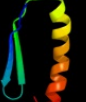
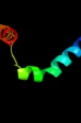


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gy9i1	 Alignment		100.0	100	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
2	d2vqe1	 Alignment		100.0	54	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
3	c3bbn1	 Alignment		100.0	46	PDB header: ribosome Chain: I: PDB Molecule: ribosomal protein s9; PDBTitle: homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
4	c2xzml	 Alignment		100.0	25	PDB header: ribosome Chain: I: PDB Molecule: rps16e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
5	c2zkqi	 Alignment		100.0	33	PDB header: ribosomal protein/rna Chain: I: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
6	c1s1hl	 Alignment		100.0	36	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s16; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
7	c3iz6l	 Alignment		100.0	36	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s16 (s9p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
8	c1s3bB	 Alignment		54.6	50	PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase [flavin-containing] b; PDBTitle: crystal structure of maob in complex with n-methyl-n-2 propargyl-1(r)-aminoindan
9	d1d5ta1	 Alignment		50.8	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
10	c1v0jB	 Alignment		46.8	38	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: udp-galactopyranose mutase from mycobacterium tuberculosis
11	c2rrlA	 Alignment		42.5	15	PDB header: protein transport Chain: A: PDB Molecule: flagellar hook-length control protein; PDBTitle: solution structure of the c-terminal domain of the flik

12	c1ltxR_	Alignment		39.5	20	PDB header: transferase/protein binding Chain: R: PDB Molecule: rab escort protein 1; PDBTitle: structure of rab escort protein-1 in complex with rab2 geranylgeranyl transferase and isoprenoid
13	c2hydB_	Alignment		35.6	21	PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
14	d1hyua1	Alignment		35.2	30	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
15	c3cp8C_	Alignment		33.7	32	PDB header: oxidoreductase Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from chlorobium tepidum
16	c2uzzD_	Alignment		33.2	38	PDB header: oxidoreductase Chain: D: PDB Molecule: n-methyl-l-tryptophan oxidase; PDBTitle: x-ray structure of n-methyl-l-tryptophan oxidase (mtox)
17	c2v6oA_	Alignment		33.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin glutathione reductase; PDBTitle: structure of schistosoma mansoni thioredoxin-gluthathione2 reductase (smtgr)
18	c3jskN_	Alignment		32.8	24	PDB header: biosynthetic protein Chain: N: PDB Molecule: cypbp37 protein; PDBTitle: thiazole synthase from neurospora crassa
19	d2bcgg1	Alignment		32.7	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
20	d1gesa1	Alignment		30.9	32	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
21	c3k7tB_	Alignment	not modelled	30.7	45	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-hydroxy-l-nicotine oxidase; PDBTitle: crystal structure of apo-form 6-hydroxy-l-nicotine oxidase,2 crystal form p3121
22	d1rbla1	Alignment	not modelled	30.4	25	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
23	d1wdda1	Alignment	not modelled	28.9	22	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
24	c2vv1D_	Alignment	not modelled	28.5	36	PDB header: oxidoreductase Chain: D: PDB Molecule: monoamine oxidase n; PDBTitle: the structure of mao-n-d3, a variant of monoamine oxidase2 from aspergillus niger.
25	c2yl4A_	Alignment	not modelled	27.8	26	PDB header: membrane protein Chain: A: PDB Molecule: atp-binding cassette sub-family b member 10, PDBTitle: structure of the human mitochondrial abc transporter, abcb10
26	c4a1eU_	Alignment	not modelled	27.0	29	PDB header: ribosome Chain: U: PDB Molecule: rpl35; PDBTitle: t thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
27	c2zxiC_	Alignment	not modelled	26.7	33	PDB header: fad-binding protein Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: structure of aquifex aeolicus gida in the form ii crystal
28	c3cqvA_	Alignment	not modelled	25.7	36	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: geranylgeranyl reductase related protein;

