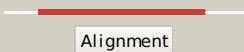

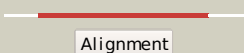

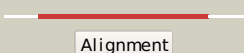

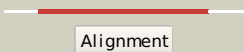

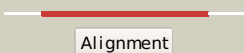

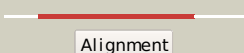



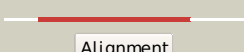

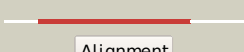

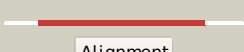

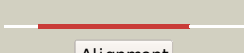

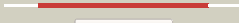

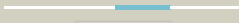




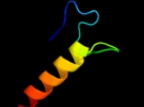



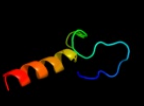









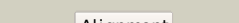
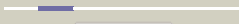





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c8fA_	 Alignment		99.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate formate-lyase 1-activating enzyme; PDBTitle: 4fe-4s-pyruvate formate-lyase activating enzyme with2 partially disordered adomet
2	d1tv8a_	 Alignment		99.5	19	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: MoCo biosynthesis proteins
3	c2yx0A_	 Alignment		99.5	12	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
4	c3rfaA_	 Alignment		99.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: ribosomal rna large subunit methyltransferase n; PDBTitle: x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
5	c2z2uA_	 Alignment		98.8	10	PDB header: metal binding protein Chain: A: PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaeal tyw1
6	c2a5hC_	 Alignment		98.8	14	PDB header: isomerase Chain: C: PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
7	c3canA_	 Alignment		98.5	15	PDB header: lyase activator Chain: A: PDB Molecule: pyruvate-formate lyase-activating enzyme; PDBTitle: crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
8	d1r30a_	 Alignment		98.1	11	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
9	c1r30A_	 Alignment		98.1	11	PDB header: transferase Chain: A: PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-2 adenosylmethionine-dependent radical enzyme
10	c3t7vA_	 Alignment		98.0	16	PDB header: transferase Chain: A: PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
11	c3cixA_	 Alignment		97.9	15	PDB header: adomet binding protein Chain: A: PDB Molecule: fefe-hydrogenase maturase; PDBTitle: x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate

12	d1olta_		Alignment		97.2	15	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
13	d1lbua2		Alignment		33.4	27	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: Muramoyl-pentapeptide carboxypeptidase
14	c2klxA_		Alignment		30.9	41	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin; PDBTitle: solution structure of glutaredoxin from bartonella henselae str.2 houston
15	c2hl7A_		Alignment		28.1	28	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c-type biogenesis protein ccmh; PDBTitle: crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
16	c2qggF_		Alignment		27.8	17	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: protein tm_1862; PDBTitle: crystal structure of tm_1862 from thermotoga maritima.2 northeast structural genomics consortium target vr77
17	c2kw0A_		Alignment		26.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ccmh protein; PDBTitle: solution structure of n-terminal domain of ccmh from escherichia.coli
18	c2kl5A_		Alignment		25.7	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yutd; PDBTitle: solution nmr structure of protein yutd from b.subtilis, northeast2 structural genomics consortium target sr232
19	c3gv1A_		Alignment		25.2	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: disulfide interchange protein; PDBTitle: crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
20	c3kc2A_		Alignment		24.0	10	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
21	c3gn3B_		Alignment	not modelled	21.3	23	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.
22	c3h93A_		Alignment	not modelled	19.0	22	PDB header: transcription regulator Chain: A: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of pseudomonas aeruginosa dsba
23	c3dvwA_		Alignment	not modelled	17.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of reduced dsba1 from neisseria2 meningitidis
24	c2k0rA_		Alignment	not modelled	16.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbd; PDBTitle: solution structure of the c103s mutant of the n-terminal2 domain of dsbd from neisseria meningitidis
25	c1v57A_		Alignment	not modelled	16.6	24	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbg; PDBTitle: crystal structure of the disulfide bond isomerase dsbg
26	c2k9hA_		Alignment	not modelled	16.5	38	PDB header: metal binding protein Chain: A: PDB Molecule: glycoprotein; PDBTitle: the hantavirus glycoprotein g1 tail contains a dual cchc-2 type classical zinc fingers
27	c3l9vE_		Alignment	not modelled	16.4	31	PDB header: oxidoreductase Chain: E: PDB Molecule: putative thiol-disulfide isomerase or thioredoxin; PDBTitle: crystal structure of salmonella enterica serovar typhimurium srga
28	d2atcb2		Alignment	not modelled	16.2	33	Fold: Rubredoxin-like Superfamily: Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain Family: Aspartate carbamoyltransferase, Regulatory-chain, C-

