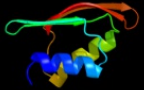
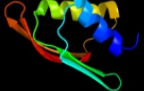
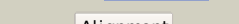
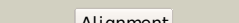
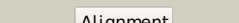
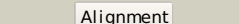
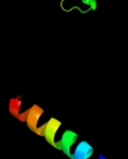
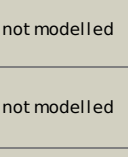


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1uv7A_	 Alignment		99.8	11	PDB header: transport Chain: A: PDB Molecule: general secretion pathway protein m; PDBTitle: periplasmic domain of epsm from vibrio cholerae
2	d1uv7a_	 Alignment		99.8	11	Fold: RRF/tRNA synthetase additional domain-like Superfamily: General secretion pathway protein M, EpsM Family: General secretion pathway protein M, EpsM
3	c2rjzA_	 Alignment		97.7	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pilo protein; PDBTitle: crystal structure of the type 4 fimbrial biogenesis protein pilo from2 pseudomonas aeruginosa
4	c2rddB_	 Alignment		57.7	17	PDB header: membrane protein/transport protein Chain: B: PDB Molecule: upf0092 membrane protein yajc; PDBTitle: x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
5	c2y9kG_	 Alignment		47.2	9	PDB header: protein transport Chain: G: PDB Molecule: protein invg; PDBTitle: three-dimensional model of salmonella's needle complex at2 subnanometer resolution
6	d1bjna_	 Alignment		29.5	9	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
7	c3gr5A_	 Alignment		28.1	10	PDB header: membrane protein Chain: A: PDB Molecule: escs; PDBTitle: periplasmic domain of the outer membrane secretin escs from2 enteropathogenic e.coli (epec)
8	d1ppic2	 Alignment		26.1	9	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
9	d1tp6a_	 Alignment		24.9	22	Fold: Cystatin-like Superfamily: NTF2-like Family: PA1314-like
10	d1dnla_	 Alignment		24.9	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
11	c3hd7A_	 Alignment		22.9	22	PDB header: exocytosis Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1

12	dlyioa1	Alignment		21.4	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
13	d2c0ra1	Alignment		20.2	7	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
14	d1x4pa1	Alignment		18.6	18	Fold: Surp module (SWAP domain) Superfamily: Surp module (SWAP domain) Family: Surp module (SWAP domain)
15	d1nrga_	Alignment		18.1	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
16	c1nrgA_	Alignment		18.1	11	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxine 5'-phosphate oxidase; PDBTitle: structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
17	d1t9ma_	Alignment		17.1	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
18	c2kncA_	Alignment		16.5	25	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
19	d1hywa_	Alignment		14.4	5	Fold: gpW/XkdW-like Superfamily: Head-to-tail joining protein W, gpW Family: Head-to-tail joining protein W, gpW
20	d1bccc3	Alignment		12.8	11	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
21	d1v54d_	Alignment	not modelled	12.5	27	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit IV Family: Mitochondrial cytochrome c oxidase subunit IV
22	c3mn7S_	Alignment	not modelled	12.1	20	PDB header: contractile protein/protein binding Chain: S: PDB Molecule: spire ddd; PDBTitle: structures of actin-bound wh2 domains of spire and the implication for2 filament nucleation
23	c2rnjA_	Alignment	not modelled	11.8	19	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrrA; PDBTitle: nmr structure of the s. aureus vrrA dna binding domain
24	c3mn5S_	Alignment	not modelled	11.8	20	PDB header: contractile protein/protein binding Chain: S: PDB Molecule: protein spire; PDBTitle: structures of actin-bound wh2 domains of spire and the implication for2 filament nucleation
25	c3qm2A_	Alignment	not modelled	11.4	9	PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase; PDBTitle: 2.25 angstrom crystal structure of phosphoserine aminotransferase2 (serc) from salmonella enterica subsp. enterica serovar typhimurium
26	c2d89A_	Alignment	not modelled	10.7	19	PDB header: structural protein, protein binding Chain: A: PDB Molecule: ehbp1 protein; PDBTitle: solution structure of the ch domain from human eh domain2 binding protein 1
27	c2v69Q_	Alignment	not modelled	10.6	27	PDB header: electron transport Chain: Q: PDB Molecule: cytochrome c oxidase subunit 4 isoform 1; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
28	c2w7vB_	Alignment	not modelled	10.5	11	PDB header: transport protein Chain: B: PDB Molecule: general secretion pathway protein I; PDBTitle: periplasmic domain of epsI from vibrio

						parahaemolyticus
29	d2csua2	Alignment	not modelled	10.4	7	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
30	c2d88A	Alignment	not modelled	10.3	24	PDB header: signaling protein, protein binding Chain: A: PDB Molecule: protein mical-3; PDBTitle: solution structure of the ch domain from human mical-32 protein
31	d1ty9a	Alignment	not modelled	10.0	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
32	d2p8ia1	Alignment	not modelled	9.4	14	Fold: Ferredoxin-like Superfamily: DOPA-like Family: DOPA dioxygenase-like
33	c2yv2A	Alignment	not modelled	9.2	9	PDB header: ligase Chain: A: PDB Molecule: succinyl-coa synthetase alpha chain; PDBTitle: crystal structure of succinyl-coa synthetase alpha chain from <i>Aeropyrum pernix</i> k1
34	c3adyA	Alignment	not modelled	8.9	16	PDB header: proton transport Chain: A: PDB Molecule: dotd; PDBTitle: crystal structure of dotd from <i>Legionella</i>
35	d1dwka2	Alignment	not modelled	8.8	13	Fold: Cyanase C-terminal domain Superfamily: Cyanase C-terminal domain Family: Cyanase C-terminal domain
36	c2k1aA	Alignment	not modelled	8.8	29	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: bicelle-embedded integrin alpha(iiB) transmembrane segment
37	d2f06a2	Alignment	not modelled	8.6	15	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
38	c2iv1J	Alignment	not modelled	8.5	13	PDB header: lyase Chain: J: PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the 2 catalytic mechanism of cyanase
39	d1dxxa2	Alignment	not modelled	8.4	10	Fold: CH domain-like Superfamily: Calponin-homology domain, CH-domain Family: Calponin-homology domain, CH-domain
40	d1sh5a2	Alignment	not modelled	8.3	19	Fold: CH domain-like Superfamily: Calponin-homology domain, CH-domain Family: Calponin-homology domain, CH-domain
41	c1wylA	Alignment	not modelled	8.3	30	PDB header: signaling protein Chain: A: PDB Molecule: nedd9 interacting protein with calponin homology PDBTitle: solution structure of the ch domain of human nedd92 interacting protein with calponin homology and lim domains
42	d2a2ja1	Alignment	not modelled	8.2	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
43	c2kncB	Alignment	not modelled	7.9	14	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
44	c1x3uA	Alignment	not modelled	7.7	26	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein fixj; PDBTitle: solution structure of the c-terminal transcriptional2 activator domain of fixj from <i>Sinorhizobium melilot</i>
45	c2a2jA	Alignment	not modelled	7.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of a putative pyridoxine 5'-phosphate oxidase2 (rv2607) from <i>Mycobacterium tuberculosis</i>
46	d1ku3a	Alignment	not modelled	7.6	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
47	c2pebB	Alignment	not modelled	7.4	10	PDB header: oxidoreductase Chain: B: PDB Molecule: putative dioxygenase; PDBTitle: crystal structure of a putative dioxygenase (npun_f1925) from <i>Nostoc punctiforme</i> pcc 73102 at 1.46 a resolution
48	d3e9va1	Alignment	not modelled	7.4	14	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
