospira halophila
40	dlwe0a1	Alignment	not modelled	27.0	23	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
41	dlq44a	Alignment	not modelled	26.6	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
42	c3d0fA	Alignment	not modelled	26.4	18	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding 1 transmembrane protein mrca; PDBTitle: structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
43	dlqmva	Alignment	not modelled	26.3	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
44	dlj3pa	Alignment	not modelled	26.0	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Glucose-6-phosphate isomerase, GPI
45	c2h8kA	Alignment	not modelled	25.3	14	PDB header: transferase Chain: A: PDB Molecule: sult1c3 splice variant d; PDBTitle: human sulfotranferase sult1c3 in complex with pap
46	c3cmiA	Alignment	not modelled	25.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: peroxiredoxin hyr1; PDBTitle: crystal structure of glutathione-dependent phospholipid peroxidase2 hyr1 from the yeast saccharomyces cerevisiae
47	d2dsya1	Alignment	not modelled	24.6	20	Fold: TTHA1013/TTHA0281-like Superfamily: TTHA1013/TTHA0281-like Family: TTHA0281-like
48	c3kh7A	Alignment	not modelled	24.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbe; PDBTitle: crystal structure of the periplasmic soluble domain of reduced ccmg2 from pseudomonas aeruginosa
49	c3d82A	Alignment	not modelled	24.3	30	PDB header: metal binding protein Chain: A: PDB Molecule: cupin 2, conserved barrel domain protein; PDBTitle: crystal structure of a cupin-2 domain containing protein (sfri_3543)2 from shewanella frigidimarina ncimb 400 at 2.05 a resolution
50	dlknga	Alignment	not modelled	23.9	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
51	dluija2	Alignment	not modelled	23.6	8	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
52	c2v1mA	Alignment	not modelled	23.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione peroxidase; PDBTitle: crystal structure of schistosoma mansoni glutathione2 peroxidase
53	c3or5A	Alignment	not modelled	22.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein, thioredoxin family PDBTitle: crystal structure of thiol:disulfide interchange protein, thioredoxin2 family protein from chlorobium tepidum t1s PDB header: metal binding protein

54	c2rogA	Alignment	not modelled	22.7	30	Chain: A: PDB Molecule: heavy metal binding protein; PDBTitle: solution structure of thermus thermophilus hb8 tha17182 protein in living e. coli cells
55	c3h8uA	Alignment	not modelled	22.5	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein with double-stranded PDBTitle: crystal structure of uncharacterized conserved protein with double-2 stranded beta-helix domain (yp_001338853.1) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.80 a resolution
56	d1fmja	Alignment	not modelled	22.5	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
57	c2hhzA	Alignment	not modelled	22.3	11	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related; PDBTitle: crystal structure of a pyridoxamine 5'-phosphate oxidase-related2 protein (ssuidraft_2804) from streptococcus suis 89/1591 at 2.00 a3 resolution
58	c3lwaA	Alignment	not modelled	22.3	9	PDB header: isomerase Chain: A: PDB Molecule: secreted thiol-disulfide isomerase; PDBTitle: the crystal structure of a secreted thiol-disulfide2 isomerase from corynebacterium glutamicum to 1.75a
59	c3jxoB	Alignment	not modelled	22.3	11	PDB header: transport protein Chain: B: PDB Molecule: trka-n domain protein; PDBTitle: crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
60	c3drnB	Alignment	not modelled	22.3	8	PDB header: oxidoreductase Chain: B: PDB Molecule: peroxiredoxin, bacterioferritin comigratory protein PDBTitle: the crystal structure of bcp1 from sulfolobus sulfataricus
61	d1prxa	Alignment	not modelled	22.1	4	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
62	d1gp1a	Alignment	not modelled	22.0	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
63	c3h7hA	Alignment	not modelled	22.0	21	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt4; PDBTitle: crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
64	d1uika2	Alignment	not modelled	21.9	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
65	d1te7a	Alignment	not modelled	21.3	20	Fold: PUA domain-like Superfamily: PUA domain-like Family: yqfB-like
66	d2d40a1	Alignment	not modelled	21.3	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
67	c2wbqA	Alignment	not modelled	21.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: l-arginine beta-hydroxylase; PDBTitle: crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine
68	d1pmia	Alignment	not modelled	20.4	7	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Type I phosphomannose isomerase
69	c2q30C	Alignment	not modelled	20.4	17	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a rmlc-like cupin protein (dde_2303) from2 desulfovibrio desulfuricans subsp. at 1.94 a resolution
70	c3h1yA	Alignment	not modelled	20.1	15	PDB header: isomerase Chain: A: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose 6-phosphate isomerase from2 salmonella typhimurium bound to substrate (f6p)and metal3 atom (zn)
71	d1xv1a	Alignment	not modelled	20.1	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
72	d2phna1	Alignment	not modelled	19.8	14	Fold: CofE-like Superfamily: CofE-like Family: CofE-like
73	d1q20a	Alignment	not modelled	19.4	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
74	c2h66G	Alignment	not modelled	19.3	12	PDB header: structural genomics/oxidoreductase Chain: G: PDB Molecule: pv-pf14_0368; PDBTitle: the crystal structure of plasmodium vivax 2-cys2 peroxiredoxin
75	d1yexa1	Alignment	not modelled	19.2	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
76	c2og5A	Alignment	not modelled	19.1	23	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxygenase; PDBTitle: crystal structure of asparagine oxygenase (asno)
77	d1e2ya	Alignment	not modelled	18.9	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
78	d1ds1a	Alignment	not modelled	18.7	38	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Clavamate synthase

79	d2b8ma1	Alignment	not modelled	18.7	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: MJ0764-like
80	c3bcwB	Alignment	not modelled	18.5	23	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf861 family protein with a rmlc-like cupin2 fold (bb1179) from bordetella bronchiseptica rb50 at 1.60 a3 resolution
81	d1o5ua	Alignment	not modelled	18.1	27	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Hypothetical protein TM1112
82	c3kw0D	Alignment	not modelled	18.0	17	PDB header: hydrolase Chain: D: PDB Molecule: cysteine peptidase; PDBTitle: crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution
83	d1j99a	Alignment	not modelled	18.0	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
84	c3ia1A	Alignment	not modelled	17.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: thio-disulfide isomerase/thioredoxin; PDBTitle: crystal structure of thio-disulfide isomerase from thermus2 thermophilus
85	c2v2gC	Alignment	not modelled	17.7	9	PDB header: oxidoreductase Chain: C: PDB Molecule: peroxiredoxin 6; PDBTitle: crystal structure of the c45s mutant of the peroxiredoxin 62 of arenicola marina. monoclinic form
86	c2hc8A	Alignment	not modelled	17.5	21	PDB header: transport protein Chain: A: PDB Molecule: cation-transporting atpase, p-type; PDBTitle: structure of the a. fulgidus copa a-domain
87	d1sb6a	Alignment	not modelled	17.4	21	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
88	c3jzvA	Alignment	not modelled	17.4	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein rru_a2000; PDBTitle: crystal structure of rru_a2000 from rhodospirillum rubrum: a cupin-22 domain.
89	c3gl3D	Alignment	not modelled	16.9	16	PDB header: oxidoreductase Chain: D: PDB Molecule: putative thiol:disulfide interchange protein PDBTitle: crystal structure of a putative thiol:disulfide interchange2 protein dsbe from chlorobium tepidum
90	d1zud21	Alignment	not modelled	16.9	7	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
91	d1qq2a	Alignment	not modelled	16.9	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
92	c2fpeB	Alignment	not modelled	16.9	20	PDB header: signaling protein Chain: B: PDB Molecule: c-jun-amino-terminal kinase interacting protein PDBTitle: conserved dimerization of the ib1 src-homology 3 domain
93	c2rqeA	Alignment	not modelled	16.7	17	PDB header: sugar binding protein Chain: A: PDB Molecule: beta-1,3-glucan-binding protein; PDBTitle: solution structure of the silkworm bgrp/gnbp3 n-terminal2 domain reveals the mechanism for b-1,3-glucan specific3 recognition
94	c3k6qB	Alignment	not modelled	16.1	15	PDB header: ligand binding protein Chain: B: PDB Molecule: putative ligand binding protein; PDBTitle: crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
95	c2kytA	Alignment	not modelled	16.1	14	PDB header: hydrolase Chain: A: PDB Molecule: group xvi phospholipase a2; PDBTitle: solution struture of the h-rev107 n-terminal domain
96	d1qwra	Alignment	not modelled	16.0	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Type I phosphomannose isomerase
97	d1g3ma	Alignment	not modelled	15.4	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
98	c2gu9B	Alignment	not modelled	15.4	20	PDB header: immune system Chain: B: PDB Molecule: tetracenomycin polyketide synthesis protein; PDBTitle: crystal structure of xc5357 from xanthomonas campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure
99	d1xcca	Alignment	not modelled	15.4	9	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like