						terminal domain
29	c2l7xA	Alignment	not modelled	16.1	40	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein; PDBTitle: crimean congo hemorrhagic fever gn zinc finger
30	c3ct7E	Alignment	not modelled	16.0	15	PDB header: isomerase Chain: E: PDB Molecule: d-allulose-6-phosphate 3-epimerase; PDBTitle: crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
31	c3c7mB	Alignment	not modelled	15.5	23	PDB header: oxidoreductase Chain: B: PDB Molecule: thiol:disulfide interchange protein dsba-like; PDBTitle: crystal structure of reduced dsbl
32	c3feuA	Alignment	not modelled	14.3	22	PDB header: oxidoreductase Chain: A: PDB Molecule: putative lipoprotein; PDBTitle: crystal structure of dsba-like thioredoxin domain vf_a0457 from vibrio2 fischeri
33	c1nl0G	Alignment	not modelled	14.1	50	PDB header: immune system Chain: G: PDB Molecule: factor ix; PDBTitle: crystal structure of human factor ix gla domain in complex2 of an inhibitory antibody, 10c12
34	c3cu2A	Alignment	not modelled	14.0	11	PDB header: isomerase Chain: A: PDB Molecule: ribulose-5-phosphate 3-epimerase; PDBTitle: crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
35	d1vsra	Alignment	not modelled	13.4	42	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
36	d1beda	Alignment	not modelled	13.3	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbA-like
37	d1ckqa	Alignment	not modelled	13.2	22	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease EcoRI
38	d2fzcb2	Alignment	not modelled	13.2	33	Fold: Rubredoxin-like Superfamily: Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain Family: Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain
39	d1abaa	Alignment	not modelled	13.1	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
40	d1eysc	Alignment	not modelled	13.0	22	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Photosynthetic reaction centre (cytochrome subunit)
41	c1eysC	Alignment	not modelled	13.0	22	PDB header: electron transport Chain: C: PDB Molecule: photosynthetic reaction center; PDBTitle: crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
42	c2znmA	Alignment	not modelled	12.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: oxidoreductase nmdsba3 from neisseria meningitidis
43	c2khpA	Alignment	not modelled	12.4	35	PDB header: electron transport Chain: A: PDB Molecule: glutaredoxin; PDBTitle: solution structure of glutaredoxin from brucella melitensis
44	d1legoa	Alignment	not modelled	12.3	31	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
45	c2bpbB	Alignment	not modelled	12.3	12	PDB header: oxidoreductase Chain: B: PDB Molecule: sulfite\cytochrome c oxidoreductase subunit b; PDBTitle: sulfite dehydrogenase from starkeya novella
46	c2he3A	Alignment	not modelled	12.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione peroxidase 2; PDBTitle: crystal structure of the selenocysteine to cysteine mutant of human2 glutathione peroxidase 2 (gpx2)
47	d1pg5b2	Alignment	not modelled	12.0	33	Fold: Rubredoxin-like Superfamily: Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain Family: Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain
48	d2i5nc1	Alignment	not modelled	11.4	12	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Photosynthetic reaction centre (cytochrome subunit)
49	c2jblC	Alignment	not modelled	11.4	12	PDB header: electron transport Chain: C: PDB Molecule: photosynthetic reaction center cytochrome c PDBTitle: photosynthetic reaction center from blastochloris viridis
50	d1wjpa2	Alignment	not modelled	11.1	30	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
51	c2be7E	Alignment	not modelled	10.5	33	PDB header: transferase Chain: E: PDB Molecule: aspartate carbamoyltransferase regulatory chain; PDBTitle: crystal structure of the unliganded (t-state) aspartate2 transcarbamoylase of the psychrophilic bacterium moritella profunda
52	d1t3ba1	Alignment	not modelled	9.3	29	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
53	d1h75a	Alignment	not modelled	9.2	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase

54	d3c7bb3	Alignment	not modelled	9.2	20	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
55	c2e2zA	Alignment	not modelled	9.0	13	PDB header: protein transport, chaperone regulator Chain: A: PDB Molecule: tim15; PDBTitle: solution nmr structure of yeast tim15, co-chaperone of2 mitochondrial hsp70
56	d1x5wa2	Alignment	not modelled	8.9	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
57	c3qr7A	Alignment	not modelled	8.5	11	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
58	d1atxa	Alignment	not modelled	8.5	39	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
59	c3kwpA	Alignment	not modelled	8.2	15	PDB header: transferase Chain: A: PDB Molecule: predicted methyltransferase; PDBTitle: crystal structure of putative methyltransferase from lactobacillus2 brevis
60	d2hfqa1	Alignment	not modelled	8.1	43	Fold: NE1680-like Superfamily: NE1680-like Family: NE1680-like
61	c2hfqa	Alignment	not modelled	8.1	43	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: nmr structure of protein ne1680 from nitrosomonas europaea:2 northeast structural genomics consortium target net5
62	d1pbya1	Alignment	not modelled	8.1	17	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
63	d1eeja1	Alignment	not modelled	8.0	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
64	c2elpA	Alignment	not modelled	8.0	50	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
65	d2akja3	Alignment	not modelled	7.9	25	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
66	c2remB	Alignment	not modelled	7.8	21	PDB header: oxidoreductase Chain: B: PDB Molecule: disulfide oxidoreductase; PDBTitle: crystal structure of oxidoreductase dsba from xylella2 fastidiosa
67	d1cw0a	Alignment	not modelled	7.8	42	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
68	c3bciA	Alignment	not modelled	7.6	33	PDB header: oxidoreductase Chain: A: PDB Molecule: disulfide bond protein a; PDBTitle: crystal structure of staphylococcus aureus dsba
69	d1z6ma1	Alignment	not modelled	7.6	38	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbA-like
70	c3omzG	Alignment	not modelled	7.5	25	PDB header: immune system Chain: G: PDB Molecule: human vdelta1 gamma delta t cell receptor delta1a/b-3; PDBTitle: crystal structure of mica-specific human gamma delta t cell receptor
71	c3hf3A	Alignment	not modelled	7.3	11	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
72	d1luxja1	Alignment	not modelled	7.3	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
73	d1r7ha	Alignment	not modelled	7.2	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
74	c1u83A	Alignment	not modelled	7.2	15	PDB header: lyase Chain: A: PDB Molecule: phosphosulfolactate synthase; PDBTitle: psl synthase from bacillus subtilis
75	d1u83a	Alignment	not modelled	7.2	15	Fold: TIM beta/alpha-barrel Superfamily: (2r)-phospho-3-sulfolactate synthase ComA Family: (2r)-phospho-3-sulfolactate synthase ComA
76	d2ouwa1	Alignment	not modelled	7.1	17	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
77	c1i7mD	Alignment	not modelled	7.0	18	PDB header: lyase Chain: D: PDB Molecule: s-adenosylmethionine decarboxylase beta chain; PDBTitle: human s-adenosylmethionine decarboxylase with covalently bound2 pyruvoyl group and complexed with 4-amidinoidan-1-one-2'-3 amidinohydrazone
78	d1vkea	Alignment	not modelled	7.0	11	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
79	c2w95B	Alignment	not modelled	6.9	11	PDB header: cell adhesion Chain: B: PDB Molecule: discoidin-1 subunit a; PDBTitle: structure of the discoidin i from dictyostelium discoideum2 in complex with galnac at 1.75 angstrom resolution
						Fold: Thioredoxin fold

80	d1fova_	Alignment	not modelled	6.9	23	Superfamily: Thioredoxin-like Family: Thioltransferase
81	d1jmxal	Alignment	not modelled	6.7	19	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
82	d1aopa4	Alignment	not modelled	6.5	40	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
83	d1un2a_	Alignment	not modelled	6.5	36	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbA-like
84	d1fvka_	Alignment	not modelled	6.4	36	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbA-like
85	d1dl6a_	Alignment	not modelled	6.3	15	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
86	d1tzaa_	Alignment	not modelled	6.3	39	Fold: Immunoglobulin-like beta-sandwich Superfamily: ApaG-like Family: ApaG-like
87	d2v4jb3	Alignment	not modelled	6.2	18	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
88	c1t3ba_	Alignment	not modelled	6.2	29	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: x-ray structure of dsbc from haemophilus influenzae
89	d1adta2	Alignment	not modelled	6.1	23	Fold: Zn-binding domains of ADDBP Superfamily: Zn-binding domains of ADDBP Family: Zn-binding domains of ADDBP
90	c2f1eA_	Alignment	not modelled	6.1	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein apag; PDBTitle: solution structure of apag protein
91	d1ekqa_	Alignment	not modelled	6.1	13	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Thiamin biosynthesis kinases
92	d2o4da1	Alignment	not modelled	6.0	15	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
93	d1r4wa_	Alignment	not modelled	6.0	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbA-like
94	d2drpa2	Alignment	not modelled	5.9	60	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
95	c2k5cA_	Alignment	not modelled	5.8	17	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein pf0385; PDBTitle: nmr structure for pf0385
96	d2fug21	Alignment	not modelled	5.8	12	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: NQO2-like
97	d1twia2	Alignment	not modelled	5.7	14	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
98	c3f4tA_	Alignment	not modelled	5.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of wolbachia pipientis alpha-dsba1 c97a/c146a
99	d1tdha3	Alignment	not modelled	5.6	29	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins