












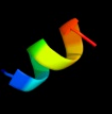



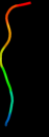



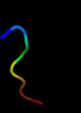





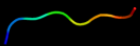


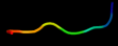


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2rddB_</a>	 Alignment		11.7	18	<b>PDB header:</b> membrane protein/transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> upf0092 membrane protein yajc; <b>PDBTitle:</b> x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
2	<a href="#">c2ostC_</a>	 Alignment		10.6	67	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> C: <b>PDB Molecule:</b> putative endonuclease; <b>PDBTitle:</b> the structure of a bacterial homing endonuclease : i-ssp6803i
3	<a href="#">d2al6a2</a>	 Alignment		8.7	50	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Third domain of FERM
4	<a href="#">d1uerc2</a>	 Alignment		8.7	63	<b>Fold:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain
5	<a href="#">c2bf9A_</a>	 Alignment		8.6	18	<b>PDB header:</b> hormone <b>Chain:</b> A: <b>PDB Molecule:</b> pancreatic hormone; <b>PDBTitle:</b> anisotropic refinement of avian (turkey) pancreatic2 polypeptide at 0.99 angstroms resolution.
6	<a href="#">c2nr1A_</a>	 Alignment		7.7	100	<b>PDB header:</b> receptor <b>Chain:</b> A: <b>PDB Molecule:</b> nr1 m2; <b>PDBTitle:</b> transmembrane segment 2 of nmda receptor nr1, nmr, 102 structures
7	<a href="#">c3gycB_</a>	 Alignment		7.5	40	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative glycoside hydrolase; <b>PDBTitle:</b> crystal structure of putative glycoside hydrolase (yp_001304622.1)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
8	<a href="#">c1wqsA_</a>	 Alignment		7.1	71	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 3c-like protease; <b>PDBTitle:</b> crystal structure of norovirus 3c-like protease
9	<a href="#">c3h1sB_</a>	 Alignment		6.9	63	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> crystal structure of superoxide dismutase from francisella tularensis2 subsp. tularensis schu s4
10	<a href="#">c2dezA_</a>	 Alignment		6.6	55	<b>PDB header:</b> neuropeptide <b>Chain:</b> A: <b>PDB Molecule:</b> peptide yy; <b>PDBTitle:</b> structure of human pyy
11	<a href="#">c1dt0A_</a>	 Alignment		6.6	75	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> cloning, sequence, and crystallographic structure of2 recombinant iron superoxide dismutase from pseudomonas3 ovalis

12	<a href="#">c1ronA_</a>	Alignment		6.6	64	<b>PDB header:</b> neuropeptide <b>Chain:</b> A: <b>PDB Molecule:</b> neuropeptide y; <b>PDBTitle:</b> nmr solution structure of human neuropeptide y
13	<a href="#">c2vdaB_</a>	Alignment		6.4	50	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> maltoporin; <b>PDBTitle:</b> solution structure of the seca-signal peptide complex
14	<a href="#">d2z0da1</a>	Alignment		6.2	50	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Autophagin-like
15	<a href="#">c2hv8D_</a>	Alignment		6.2	43	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> rab11 family-interacting protein 3; <b>PDBTitle:</b> crystal structure of gtp-bound rab11 in complex with fip3
16	<a href="#">c1tz5A_</a>	Alignment		6.1	45	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> chimera of pancreatic hormone and neuropeptide y; <b>PDBTitle:</b> [pnpy19-23]-hpp bound to dpc micelles
17	<a href="#">d1kkca2</a>	Alignment		5.7	75	<b>Fold:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain
18	<a href="#">d2j0lp1</a>	Alignment		5.5	63	<b>Fold:</b> Ribosomal proteins L15p and L18e <b>Superfamily:</b> Ribosomal proteins L15p and L18e <b>Family:</b> Ribosomal proteins L15p and L18e
19	<a href="#">c1qnnD_</a>	Alignment		5.5	63	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> cambialistic superoxide dismutase from porphyromonas2 gingivalis
20	<a href="#">c1my6A_</a>	Alignment		5.4	63	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> iron (iii) superoxide dismutase; <b>PDBTitle:</b> the 1.6 a structure of fe-superoxide dismutase from the2 thermophilic cyanobacterium thermosynechococcus elongatus3 : correlation of epr and structural characteristics
21	<a href="#">d3sdpa2</a>	Alignment	not modelled	5.3	63	<b>Fold:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain
22	<a href="#">c3ceiA_</a>	Alignment	not modelled	5.3	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> crystal structure of superoxide dismutase from helicobacter2 pylori
23	<a href="#">dlix9a2</a>	Alignment	not modelled	5.3	63	<b>Fold:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain
24	<a href="#">c3js4C_</a>	Alignment	not modelled	5.2	63	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> crystal structure of iron superoxide dismutase from anaplasma2 phagocytophilum
25	<a href="#">d1y67a2</a>	Alignment	not modelled	5.2	63	<b>Fold:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain
26	<a href="#">c3tqjB_</a>	Alignment	not modelled	5.2	63	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> superoxide dismutase [fe]; <b>PDBTitle:</b> structure of the superoxide dismutase (fe) (sodb) from coxiella2 burnetii
27	<a href="#">c2nybC_</a>	Alignment	not modelled	5.1	63	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> superoxide dismutase [fe]; <b>PDBTitle:</b> crystal structure of e.coli iron superoxide dismutase q69e2 at 1.1 angstrom resolution
28	<a href="#">c2a03A_</a>	Alignment	not modelled	5.1	75	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fe-superoxide dismutase homolog; <b>PDBTitle:</b> superoxide dismutase protein from plasmodium berghei