



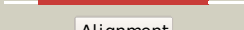

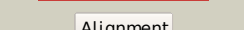

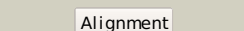





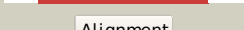

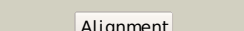

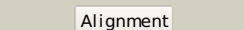














#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2nybC_</a>	 Alignment		100.0	99	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> superoxide dismutase [fe]; <b>PDBTitle:</b> crystal structure of e.coli iron superoxide dismutase q69e2 at 1.1 angstrom resolution
2	<a href="#">c3tqjB_</a>	 Alignment		100.0	61	<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
3	<a href="#">c3h1sB_</a>	 Alignment		100.0	66	<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
4	<a href="#">c1dt0A_</a>	 Alignment		100.0	68	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> cloning, sequence, and crystallographic structure of 2 recombinant iron superoxide dismutase from pseudomonas3 ovalis
5	<a href="#">c1gv3B_</a>	 Alignment		100.0	45	<b>PDB header:</b> manganese superoxide dismutase <b>Chain:</b> B: <b>PDB Molecule:</b> manganese superoxide dismutase; <b>PDBTitle:</b> the 2.0 angstrom resolution structure of the catalytic2 portion of a cyanobacterial membrane-bound manganese3 superoxide dismutase
6	<a href="#">c2a03A_</a>	 Alignment		100.0	53	<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
7	<a href="#">c1mngA_</a>	 Alignment		100.0	41	<b>PDB header:</b> oxidoreductase(superoxide acceptor) <b>Chain:</b> A: <b>PDB Molecule:</b> manganese superoxide dismutase; <b>PDBTitle:</b> structure-function in e. coli iron superoxide dismutase: comparisons2 with the manganese enzyme from t. thermophilus
8	<a href="#">c1qnnD_</a>	 Alignment		100.0	51	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> cambialistic superoxide dismutase from porphyromonas2 gingivalis
9	<a href="#">c3lj9A_</a>	 Alignment		100.0	70	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> iron superoxide dismutase; <b>PDBTitle:</b> x-ray structure of the iron superoxide dismutase from2 pseudoalteromonas haloplanktis in complex with sodium azide
10	<a href="#">c1my6A_</a>	 Alignment		100.0	57	<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
11	<a href="#">c1xreB_</a>	 Alignment		100.0	43	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> crystal structure of soda-2 (ba5696) from bacillus2 anthracis at 1.8a resolution.

12	<a href="#">c3ceiA_</a>	Alignment		100.0	53	<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
13	<a href="#">c2cw2B_</a>	Alignment		100.0	57	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> superoxide dismutase 1; <b>PDBTitle:</b> crystal structure of superoxide dismutase from p. marinus
14	<a href="#">c1gn4B_</a>	Alignment		100.0	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> h145e mutant of mycobacterium tuberculosis iron-superoxide2 dismutase.
15	<a href="#">c2rcvA_</a>	Alignment		100.0	54	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase [mn]; <b>PDBTitle:</b> crystal structure of the bacillus subtilis superoxide2 dismutase
16	<a href="#">c1ma1E_</a>	Alignment		100.0	41	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> structure and properties of the atypical iron superoxide2 dismutase from methanobacterium thermoautotrophicum
17	<a href="#">c1y67D_</a>	Alignment		100.0	51	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> manganese superoxide dismutase; <b>PDBTitle:</b> crystal structure of manganese superoxide dismutase from2 deinococcus radiodurans
18	<a href="#">c1p7qL_</a>	Alignment		100.0	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> crystal structure of superoxide dismutase from pyrobaculum2 aerophilum
19	<a href="#">c3js4C_</a>	Alignment		100.0	50	<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
20	<a href="#">c1avmA_</a>	Alignment		100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> the cambialistic superoxide dismutase (fe-sod) of p. shermanii2 coordinated by azide
21	<a href="#">c1en4C_</a>	Alignment	not modelled	100.0	45	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> manganese superoxide dismutase; <b>PDBTitle:</b> crystal structure analysis of the e. coli manganese2 superoxide dismutase q146h mutant
22	<a href="#">c1n0nB_</a>	Alignment	not modelled	100.0	41	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> superoxide dismutase [mn]; <b>PDBTitle:</b> catalytic and structural effects of amino-acid substitution at his302 in human manganese superoxide dismutase
23	<a href="#">c1b06A_</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (superoxide dismutase); <b>PDBTitle:</b> superoxide dismutase from sulfolobus acidocaldarius
24	<a href="#">c1unfX_</a>	Alignment	not modelled	100.0	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> iron superoxide dismutase; <b>PDBTitle:</b> the crystal structure of the eukaryotic fesod from vigna2 unguiculata suggests a new enzymatic mechanism
25	<a href="#">c1kkcB_</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> manganese superoxide dismutase; <b>PDBTitle:</b> crystal structure of aspergillus fumigatus mnsod
26	<a href="#">c2gpcB_</a>	Alignment	not modelled	100.0	54	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> iron superoxide dismutase; <b>PDBTitle:</b> the crystal structure of the enzyme fe-superoxide dismutase2 from trypanosoma cruzi
27	<a href="#">c2cw3A_</a>	Alignment	not modelled	100.0	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> iron superoxide dismutase; <b>PDBTitle:</b> x-ray structure of pmsod2, superoxide dismutase from2 perkinsus marinus
28	<a href="#">c3bfrA_</a>	Alignment	not modelled	100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase [mn]; <b>PDBTitle:</b> the crystal structure of sod2 from saccharomyces cerevisiae
						<b>PDB header:</b> oxidoreductase

29	<a href="#">c3dc5C_</a>	Alignment	not modelled	100.0	35	<b>Chain:</b> C: <b>PDB Molecule:</b> superoxide dismutase [mn] 2; <b>PDBTitle:</b> crystal structure of a manganese superoxide dismutases from2 caenorhabditis elegans
30	<a href="#">c1cojA_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (superoxide dismutase); <b>PDBTitle:</b> fe-sod from aquifex pyrophilus, a hyperthermophilic bacterium
31	<a href="#">d2nyba2</a>	Alignment	not modelled	100.0	100	<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
32	<a href="#">d1gv3a2</a>	Alignment	not modelled	100.0	47	<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
33	<a href="#">d1mnga2</a>	Alignment	not modelled	100.0	42	<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
34	<a href="#">d1b06a2</a>	Alignment	not modelled	100.0	38	<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
35	<a href="#">d1idsa2</a>	Alignment	not modelled	100.0	43	<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
36	<a href="#">d1wb8a2</a>	Alignment	not modelled	100.0	35	<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
37	<a href="#">d1dt0a2</a>	Alignment	not modelled	100.0	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
38	<a href="#">d1my6a2</a>	Alignment	not modelled	100.0	58	<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
39	<a href="#">d1uera2</a>	Alignment	not modelled	100.0	47	<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
40	<a href="#">d2p4ka2</a>	Alignment	not modelled	100.0	48	<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
41	<a href="#">d1ma1a2</a>	Alignment	not modelled	100.0	46	<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
42	<a href="#">d1p7ga2</a>	Alignment	not modelled	100.0	42	<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
43	<a href="#">d1jr9a2</a>	Alignment	not modelled	100.0	49	<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
44	<a href="#">d1bsma2</a>	Alignment	not modelled	100.0	38	<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
45	<a href="#">d1unfx2</a>	Alignment	not modelled	100.0	47	<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
46	<a href="#">dlix9a2</a>	Alignment	not modelled	100.0	47	<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
47	<a href="#">d1y67a2</a>	Alignment	not modelled	100.0	56	<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
48	<a href="#">d1kkca2</a>	Alignment	not modelled	100.0	35	<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
49	<a href="#">d1coja2</a>	Alignment	not modelled	100.0	29	<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
50	<a href="#">d3sdpa2</a>	Alignment	not modelled	100.0	65	<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
51	<a href="#">d1uerc2</a>	Alignment	not modelled	100.0	48	<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
52	<a href="#">d1uera1</a>	Alignment	not modelled	100.0	57	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
53	<a href="#">d1dt0a1</a>	Alignment	not modelled	100.0	75	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
54	<a href="#">d2nyba1</a>	Alignment	not modelled	100.0	99	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain

55	<a href="#">d1p7ga1</a>	Alignment	not modelled	100.0	33	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
56	<a href="#">d1mnga1</a>	Alignment	not modelled	100.0	41	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
57	<a href="#">d1gv3a1</a>	Alignment	not modelled	100.0	43	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
58	<a href="#">d1my6a1</a>	Alignment	not modelled	100.0	56	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
59	<a href="#">d1jr9a1</a>	Alignment	not modelled	100.0	45	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
60	<a href="#">d1bsma1</a>	Alignment	not modelled	100.0	35	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
61	<a href="#">d1idsa1</a>	Alignment	not modelled	100.0	35	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
62	<a href="#">d2p4ka1</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
63	<a href="#">dlix9a1</a>	Alignment	not modelled	100.0	43	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
64	<a href="#">d1ma1a1</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
65	<a href="#">d1y67a1</a>	Alignment	not modelled	100.0	46	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
66	<a href="#">d1kkca1</a>	Alignment	not modelled	100.0	37	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
67	<a href="#">d1wb8a1</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
68	<a href="#">d1unfx1</a>	Alignment	not modelled	100.0	54	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
69	<a href="#">d1b06a1</a>	Alignment	not modelled	100.0	35	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
70	<a href="#">d3sdpa1</a>	Alignment	not modelled	100.0	77	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
71	<a href="#">d1coja1</a>	Alignment	not modelled	99.9	31	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
72	<a href="#">d2gykb1</a>	Alignment	not modelled	61.6	27	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> HNH-motif
73	<a href="#">d2jb0b1</a>	Alignment	not modelled	47.9	32	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> HNH-motif
74	<a href="#">c7ceiB_</a>	Alignment	not modelled	45.4	32	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> protein (colicin e7 immunity protein); <b>PDBTitle:</b> the endonuclease domain of colicin e7 in complex with its inhibitor2 im7 protein
75	<a href="#">d1kfta_</a>	Alignment	not modelled	28.6	12	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Excinuclease UvrC C-terminal domain
76	<a href="#">c1kftA_</a>	Alignment	not modelled	28.6	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> excinuclease abc subunit c; <b>PDBTitle:</b> solution structure of the c-terminal domain of uvrc from e-2 coli
77	<a href="#">d2a1jb1</a>	Alignment	not modelled	21.4	18	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Hef domain-like
78	<a href="#">c1wqsA_</a>	Alignment	not modelled	19.1	47	<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
79	<a href="#">c2jesG_</a>	Alignment	not modelled	19.0	11	<b>PDB header:</b> viral protein <b>Chain:</b> G: <b>PDB Molecule:</b> portal protein; <b>PDBTitle:</b> portal protein from bacteriophage spp1
80	<a href="#">d1tlua1</a>	Alignment	not modelled	17.6	26	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
						<b>Fold:</b> SAM domain-like

81	<a href="#">d2bgwa1</a>	Alignment	not modelled	16.9	30	<b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Hef domain-like
82	<a href="#">d1x2ia1</a>	Alignment	not modelled	16.8	21	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Hef domain-like
83	<a href="#">d1xl7a1</a>	Alignment	not modelled	15.8	27	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
84	<a href="#">d3cjsb1</a>	Alignment	not modelled	14.4	18	<b>Fold:</b> Ribosomal L11/L12e N-terminal domain <b>Superfamily:</b> Ribosomal L11/L12e N-terminal domain <b>Family:</b> Ribosomal L11/L12e N-terminal domain
85	<a href="#">c2rnnA</a>	Alignment	not modelled	14.3	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 sumo-protein ligase siz1; <b>PDBTitle:</b> solution structure of the n-terminal sap domain of sumo e3 ligases2 from saccharomyces cerevisiae
86	<a href="#">c1xl8B</a>	Alignment	not modelled	13.4	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal carnitine o-octanoyltransferase; <b>PDBTitle:</b> crystal structure of mouse carnitine octanoyltransferase in2 complex with octanoylcarnitine
87	<a href="#">c1skoA</a>	Alignment	not modelled	12.8	24	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> mitogen-activated protein kinase kinase 1 <b>PDBTitle:</b> mp1-p14 complex
88	<a href="#">d1nm8a1</a>	Alignment	not modelled	12.7	41	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
89	<a href="#">d1ndba1</a>	Alignment	not modelled	12.0	41	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
90	<a href="#">c2fy2A</a>	Alignment	not modelled	11.7	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> choline o-acetyltransferase; <b>PDBTitle:</b> structures of ligand bound human choline acetyltransferase2 provide insight into regulation of acetylcholine synthesis
91	<a href="#">c3cjtP</a>	Alignment	not modelled	11.7	18	<b>PDB header:</b> transferase/ribosomal protein <b>Chain:</b> P: <b>PDB Molecule:</b> 50s ribosomal protein l11; <b>PDBTitle:</b> ribosomal protein l11 methyltransferase (prma) in complex with2 dimethylated ribosomal protein l11
92	<a href="#">c2h4tB</a>	Alignment	not modelled	10.8	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> carnitine o-palmitoyltransferase ii, <b>PDBTitle:</b> crystal structure of rat carnitine palmitoyltransferase ii
93	<a href="#">d2dlka1</a>	Alignment	not modelled	10.5	16	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
94	<a href="#">c1t7qA</a>	Alignment	not modelled	10.5	41	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carnitine acetyltransferase; <b>PDBTitle:</b> crystal structure of the f565a mutant of murine carnitine2 acetyltransferase in complex with carnitine and coa
95	<a href="#">c2nrzB</a>	Alignment	not modelled	9.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uvrabc system protein c; <b>PDBTitle:</b> crystal structure of the c-terminal half of uvrc bound to2 its catalytic divalent cation
96	<a href="#">d2hu7a1</a>	Alignment	not modelled	8.9	50	<b>Fold:</b> 7-bladed beta-propeller <b>Superfamily:</b> Peptidase/esterase 'gauge' domain <b>Family:</b> Acylamino-acid-releasing enzyme, N-terminal donain
97	<a href="#">d1mmsa2</a>	Alignment	not modelled	8.4	18	<b>Fold:</b> Ribosomal L11/L12e N-terminal domain <b>Superfamily:</b> Ribosomal L11/L12e N-terminal domain <b>Family:</b> Ribosomal L11/L12e N-terminal domain
98	<a href="#">c2fyoA</a>	Alignment	not modelled	8.3	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carnitine o-palmitoyltransferase ii, <b>PDBTitle:</b> crystal structure of rat carnitine palmitoyltransferase 22 in space group p43212
99	<a href="#">c1q6xA</a>	Alignment	not modelled	8.2	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> choline o-acetyltransferase; <b>PDBTitle:</b> crystal structure of rat choline acetyltransferase