

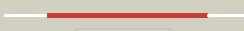
























































#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1oftC_	 Alignment		100.0	26	PDB header: bacterial cell division inhibitor Chain: C: PDB Molecule: hypothetical protein pa3008; PDBTitle: crystal structure of sula from pseudomonas aeruginosa
2	d1ofux_	 Alignment		100.0	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Bacterial cell division inhibitor SulA
3	d1xp8a1	 Alignment		99.5	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
4	c1xp8A_	 Alignment		99.5	16	PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: "deinococcus radiodurans reca in complex with atp-gamma-s"
5	d1ubea1	 Alignment		99.4	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
6	d1u94a1	 Alignment		99.4	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
7	c2zroA_	 Alignment		99.2	11	PDB header: hydrolase Chain: A: PDB Molecule: protein reca; PDBTitle: msreca adp form iv
8	c3hr8A_	 Alignment		99.2	14	PDB header: recombination Chain: A: PDB Molecule: protein reca; PDBTitle: crystal structure of thermotoga maritima reca
9	c2recB_	 Alignment		99.2	15	PDB header: helicase PDB COMPND:
10	d1mo6a1	 Alignment		99.1	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
11	c3cmwA_	 Alignment		98.9	13	PDB header: recombination/dna Chain: A: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-2 ssdna/dsna structures

12	c3cmvG_	Alignment		98.1	13	PDB header: recombination Chain: G: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
13	c3io5B_	Alignment		97.9	14	PDB header: dna binding protein Chain: B: PDB Molecule: recombination and repair protein; PDBTitle: crystal structure of a dimeric form of the uvsx recombinase core2 domain from enterobacteria phage t4
14	c3cmuA_	Alignment		97.4	16	PDB header: recombination/dna Chain: A: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
15	d1tf7a2	Alignment		72.1	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
16	c2w0mA_	Alignment		60.4	10	PDB header: unknown function Chain: A: PDB Molecule: sso2452; PDBTitle: crystal structure of sso2452 from sulfolobus solfataricus2 p2
17	c2ztsB_	Alignment		59.7	11	PDB header: atp-binding protein Chain: B: PDB Molecule: putative uncharacterized protein ph0186; PDBTitle: crystal structure of kaic-like protein ph0186 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
18	d1j5pa4	Alignment		58.4	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
19	c2dc1A_	Alignment		55.9	7	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
20	c3ldaA_	Alignment		40.8	18	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: yeast rad51 h352y filament interface mutant
21	d1rvv1_	Alignment	not modelled	37.4	10	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
22	c2pjka_	Alignment	not modelled	37.3	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 178aa long hypothetical molybdenum cofactor PDBTitle: structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
23	d1nqua_	Alignment	not modelled	33.5	10	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
24	c2obxH_	Alignment	not modelled	33.3	17	PDB header: transferase Chain: H: PDB Molecule: 6,7-dimethyl-8-ribityllumazine synthase 1; PDBTitle: lumazine synthase ribh2 from mesorhizobium loti (gene ml17281, swiss-2 prot entry q986n2) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
25	c1t4ga_	Alignment	not modelled	31.0	11	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: atpase in complex with amp-pnp
26	d1di0a_	Alignment	not modelled	31.0	16	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
27	c2de4B_	Alignment	not modelled	30.5	17	PDB header: hydrolase Chain: B: PDB Molecule: dibenzothiophene desulfurization enzyme b; PDBTitle: crystal structure of dszb c27s mutant in complex with biphenyl-2-2 sulfinic acid
						PDB header: structural genomics, unknown function

28	c2dr3A_	Alignment	not modelled	27.9	3	Chain: A: PDB Molecule: upf0273 protein ph0284; PDBTitle: crystal structure of reca superfamily atpase ph0284 from pyrococcus2 horikoshii ot3
29	c1j5pA_	Alignment	not modelled	27.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartate dehydrogenase; PDBTitle: crystal structure of aspartate dehydrogenase (tm1643) from thermotoga2 maritima at 1.9 a resolution
30	c3k2gA_	Alignment	not modelled	25.6	12	PDB header: resiniferatoxin binding protein Chain: A: PDB Molecule: resiniferatoxin-binding, phosphotriesterase- PDBTitle: crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
31	c2is8A_	Alignment	not modelled	24.1	7	PDB header: structural protein Chain: A: PDB Molecule: molybdopterin biosynthesis enzyme, moab; PDBTitle: crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
32	d1y5ea1	Alignment	not modelled	23.5	12	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
33	d1n0wa_	Alignment	not modelled	22.7	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
34	d1szpa2	Alignment	not modelled	21.9	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
35	c2i4cA_	Alignment	not modelled	21.7	19	PDB header: transport protein Chain: A: PDB Molecule: bicarbonate transporter; PDBTitle: crystal structure of bicarbonate transport protein cmpa from2 synechocystis sp. pcc 6803 in complex with bicarbonate and calcium
36	d1srva_	Alignment	not modelled	20.9	37	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
37	d1dk7a_	Alignment	not modelled	19.8	21	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
38	d1ydw1	Alignment	not modelled	18.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
39	d2ilqa2	Alignment	not modelled	17.9	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
40	c2wv9A_	Alignment	not modelled	17.5	14	PDB header: hydrolase Chain: A: PDB Molecule: flavivirin protease ns2b regulatory subunit, flavivirin PDBTitle: crystal structure of the ns3 protease-helicase from murray2 valley encephalitis virus
41	d1v5wa_	Alignment	not modelled	16.0	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
42	d1c2ya_	Alignment	not modelled	15.7	5	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
43	d1we3a2	Alignment	not modelled	15.5	37	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
44	d1oela2	Alignment	not modelled	15.4	21	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
45	d1sjpa2	Alignment	not modelled	15.3	32	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
46	d7aata_	Alignment	not modelled	14.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
47	d1kida_	Alignment	not modelled	13.9	21	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
48	c3gr1A_	Alignment	not modelled	13.6	9	PDB header: membrane protein Chain: A: PDB Molecule: protein prgh; PDBTitle: periplasmic domain of the t3ss inner membrane protein prgh2 from s.typhimurium (fragment 170-392)
49	d1o6za1	Alignment	not modelled	13.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
50	d1i0za1	Alignment	not modelled	12.9	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
51	d1o4sa_	Alignment	not modelled	12.2	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
52	d1tf7a1	Alignment	not modelled	12.1	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
53	d2ay1a_	Alignment	not modelled	12.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like

54	d1ldma1	 Alignment	not modelled	11.9	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
55	c3m6cA	 Alignment	not modelled	11.9	32	PDB header: chaperone Chain: A: PDB Molecule: 60 kda chaperonin 1; PDBTitle: crystal structure of mycobacterium tuberculosis groel1 apical domain
56	c3mk3L	 Alignment	not modelled	11.3	10	PDB header: transferase Chain: L: PDB Molecule: 6,7-dimethyl-8-ribityllumazine synthase; PDBTitle: crystal structure of lumazine synthase from salmonella typhimurium lt2
57	c3oirA	 Alignment	not modelled	11.2	7	PDB header: transport protein Chain: A: PDB Molecule: sulfate transporter sulfate transporter family protein; PDBTitle: crystal structure of sulfate transporter family protein from wolinetella2 succinogenes
58	c1ofgF	 Alignment	not modelled	10.9	20	PDB header: oxidoreductase Chain: F: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: glucose-fructose oxidoreductase
59	d1c7na	 Alignment	not modelled	10.7	6	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
60	d1bw0a	 Alignment	not modelled	10.5	10	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
61	d2q7wa1	 Alignment	not modelled	10.4	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
62	c2df1A	 Alignment	not modelled	10.4	13	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: crystal structure of left-handed rada filament
63	c3o82B	 Alignment	not modelled	10.3	11	PDB header: ligase Chain: B: PDB Molecule: peptide arylation enzyme; PDBTitle: structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
64	c3ix1A	 Alignment	not modelled	10.1	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding PDBTitle: periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
65	c3ix1B	 Alignment	not modelled	10.1	18	PDB header: biosynthetic protein Chain: B: PDB Molecule: n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding PDBTitle: periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
66	c3un6A	 Alignment	not modelled	9.5	10	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein saouhsc_00137; PDBTitle: 2.0 angstrom crystal structure of ligand binding component of abc-type2 import system from staphylococcus aureus with zinc bound
67	d1ebfa1	 Alignment	not modelled	9.2	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
68	d1ldna1	 Alignment	not modelled	9.1	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
69	d1mkza	 Alignment	not modelled	9.1	12	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
70	c3btuD	 Alignment	not modelled	8.9	14	PDB header: transcription Chain: D: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal structure of the super-repressor mutant of gal80p2 from saccharomyces cerevisiae; gal80(s2) [e351k]
71	c1szpC	 Alignment	not modelled	8.6	14	PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein rad51; PDBTitle: a crystal structure of the rad51 filament
72	c3f41F	 Alignment	not modelled	8.4	19	PDB header: oxidoreductase Chain: F: PDB Molecule: putative oxidoreductase yhhx; PDBTitle: crystal structure of a probable oxidoreductase yhhx in2 triclinic form. northeast structural genomics target er647
73	d2nu7a1	 Alignment	not modelled	8.3	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
74	d1lc0a1	 Alignment	not modelled	8.2	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
75	d1m5wa	 Alignment	not modelled	8.2	13	Fold: TIM beta/alpha-barrel Superfamily: Pyridoxine 5'-phosphate synthase Family: Pyridoxine 5'-phosphate synthase
76	c1h6dL	 Alignment	not modelled	7.9	18	PDB header: protein translocation Chain: L: PDB Molecule: precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
77	c3gr0D	 Alignment	not modelled	7.7	9	PDB header: membrane protein Chain: D: PDB Molecule: protein prgh; PDBTitle: periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-362)
78	d1np7a2	 Alignment	not modelled	7.6	29	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
		 Alignment				PDB header: ligase

79	c3kxwA	Alignment	not modelled	7.6	12	Chain: A: PDB Molecule: saframycin mx1 synthetase b; PDBTitle: the crystal structure of fatty acid amp ligase from legionella2 pneumophila
80	d2j07a2	Alignment	not modelled	7.5	24	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
81	c3r4rB	Alignment	not modelled	7.4	25	PDB header: cell adhesion Chain: B: PDB Molecule: hypothetical fimbrial assembly protein; PDBTitle: crystal structure of a hypothetical fimbrial assembly protein2 (bdi_3522) from parabacteroides distasonis atcc 8503 at 2.38 a3 resolution
82	c2x7pA	Alignment	not modelled	7.2	7	PDB header: unknown function Chain: A: PDB Molecule: possible thiamine biosynthesis enzyme; PDBTitle: the conserved candida albicans ca3427 gene product defines a new2 family of proteins exhibiting the generic periplasmic binding3 protein structural fold
83	c3dtyA	Alignment	not modelled	7.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from pseudomonas2 syringae
84	c3e2yB	Alignment	not modelled	6.9	12	PDB header: transferase, lyase Chain: B: PDB Molecule: kynurenine-oxoglutarate transaminase 3; PDBTitle: crystal structure of mouse kynurenine aminotransferase iii in complex2 with glutamine
85	d1owla2	Alignment	not modelled	6.9	16	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
86	d2gdtal	Alignment	not modelled	6.7	18	Fold: SARS Nsp1-like Superfamily: SARS Nsp1-like Family: SARS Nsp1-like
87	d1xi9a	Alignment	not modelled	6.7	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
88	c3bgwD	Alignment	not modelled	6.6	8	PDB header: replication Chain: D: PDB Molecule: dnab-like replicative helicase; PDBTitle: the structure of a dnab-like replicative helicase and its interactions2 with primase
89	d1wu2a3	Alignment	not modelled	6.5	10	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
90	c2g29A	Alignment	not modelled	6.3	19	PDB header: transport protein Chain: A: PDB Molecule: nitrate transport protein nrtA; PDBTitle: crystal structure of the periplasmic nitrate-binding2 protein nrtA from synechocystis pcc 6803
91	c3fd8A	Alignment	not modelled	6.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
92	c3umvB	Alignment	not modelled	6.3	22	PDB header: lyase Chain: B: PDB Molecule: deoxyribodipyrimidine photo-lyase; PDBTitle: eukaryotic class ii cpd photolyase structure reveals a basis for2 improved uv-tolerance in plants
93	d1to3a	Alignment	not modelled	6.1	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
94	d1luxja1	Alignment	not modelled	6.1	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
95	d1y6ja1	Alignment	not modelled	6.1	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
96	c3r0zA	Alignment	not modelled	5.5	22	PDB header: lyase Chain: A: PDB Molecule: d-serine dehydratase; PDBTitle: crystal structure of apo d-serine deaminase from salmonella2 typhimurium
97	d1guza1	Alignment	not modelled	5.5	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
98	c3ahhA	Alignment	not modelled	5.5	7	PDB header: lyase Chain: A: PDB Molecule: xylulose 5-phosphate/fructose 6-phosphate phosphoketolase; PDBTitle: h142a mutant of phosphoketolase from bifidobacterium breve complexed2 with acetyl thiamine diphosphate
99	c3kbqA	Alignment	not modelled	5.5	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ta0487; PDBTitle: the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum