



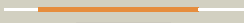








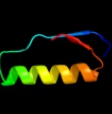

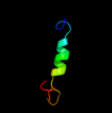

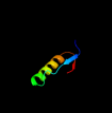

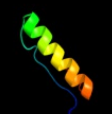


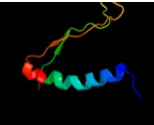
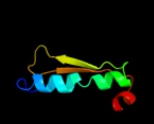
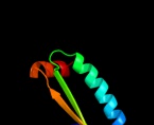
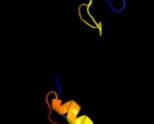
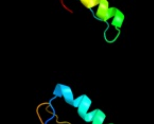
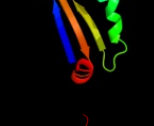
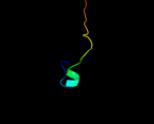
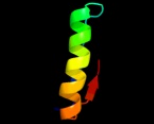



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2okqa1	 Alignment		100.0	100	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: YbaA-like
2	c2okqB_	 Alignment		100.0	100	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ybaa; PDBTitle: crystal structure of unknown conserved ybaa protein from <i>Shigella flexneri</i>
3	d1vqsa_	 Alignment		87.4	19	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: NIPSNAP
4	d1vqya1	 Alignment		86.1	19	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: NIPSNAP
5	d2fiua1	 Alignment		80.5	23	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Atu0297-like
6	c3lo3E_	 Alignment		75.2	18	PDB header: structure genomics, unknown function Chain: E: PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved functionally unknown2 protein from <i>Colwellia psychrerythraea</i> 34h.
7	c2wqhA_	 Alignment		53.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase large PDBTitle: human ribonucleotide reductase r1 subunit (rrm1) in complex2 with datp and mg.
8	c3nfgA_	 Alignment		52.2	25	PDB header: transcription Chain: A: PDB Molecule: transcription factor iws1; PDBTitle: crystal structure of the conserved central domain of yeast spn1/iws1
9	c2cvuA_	 Alignment		51.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase large chain PDBTitle: structures of yeast ribonucleotide reductase i
10	c3hnfA_	 Alignment		45.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase large subunit; PDBTitle: crystal structure of human ribonucleotide reductase 1 bound to the2 effectors ttp and datp
11	c2xpnA_	 Alignment		44.7	18	PDB header: transcription Chain: A: PDB Molecule: iws1; PDBTitle: crystal structure of a spt6-iws1 (spn1) complex from <i>Encephalitozoon cuniculi</i> , form i

12	c3dcaC	Alignment		33.2	19	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: rpa0582; PDBTitle: crystal structure of the rpa0582- protein of unknown2 function from rhodopseudomonas palustris- a structural3 genomics target
13	c3bm7A	Alignment		31.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: protein of unknown function with ferredoxin-like fold; PDBTitle: crystal structure of a putative antibiotic biosynthesis monooxygenase2 (cc_2132) from caulobacter crescentus cb15 at 1.35 a resolution
14	c2rliA	Alignment		29.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of a putative monooxygenase (yp_001095275.1) from2 shewanella loihica pv-4 at 1.26 a resolution
15	c1pemA	Alignment		22.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase 2 alpha PDBTitle: ribonucleotide reductase protein r1e from salmonella2 typhimurium
16	d1iuja	Alignment		21.9	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
17	d1edqa1	Alignment		21.1	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
18	d1peqa2	Alignment		20.6	21	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: R1 subunit of ribonucleotide reductase, C-terminal domain
19	d1xbwa	Alignment		19.4	17	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
20	c3chgB	Alignment		17.5	9	PDB header: ligand binding protein Chain: B: PDB Molecule: glycine betaine-binding protein; PDBTitle: the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
21	c2qlxA	Alignment	not modelled	17.3	21	PDB header: isomerase Chain: A: PDB Molecule: l-rhamnose mutarotase; PDBTitle: crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose
22	c2qlwA	Alignment	not modelled	17.2	21	PDB header: isomerase Chain: A: PDB Molecule: rhau; PDBTitle: crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
23	d2k8ea1	Alignment	not modelled	16.6	27	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
24	d1rlra2	Alignment	not modelled	16.2	9	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: R1 subunit of ribonucleotide reductase, C-terminal domain
25	d2k49a2	Alignment	not modelled	15.9	22	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
26	d1iwpA	Alignment	not modelled	14.3	39	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: Diol dehydratase, alpha subunit
27	d1x4ha1	Alignment	not modelled	12.5	9	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
28	d1fnxh2	Alignment	not modelled	12.5	14	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
29	d2ix0a1	Alignment	not modelled	12.4	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like

30	d1lmta2	Alignment	not modelled	11.7	56	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Colipase-like Family: Colipase-like
31	d2qtva2	Alignment	not modelled	11.1	50	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: beta-sandwich domain of Sec23/24 Family: beta-sandwich domain of Sec23/24
32	c3r1rB_	Alignment	not modelled	10.6	8	PDB header: complex (oxidoreductase/peptide) Chain: B: PDB Molecule: ribonucleotide reductase r1 protein; PDBTitle: ribonucleotide reductase r1 protein with amppnp occupying2 the activity site from escherichia coli
33	d3bida1	Alignment	not modelled	9.8	28	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
34	d2omoa1	Alignment	not modelled	9.4	19	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
35	dleexa_	Alignment	not modelled	9.3	35	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: Diol dehydratase, alpha subunit
36	c1xjeA_	Alignment	not modelled	9.3	25	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleotide reductase, b12-dependent; PDBTitle: structural mechanism of allosteric substrate specificity in a2 ribonucleotide reductase: dtp-gdp complex
37	c3gh7A_	Alignment	not modelled	8.8	13	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of beta-hexosaminidase from paenibacillus2 sp. ts12 in complex with galnac
38	d2k7ia1	Alignment	not modelled	8.1	26	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
39	c2k7iB_	Alignment	not modelled	8.1	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: upf0339 protein atu0232; PDBTitle: solution nmr structure of protein atu0232 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att3. ontario center for structural proteomics target atc0223.
40	d2zdpa1	Alignment	not modelled	7.4	8	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
41	c3p6yD_	Alignment	not modelled	7.4	13	PDB header: rna binding protein/rna Chain: D: PDB Molecule: cleavage and polyadenylation specificity factor subunit 6; PDBTitle: cf im25-cf im68-uguaa complex
42	c2i38A_	Alignment	not modelled	7.1	26	PDB header: rna binding protein/chimera Chain: A: PDB Molecule: fusion protein consists of immunoglobulin g- PDBTitle: solution structure of the rrm of srp20
43	c2kdbA_	Alignment	not modelled	6.6	19	PDB header: protein binding Chain: A: PDB Molecule: homocysteine-responsive endoplasmic reticulum- PDBTitle: solution structure of human ubiquitin-like domain of 2 herpud2_9_85, northeast structural genomics consortium3 (nesg) target ht53a
44	c2k49A_	Alignment	not modelled	6.6	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0339 protein so_3888; PDBTitle: solution nmr structure of upf0339 protein so3888 from shewanella2 oneidensis. northeast structural genomics consortium target sor190
45	c2f3ja_	Alignment	not modelled	6.5	17	PDB header: transport protein Chain: A: PDB Molecule: rna and export factor binding protein 2; PDBTitle: the solution structure of the ref2-i mrna export factor2 (residues 1-155).
46	c1ylhA_	Alignment	not modelled	5.6	14	PDB header: lyase Chain: A: PDB Molecule: phosphoenolpyruvate carboxykinase; PDBTitle: crystal structure of phosphoenolpyruvate carboxykinase from2 actinobacillus succinogenes in complex with manganese and3 pyruvate
47	d1v3va1	Alignment	not modelled	5.5	25	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
48	d1tz0a_	Alignment	not modelled	5.3	24	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
49	c2omoC_	Alignment	not modelled	5.3	19	PDB header: oxidoreductase Chain: C: PDB Molecule: duf176; PDBTitle: putative antibiotic biosynthesis monooxygenase from nitrosomonas2 europaea