
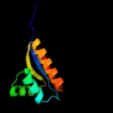


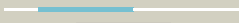


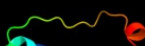

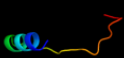


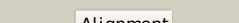


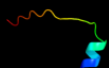




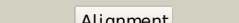












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1r6oc1	 Alignment		100.0	100	Fold: ClpS-like Superfamily: ClpS-like Family: Adaptor protein ClpS (YljA)
2	c3dnjB_	 Alignment		100.0	59	PDB header: peptide binding protein Chain: B: PDB Molecule: atp-dependent clp protease adapter protein clps; PDBTitle: the structure of the caulobacter crescentus clps protease2 adaptor protein in complex with a n-end rule peptide
3	c2jwlB_	 Alignment		30.9	14	PDB header: membrane protein Chain: B: PDB Molecule: protein tolR; PDBTitle: solution structure of periplasmic domain of tolR from h.2 influenzae with saxes data
4	c3ge5A_	 Alignment		29.5	22	PDB header: oxidoreductase Chain: A: PDB Molecule: putative nad(p)h:fmn oxidoreductase; PDBTitle: crystal structure of a putative nad(p)h:fmn oxidoreductase (pg0310)2 from porphyromonas gingivalis w83 at 1.70 a resolution
5	c2r01A_	 Alignment		21.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nitroreductase family protein; PDBTitle: crystal structure of a putative fmN-dependent nitroreductase (ct0345)2 from chlorobium tepidum t1s at 1.15 a resolution
6	d1xdya_	 Alignment		19.8	18	Fold: Oxidoreductase molybdopterin-binding domain Superfamily: Oxidoreductase molybdopterin-binding domain Family: Oxidoreductase molybdopterin-binding domain
7	c1xdyC_	 Alignment		19.4	18	PDB header: oxidoreductase Chain: C: PDB Molecule: bacterial sulfite oxidase; PDBTitle: structural and biochemical identification of a novel2 bacterial oxidoreductase, w-containing cofactor
8	d2giaa1	 Alignment		17.0	19	Fold: ssDNA-binding transcriptional regulator domain Superfamily: ssDNA-binding transcriptional regulator domain Family: Guide RNA binding protein gBP
9	d1ogpa2	 Alignment		15.9	27	Fold: Oxidoreductase molybdopterin-binding domain Superfamily: Oxidoreductase molybdopterin-binding domain Family: Oxidoreductase molybdopterin-binding domain
10	c2biiA_	 Alignment		15.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrate reductase [nadph]; PDBTitle: crystal structure of nitrate-reducing fragment of2 assimilatory nitrate reductase from pichia angusta
11	c1soxB_	 Alignment		15.3	18	PDB header: oxidoreductase Chain: B: PDB Molecule: sulfite oxidase; PDBTitle: sulfite oxidase from chicken liver

12	c2bihA_	Alignment		15.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrate reductase [nadph]; PDBTitle: crystal structure of the molybdenum-containing nitrate2 reducing fragment of pichia angusta assimilatory nitrate3 reductase
13	c2xtsC_	Alignment		14.8	18	PDB header: oxidoreductase/electron transport Chain: C: PDB Molecule: sulfite dehydrogenase; PDBTitle: crystal structure of the sulfane dehydrogenase soxcd from paracoccus2 pantotrophus
14	c2bpbA_	Alignment		14.7	27	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite\cytochrome c oxidoreductase subunit a; PDBTitle: sulfite dehydrogenase from starkeya novella
15	d3etja2	Alignment		14.0	16	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
16	c2gidP_	Alignment		12.9	19	PDB header: translation Chain: P: PDB Molecule: mitochondrial rna-binding protein 2; PDBTitle: crystal structures of trypanosoma brucei mrp1/mrp2
17	d1vkwa_	Alignment		12.6	26	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: Putative nitroreductase TM1586
18	d2a9da2	Alignment		12.4	18	Fold: Oxidoreductase molybdopterin-binding domain Superfamily: Oxidoreductase molybdopterin-binding domain Family: Oxidoreductase molybdopterin-binding domain
19	c1ogpD_	Alignment		11.8	27	PDB header: oxidoreductase Chain: D: PDB Molecule: sulfite oxidase; PDBTitle: the crystal structure of plant sulfite oxidase provides2 insight into sulfite oxidation in plants and animals
20	c3hj9A_	Alignment		11.3	11	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of a putative nitroreductase (reut_a1228) from2 ralstonia eutropha jmp134 at 2.00 a resolution
21	c2a9dB_	Alignment	not modelled	10.7	18	PDB header: oxidoreductase Chain: B: PDB Molecule: sulfite oxidase; PDBTitle: crystal structure of recombinant chicken sulfite oxidase with arg at2 residue 161
22	c3koqC_	Alignment	not modelled	10.6	15	PDB header: oxidoreductase Chain: C: PDB Molecule: nitroreductase family protein; PDBTitle: crystal structure of a nitroreductase family protein (cd3355) from2 clostridium difficile 630 at 1.58 a resolution
23	d1cmga_	Alignment	not modelled	9.6	10	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
24	d1n0yb_	Alignment	not modelled	9.5	5	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
25	d2o8ra3	Alignment	not modelled	8.9	21	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
26	c3of4A_	Alignment	not modelled	8.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nitroreductase; PDBTitle: crystal structure of a fmn/fad- and nad(p)h-dependent nitroreductase2 (nfnb, il2077) from idiomarina loihiensis l2tr at 1.90 a resolution
27	c3g14B_	Alignment	not modelled	8.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: nitroreductase family protein; PDBTitle: crystal structure of nitroreductase family protein (yp_877874.1) from2 clostridium novyi nt at 1.75 a resolution
28	c2kgrA_	Alignment	not modelled	8.3	8	PDB header: protein binding Chain: A: PDB Molecule: intersectin-1; PDBTitle: solution structure of protein itsn1 from homo sapiens.2 northeast structural genomics consortium target hr5524a