49	c2d87A	Alignment	not modelled	7.2	15	PDB header: structural protein, protein binding Chain: A: PDB Molecule: smoothelin splice isoform I2; PDBTitle: solution structure of the ch domain from human smoothelin2 splice isoform I2
50	d1wb9a4	Alignment	not modelled	7.2	13	Fold: MutS N-terminal domain-like Superfamily: DNA repair protein MutS, domain I Family: DNA repair protein MutS, domain I
51	c3smtA	Alignment	not modelled	7.2	19	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase setd3; PDBTitle: crystal structure of human set domain-containing protein3
52	d1bkra	Alignment	not modelled	7.2	15	Fold: CH domain-like Superfamily: Calponin-homology domain, CH-domain Family: Calponin-homology domain, CH-domain
53	d1ewqa4	Alignment	not modelled	7.1	18	Fold: MutS N-terminal domain-like Superfamily: DNA repair protein MutS, domain I Family: DNA repair protein MutS, domain I
54	c3cwbC	Alignment	not modelled	6.8	11	PDB header: oxidoreductase Chain: C: PDB Molecule: cytochrome b; PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of 2 the polyketide crocacin-d
						Fold: BTG domain-like

55	d2z15a1	Alignment	not modelled	6.8	14	Superfamily: BTG domain-like Family: BTG domain-like
56	c3hiIB	Alignment	not modelled	6.7	38	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: sam domain of human ephrin type-a receptor 1 (epha1)
57	d3dhxa1	Alignment	not modelled	6.5	22	Fold: Ferredoxin-like Superfamily: ACT-like Family: NIL domain-like
58	d1ygga3	Alignment	not modelled	6.5	12	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
59	d2af7a1	Alignment	not modelled	6.3	6	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
60	c2ogfD	Alignment	not modelled	6.2	12	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein mj0408; PDBTitle: crystal structure of protein mj0408 from methanococcus jannaschii,2 pfam duf372
61	d1ulra	Alignment	not modelled	6.2	17	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
62	c3f6oB	Alignment	not modelled	5.9	18	PDB header: transcription regulator Chain: B: PDB Molecule: probable transcriptional regulator, arsr family PDBTitle: crystal structure of arsr family transcriptional regulator,2 rha00566
63	d2iw0a1	Alignment	not modelled	5.9	6	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
64	c2d1uA	Alignment	not modelled	5.8	10	PDB header: metal transport Chain: A: PDB Molecule: iron(iii) dicitrate transport protein fecA; PDBTitle: solution structure of the periplasmic signaling domain of2 fecA from escherichia coli
65	d1ku7a	Alignment	not modelled	5.6	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
66	c3mgjA	Alignment	not modelled	5.6	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mj1480; PDBTitle: crystal structure of the saccharop_dh_n domain of mj14802 protein from methanococcus jannaschii. northeast structural3 genomics consortium target mjr83a.
67	c3dmyA	Alignment	not modelled	5.6	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein fdra; PDBTitle: crystal structure of a predicated acyl-coa synthetase from e.coli
68	c2e8nA	Alignment	not modelled	5.4	33	PDB header: transferase, signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: solution structure of the c-terminal sam-domain of ephaa2:2 ephrin type-a receptor 2 precursor (ec 2.7.10.1)
69	d1euca2	Alignment	not modelled	5.2	11	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
70	c2yh5A	Alignment	not modelled	5.1	25	PDB header: lipid binding protein Chain: A: PDB Molecule: dapx protein; PDBTitle: structure of the c-terminal domain of bamc
71	c1zzvA	Alignment	not modelled	5.1	10	PDB header: membrane protein, metal transport Chain: A: PDB Molecule: iron(iii) dicitrate transport protein fecA; PDBTitle: solution nmr structure of the periplasmic signaling domain2 of the outer membrane iron transporter fecA from3 escherichia coli.
72	d1bhda	Alignment	not modelled	5.0	10	Fold: CH domain-like Superfamily: Calponin-homology domain, CH-domain Family: Calponin-homology domain, CH-domain