28	c3cgvA	Alignment	not modelled	23.7	30	PDBTitle: crystal structure of geranylgeranyl bacteriochlorophyll reductase-like2 fixc homolog (np_393992.1) from thermoplasma acidophilum at 1.60 a3 resolution
29	c3rhaA	Alignment	not modelled	23.8	28	PDB header: oxidoreductase Chain: A: PDB Molecule: putrescine oxidase; PDBTitle: the crystal structure of oxidoreductase from arthrobacter aureus
30	c1ryiB	Alignment	not modelled	23.4	38	PDB header: oxidoreductase Chain: B: PDB Molecule: glycine oxidase; PDBTitle: structure of glycine oxidase with bound inhibitor glycolate
31	d1rrea	Alignment	not modelled	22.5	25	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: ATP-dependent protease Lon (La), catalytic domain
32	c3g05B	Alignment	not modelled	21.7	30	PDB header: rna binding protein Chain: B: PDB Molecule: trna uridine 5-carboxymethylaminomethyl modification enzyme PDBTitle: crystal structure of n-terminal domain (2-550) of e.coli mnmg
33	c2olnA	Alignment	not modelled	21.6	38	PDB header: oxidoreductase Chain: A: PDB Molecule: nikd protein; PDBTitle: nikd, an unusual amino acid oxidase essential for2 nikkomycin biosynthesis: closed form at 1.15 a resolution
34	c3m6aC	Alignment	not modelled	21.2	25	PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent protease la 1; PDBTitle: crystal structure of bacillus subtilis lon c-terminal domain
35	c2w0hA	Alignment	not modelled	21.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: trypanothione reductase; PDBTitle: x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph
36	c2qaeA	Alignment	not modelled	19.3	32	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure analysis of trypanosoma cruzi lipoamide2 dehydrogenase
37	c1dxlC	Alignment	not modelled	19.3	30	PDB header: oxidoreductase Chain: C: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum
38	c3uo9B	Alignment	not modelled	17.8	29	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: glutaminase kidney isoform, mitochondrial; PDBTitle: crystal structure of human gac in complex with glutamate and bptes
39	c2nvkX	Alignment	not modelled	17.3	36	PDB header: oxidoreductase Chain: X: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from drosophila2 melanogaster
40	d3lada1	Alignment	not modelled	17.0	35	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
41	d1dxa1	Alignment	not modelled	16.9	30	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
42	d1d4ca2	Alignment	not modelled	15.8	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
43	d2bj7a1	Alignment	not modelled	15.5	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
44	d1reoa1	Alignment	not modelled	15.4	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
45	c1f8sA	Alignment	not modelled	15.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: l-amino acid oxidase; PDBTitle: crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
46	c3b5xB	Alignment	not modelled	15.3	31	PDB header: membrane protein Chain: B: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of msba from vibrio cholerae
47	c2r9zB	Alignment	not modelled	15.2	30	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione amide reductase; PDBTitle: glutathione amide reductase from chromatium gracile
48	c3ihgA	Alignment	not modelled	14.9	20	PDB header: flavoprotein, oxidoreductase Chain: A: PDB Molecule: rdme; PDBTitle: crystal structure of a ternary complex of aklavinone-112 hydroxylase with fad and aklavinone
49	c2e1mA	Alignment	not modelled	14.8	26	PDB header: oxidoreductase Chain: A: PDB Molecule: l-glutamate oxidase; PDBTitle: crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
50	c3dmeB	Alignment	not modelled	14.6	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved exported protein; PDBTitle: crystal structure of conserved exported protein from2 bordetella pertussis. northeast structural genomics target3 ber141
51	c1tytA	Alignment	not modelled	14.6	25	PDB header: oxidoreductase Chain: A: PDB Molecule: trypanothione reductase, oxidized form; PDBTitle: crystal and molecular structure of crithidia fasciculata2 trypanothione reductase at 2.6 angstroms resolution
52	c3ss4C	Alignment	not modelled	14.5	29	PDB header: hydrolase Chain: C: PDB Molecule: glutaminase c; PDBTitle: crystal structure of mouse glutaminase c, phosphate-bound form
53	d1kifa1	Alignment	not modelled	14.4	25	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain

						Family: D-aminoacid oxidase, N-terminal domain
54	dlh6va1	Alignment	not modelled	14.1	32	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
55	dlchua2	Alignment	not modelled	14.0	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
56	c3p4rM_	Alignment	not modelled	13.9	20	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
57	c3nyeA_	Alignment	not modelled	13.8	24	PDB header: oxidoreductase Chain: A: PDB Molecule: d-arginine dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
58	dlseza1	Alignment	not modelled	13.8	37	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
59	c3g5uB_	Alignment	not modelled	13.7	26	PDB header: membrane protein Chain: B: PDB Molecule: multidrug resistance protein 1a; PDBTitle: structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding
60	c1ndaD_	Alignment	not modelled	13.5	30	PDB header: oxidoreductase Chain: D: PDB Molecule: trypanothione oxidoreductase; PDBTitle: the structure of trypanosoma cruzi trypanothione reductase2 in the oxidized and nadph reduced state
61	d2gf3a1	Alignment	not modelled	13.3	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
62	dlv59a1	Alignment	not modelled	13.2	29	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
63	dlpj5a2	Alignment	not modelled	13.1	33	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
64	clkf6A_	Alignment	not modelled	13.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase flavoprotein; PDBTitle: e. coli quinol-fumarate reductase with bound inhibitor hqno
65	d2dw4a2	Alignment	not modelled	12.8	32	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
66	d2bi7a1	Alignment	not modelled	12.8	24	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: UDP-galactopyranose mutase, N-terminal domain
67	d2gmha1	Alignment	not modelled	12.7	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
68	dl1pfa1	Alignment	not modelled	12.6	39	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
69	d2hzaa1	Alignment	not modelled	12.3	30	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
70	c2cfyB_	Alignment	not modelled	12.3	30	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of human thioredoxin reductase 1
71	c3bnuA_	Alignment	not modelled	12.2	26	PDB header: oxidoreductase Chain: A: PDB Molecule: polyamine oxidase fms1; PDBTitle: crystal structure of polyamine oxidase fms1 from2 saccharomyces cerevisiae in complex with bis-(3s,3's)-3 methylated spermine
72	d2i0za1	Alignment	not modelled	12.1	36	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
73	c2r4jA_	Alignment	not modelled	11.9	43	PDB header: oxidoreductase Chain: A: PDB Molecule: aerobic glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of escherichia coli semet substituted2 glycerol-3-phosphate dehydrogenase in complex with dhap
74	c3bjrA_	Alignment	not modelled	11.7	23	PDB header: hydrolase Chain: A: PDB Molecule: putative carboxylesterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcf51 at 2.09 a resolution
75	c1h83A_	Alignment	not modelled	11.6	39	PDB header: oxidoreductase Chain: A: PDB Molecule: polyamine oxidase; PDBTitle: structure of polyamine oxidase in complex with2 1,8-diaminooctane
76	c3i6dA_	Alignment	not modelled	11.5	37	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of ppo from bacillus subtilis with af
77	dlrp0a1	Alignment	not modelled	11.5	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Thi4-like
78	dlvg0a1	Alignment	not modelled	11.3	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
79	c3l8kB_	Alignment	not modelled	11.3	43	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of a dihydrolipoyl dehydrogenase from2