29	d1fsha_	Alignment	not modelled	8.3	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
30	d1qnaa1	Alignment	not modelled	7.9	14	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
31	d2d8ca1	Alignment	not modelled	7.8	24	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
32	d1wzla2	Alignment	not modelled	7.6	18	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
33	c2islB_	Alignment	not modelled	7.4	26	PDB header: flavoprotein Chain: B: PDB Molecule: blub; PDBTitle: blub bound to reduced flavin (fmh2) and molecular oxygen.2 (clear crystal form)
34	c3fiaA_	Alignment	not modelled	7.3	5	PDB header: protein binding Chain: A: PDB Molecule: intersectin-1; PDBTitle: crystal structure of the eh 1 domain from human intersectin-2 1 protein. northeast structural genomics consortium target3 hr3646e.
35	d1v3fa_	Alignment	not modelled	6.7	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
36	c2kc8B_	Alignment	not modelled	6.6	33	PDB header: toxin/toxin repressor Chain: B: PDB Molecule: antitoxin relb; PDBTitle: structure of e. coli toxin rele (r81a/r83a) mutant in2 complex with antitoxin relbc (k47-l79) peptide
37	c2x2oA_	Alignment	not modelled	6.6	16	PDB header: flavoprotein Chain: A: PDB Molecule: nrld protein; PDBTitle: the flavoprotein nrld from bacillus cereus with the2 initially oxidized fmn cofactor in an intermediate3 radiation reduced state
38	c2xznM_	Alignment	not modelled	6.6	11	PDB header: ribosome Chain: M: PDB Molecule: rps18e; 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 2
39	c3pg8B_	Alignment	not modelled	6.5	8	PDB header: transferase Chain: B: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
40	d2jxca1	Alignment	not modelled	6.5	13	Fold: EF Hand-like Superfamily: EF-hand Family: Eps15 homology domain (EH domain)
41	c3bemA_	Alignment	not modelled	6.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative nad(p)h nitroreductase ydfn; PDBTitle: crystal structure of putative nitroreductase ydfn (2632848) from2 bacillus subtilis at 1.65 a resolution
42	c2kfha_	Alignment	not modelled	6.0	7	PDB header: protein binding Chain: A: PDB Molecule: eh domain-containing protein 1; PDBTitle: structure of the c-terminal domain of ehd1 with fnyestgptak
43	c3u5zA_	Alignment	not modelled	6.0	17	PDB header: dna binding protein/dna Chain: A: PDB Molecule: dna polymerase accessory protein 62; PDBTitle: structure of t4 bacteriophage clamp loader bound to the t4 clamp.2 primer-template dna, and atp analog
44	d2frea1	Alignment	not modelled	5.7	15	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
45	c2b1uA_	Alignment	not modelled	5.7	5	PDB header: metal binding protein Chain: A: PDB Molecule: calmodulin-like protein 5; PDBTitle: solution structure of calmodulin-like skin protein c2 terminal domain
46	d1c07a_	Alignment	not modelled	5.6	7	Fold: EF Hand-like Superfamily: EF-hand Family: Eps15 homology domain (EH domain)
47	d2i1sa1	Alignment	not modelled	5.3	18	Fold: MM3350-like Superfamily: MM3350-like Family: MM3350-like
48	d1w4ma_	Alignment	not modelled	5.2	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
49	c3kwkA_	Alignment	not modelled	5.2	9	PDB header: oxidoreductase Chain: A: PDB Molecule: putative nadh dehydrogenase/nad(p)h nitroreductase; PDBTitle: crystal structure of putative nadh dehydrogenase/nad(p)h2 nitroreductase (np_809094.1) from bacteroides thetaiotaomicron vpi-3 5482 at 1.54 a resolution
50	d1fi6a_	Alignment	not modelled	5.1	10	Fold: EF Hand-like Superfamily: EF-hand Family: Eps15 homology domain (EH domain)