













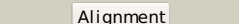



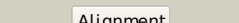

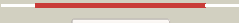



# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A0J3
Date	Tue Jul 17 17:05:07 BST 2012
Unique Job ID	9ac7f441f5c44658

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1en4C_</a>	 Alignment		100.0	55	<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
2	<a href="#">c1xreB_</a>	 Alignment		100.0	51	<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.
3	<a href="#">c1gv3B_</a>	 Alignment		100.0	54	<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
4	<a href="#">c1y67D_</a>	 Alignment		100.0	57	<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
5	<a href="#">c1mngA_</a>	 Alignment		100.0	55	<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
6	<a href="#">c2rcvA_</a>	 Alignment		100.0	73	<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
7	<a href="#">c3h1sB_</a>	 Alignment		100.0	51	<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
8	<a href="#">c1my6A_</a>	 Alignment		100.0	43	<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
9	<a href="#">c1gn4B_</a>	 Alignment		100.0	38	<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.
10	<a href="#">c3ceiA_</a>	 Alignment		100.0	38	<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
11	<a href="#">c2cw2B_</a>	 Alignment		100.0	41	<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

12	<a href="#">c1dt0A_</a>	Alignment		100.0	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> cloning, sequence, and crystallographic structure of f2 recombinant iron superoxide dismutase from pseudomonas3 ovalis
13	<a href="#">c4f2nL_</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 iron superoxide dismutase from leishmania major
14	<a href="#">c2a03A_</a>	Alignment		100.0	44	<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
15	<a href="#">c1ma1E_</a>	Alignment		100.0	40	<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
16	<a href="#">c4ffkA_</a>	Alignment		100.0	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> x-ray structure of iron superoxide dismutase from acidilobus2 saccharovorans
17	<a href="#">c3tqjB_</a>	Alignment		100.0	50	<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
18	<a href="#">c3js4C_</a>	Alignment		100.0	39	<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
19	<a href="#">c1p7qL_</a>	Alignment		100.0	37	<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
20	<a href="#">c1avmA_</a>	Alignment		100.0	37	<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="#">c3qvnA_</a>	Alignment	not modelled	100.0	41	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> manganese-containing superoxide dismutase; <b>PDBTitle:</b> crystal structure of cytosolic mnsod3 from candida albicans
22	<a href="#">c2nybC_</a>	Alignment	not modelled	100.0	51	<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
23	<a href="#">c1b06A_</a>	Alignment	not modelled	100.0	35	<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="#">c1n0nB_</a>	Alignment	not modelled	100.0	48	<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
25	<a href="#">c1unfX_</a>	Alignment	not modelled	100.0	42	<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
26	<a href="#">c1qnnD_</a>	Alignment	not modelled	100.0	45	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> cambialistic superoxide dismutase from porphyromonas2 gingivalis
27	<a href="#">c3lj9A_</a>	Alignment	not modelled	100.0	54	<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
28	<a href="#">c3bfrA_</a>	Alignment	not modelled	100.0	43	<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

29	<a href="#">c3dc5C</a>	Alignment	not modelled	100.0	42	<b>PDB header:</b> oxidoreductase <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="#">c1kkcB</a>	Alignment	not modelled	100.0	43	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> manganese superoxi de dismutase; <b>PDBTitle:</b> crystal structure of aspergillus fumigatus mnsod
31	<a href="#">c2cw3A</a>	Alignment	not modelled	100.0	37	<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
32	<a href="#">c2gpcB</a>	Alignment	not modelled	100.0	44	<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
33	<a href="#">c1coiA</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
34	<a href="#">d1bsma2</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
35	<a href="#">d1y67a2</a>	Alignment	not modelled	100.0	60	<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="#">d1ix9a2</a>	Alignment	not modelled	100.0	53	<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="#">d1idsa2</a>	Alignment	not modelled	100.0	36	<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="#">d1gv3a2</a>	Alignment	not modelled	100.0	53	<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="#">d1wb8a2</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
40	<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
41	<a href="#">d1mnga2</a>	Alignment	not modelled	100.0	51	<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="#">d2p4ka2</a>	Alignment	not modelled	100.0	51	<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="#">d1p7ga2</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
44	<a href="#">d1jr9a2</a>	Alignment	not modelled	100.0	67	<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="#">d2nyba2</a>	Alignment	not modelled	100.0	50	<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="#">d1dt0a2</a>	Alignment	not modelled	100.0	44	<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="#">d1unfx2</a>	Alignment	not modelled	100.0	44	<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="#">d1my6a2</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
49	<a href="#">d1ma1a2</a>	Alignment	not modelled	100.0	41	<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="#">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
51	<a href="#">d1kka2</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
52	<a href="#">d1coja2</a>	Alignment	not modelled	100.0	33	<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
53	<a href="#">d3sdp2</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
54	<a href="#">d1uerc2</a>	Alignment	not modelled	100.0	51	<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

						<b>Family:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
55	<a href="#">d1mnga1</a>	Alignment	not modelled	100.0	59	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
56	<a href="#">d1gv3a1</a>	Alignment	not modelled	100.0	53	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
57	<a href="#">d1ix9a1</a>	Alignment	not modelled	100.0	56	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
58	<a href="#">d1y67a1</a>	Alignment	not modelled	100.0	55	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
59	<a href="#">d1jr9a1</a>	Alignment	not modelled	100.0	72	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
60	<a href="#">d1uera1</a>	Alignment	not modelled	100.0	43	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
61	<a href="#">d1dt0a1</a>	Alignment	not modelled	100.0	57	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
62	<a href="#">d1my6a1</a>	Alignment	not modelled	100.0	36	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
63	<a href="#">d2nyba1</a>	Alignment	not modelled	100.0	50	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
64	<a href="#">d1p7ga1</a>	Alignment	not modelled	100.0	33	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
65	<a href="#">d1bsma1</a>	Alignment	not modelled	100.0	37	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
66	<a href="#">d2p4ka1</a>	Alignment	not modelled	100.0	42	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
67	<a href="#">d1idsa1</a>	Alignment	not modelled	100.0	37	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
68	<a href="#">d1unfx1</a>	Alignment	not modelled	100.0	38	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
69	<a href="#">d1ma1a1</a>	Alignment	not modelled	100.0	37	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
70	<a href="#">d1wb8a1</a>	Alignment	not modelled	100.0	33	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
71	<a href="#">d1kkca1</a>	Alignment	not modelled	100.0	48	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
72	<a href="#">d1b06a1</a>	Alignment	not modelled	99.9	29	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
73	<a href="#">d3sdpa1</a>	Alignment	not modelled	99.9	54	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
74	<a href="#">d1coja1</a>	Alignment	not modelled	99.9	25	<b>Family:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain <b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), N-terminal domain
75	<a href="#">d2gykb1</a>	Alignment	not modelled	61.2	14	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> HNH-motif
76	<a href="#">d2jb0b1</a>	Alignment	not modelled	47.5	17	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> HNH-motif
77	<a href="#">c7ceiB_</a>	Alignment	not modelled	39.1	17	<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
78	<a href="#">d1kfta_</a>	Alignment	not modelled	38.8	11	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Excinuclease UvrC C-terminal domain
79	<a href="#">c1kfta_</a>	Alignment	not modelled	38.8	11	<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
80	<a href="#">d2a1jb1</a>	Alignment	not modelled	32.1	24	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like

				Family:Hef domain-like		
81	<a href="#">d1t1ua1</a>	Alignment	not modelled	30.0	26	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
82	<a href="#">d1xl7a1</a>	Alignment	not modelled	27.1	23	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
83	<a href="#">d1nm8a1</a>	Alignment	not modelled	25.1	36	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
84	<a href="#">d2bgwa1</a>	Alignment	not modelled	24.7	28	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Hef domain-like
85	<a href="#">c1xl8B_</a>	Alignment	not modelled	24.0	23	<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
86	<a href="#">c1t7qA_</a>	Alignment	not modelled	23.5	36	<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
87	<a href="#">d1x2ia1</a>	Alignment	not modelled	23.5	15	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Hef domain-like
88	<a href="#">d1ndba1</a>	Alignment	not modelled	22.8	36	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
89	<a href="#">c2fy2A_</a>	Alignment	not modelled	22.6	27	<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
90	<a href="#">c3oruA_</a>	Alignment	not modelled	21.8	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> duf1989 family protein; <b>PDBTitle:</b> crystal structure of a duf1989 family protein (tm1040_0329) from2 silicibacter sp. tm1040 at 1.11 a resolution
91	<a href="#">c2h4tB_</a>	Alignment	not modelled	19.3	32	<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
92	<a href="#">c1q6xA_</a>	Alignment	not modelled	18.7	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
93	<a href="#">c1n6dE_</a>	Alignment	not modelled	16.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> tricorn protease; <b>PDBTitle:</b> tricorn protease in complex with tetrapeptide chloromethyl2 ketone derivative
94	<a href="#">c1k32E_</a>	Alignment	not modelled	16.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> tricorn protease; <b>PDBTitle:</b> crystal structure of the tricorn protease
95	<a href="#">c2fyoA_</a>	Alignment	not modelled	15.8	32	<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
96	<a href="#">c1wqsA_</a>	Alignment	not modelled	14.9	67	<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
97	<a href="#">c2oqqB_</a>	Alignment	not modelled	14.1	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor hy5; <b>PDBTitle:</b> crystal structure of hy5 leucine zipper homodimer from2 arabidopsis thaliana
98	<a href="#">c3di4A_</a>	Alignment	not modelled	13.5	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein duf1989; <b>PDBTitle:</b> crystal structure of a duf1989 family protein (spo0365) from2 silicibacter pomeroyi dss-3 at 1.60 a resolution
99	<a href="#">c2nrzB_</a>	Alignment	not modelled	13.3	25	<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 uvrbc bound to2 its catalytic divalent cation