						sulfolobus solfataricus
80	c2gqfA_	Alignment	not modelled	11.2	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0933; PDBTitle: crystal structure of flavoprotein hi0933 from haemophilus influenzae2 rd
81	c3hdql_	Alignment	not modelled	11.0	26	PDB header: isomerase Chain: I: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of udp-galactopyranose mutase (oxidized2 form) in complex with substrate
82	c2aczA_	Alignment	not modelled	10.9	24	PDB header: oxidoreductase/electron transport Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: complex ii (succinate dehydrogenase) from e. coli with atpenin a52 inhibitor co-crystallized at the ubiquinone binding site
83	c2yg4B_	Alignment	not modelled	10.9	32	PDB header: oxidoreductase Chain: B: PDB Molecule: putrescine oxidase; PDBTitle: structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
84	c3gyxA_	Alignment	not modelled	10.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: adenylsulfate reductase; PDBTitle: crystal structure of adenylsulfate reductase from2 desulfovibrio gigas
85	c3r9uA_	Alignment	not modelled	10.6	29	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: thioredoxin-disulfide reductase from campylobacter jejuni.
86	d1r7la_	Alignment	not modelled	10.4	20	Fold: Bacillus phage protein Superfamily: Bacillus phage protein Family: Bacillus phage protein
87	c3o0hA_	Alignment	not modelled	10.4	30	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase from bartonella henselae
88	c3nixF_	Alignment	not modelled	10.2	25	PDB header: oxidoreductase Chain: F: PDB Molecule: flavoprotein/dehydrogenase; PDBTitle: crystal structure of flavoprotein/dehydrogenase from cytophaga2 hutchinsonii. northeast structural genomics consortium target chr43.
89	c1geuA_	Alignment	not modelled	10.1	36	PDB header: oxidoreductase(flavoenzyme) Chain: A: PDB Molecule: glutathione reductase; PDBTitle: anatomy of an engineered nad-binding site
90	c2gmhA_	Alignment	not modelled	10.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: electron transfer flavoprotein-ubiquinone PDBTitle: structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
91	d2gjca1	Alignment	not modelled	10.0	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Thi4-like
92	d1onfa1	Alignment	not modelled	9.9	45	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
93	c1yvvB_	Alignment	not modelled	9.8	30	PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase, flavin-containing; PDBTitle: x-ray structurure of p. syringae q888a4 oxidoreductase at2 resolution 2.5a. northeast structural genomics consortium3 target psr10.
94	d1rhya2	Alignment	not modelled	9.8	15	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Imidazole glycerol phosphate dehydratase
95	c2hqmB_	Alignment	not modelled	9.8	45	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae
96	c2qa2A_	Alignment	not modelled	9.7	29	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide oxygenase cab2; PDBTitle: crystal structure of cab2, an aromatic hydroxylase from angucycline2 biosynthesis, determined to 2.7 a resolution
97	c1kifE_	Alignment	not modelled	9.7	26	PDB header: flavoprotein Chain: E: PDB Molecule: d-amino acid oxidase; PDBTitle: d-amino acid oxidase from pig kidney
98	c2b9yA_	Alignment	not modelled	9.7	29	PDB header: isomerase Chain: A: PDB Molecule: putative aminooxidase; PDBTitle: crystal structure of cla-producing fatty acid isomerase2 from p. acnes
99	d1jnra2	Alignment	not modelled	9.4	32	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain