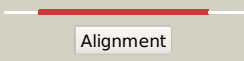

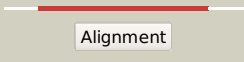

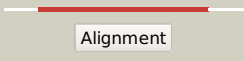

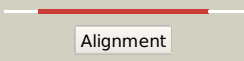

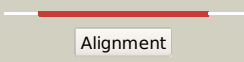

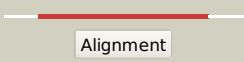

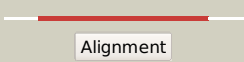

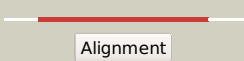

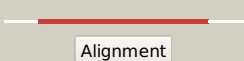

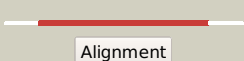

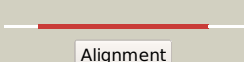












# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD3846\_(sodA)\_4320882\_4321505  
 Date Sat Aug 10 22:05:02 BST 2019  
 Unique Job ID c7a77afe07384de5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1gn4B_</a>			100.0	99	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> h145e mutant of mycobacterium tuberculosis iron-superoxide dismutase.
2	<a href="#">c3ak1C_</a>			100.0	47	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> superoxide dismutase [mn/fe]; <b>PDBTitle:</b> superoxide dismutase from aeropyrum pernix k1, apo-form
3	<a href="#">c4ffkA_</a>			100.0	40	<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
4	<a href="#">c1p7gL_</a>			100.0	47	<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
5	<a href="#">c1ma1E_</a>			100.0	44	<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
6	<a href="#">c1n0nB_</a>			100.0	51	<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
7	<a href="#">c1avmA_</a>			100.0	64	<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
8	<a href="#">c1xreB_</a>			100.0	37	<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.
9	<a href="#">c2cw2B_</a>			100.0	39	<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
10	<a href="#">c1gv3B_</a>			100.0	37	<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 catalytic portion of a2 cyanobacterial membrane-bound manganese superoxide dismutase
11	<a href="#">c3qvna_</a>			100.0	40	<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

12	<a href="#">c3ceiA_</a>	Alignment		100.0	31	<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="#">c1b06A_</a>	Alignment		100.0	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (superoxide dismutase); <b>PDBTitle:</b> superoxide dismutase from sulfolobus acidocaldarius
14	<a href="#">c1mngA_</a>	Alignment		100.0	37	<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
15	<a href="#">c5a9gB_</a>	Alignment		100.0	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> manganese superoxide dismutase; <b>PDBTitle:</b> manganese superoxide dismutase from sphingobacterium sp. t2
16	<a href="#">c6bejA_</a>	Alignment		100.0	41	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> crystal structure of manganese superoxide dismutase from xanthomonas2 citri
17	<a href="#">c4yioB_</a>	Alignment		100.0	44	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> x-ray structure of the iron/manganese cambialistic superoxide2 dismutase from streptococcus thermophilus
18	<a href="#">c1dt0A_</a>	Alignment		100.0	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> cloning, sequence, and crystallographic structure of recombinant iron2 superoxide dismutase from pseudomonas ovalis
19	<a href="#">c1kkcB_</a>	Alignment		100.0	44	<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
20	<a href="#">c4c7uB_</a>	Alignment		100.0	45	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> superoxide dismutase [mn] 1, mitochondrial; <b>PDBTitle:</b> crystal structure of manganese superoxide dismutase from arabidopsis2 thaliana
21	<a href="#">c2rcvA_</a>	Alignment	not modelled	100.0	45	<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 superoxide dismutase
22	<a href="#">c3tjtA_</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> crystal structure analysis of the superoxide dismutase from2 clostridium difficile
23	<a href="#">c4f2nL_</a>	Alignment	not modelled	100.0	36	<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
24	<a href="#">c3js4C_</a>	Alignment	not modelled	100.0	31	<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="#">c4h3eB_</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> crystal structure of a putative iron superoxide dismutase from2 trypanosoma cruzi bound to iron
26	<a href="#">c3h1sB_</a>	Alignment	not modelled	100.0	35	<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
27	<a href="#">c3tqjB_</a>	Alignment	not modelled	100.0	38	<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
28	<a href="#">c4br6B_</a>	Alignment	not modelled	100.0	49	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> crystal structure of chaetomium thermophilum mnsod
						<b>PDB header:</b> oxidoreductase

29	<a href="#">c5tirB_</a>	Alignment	not modelled	100.0	41	<b>Chain:</b> B: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> crystal structure of mn superoxide dismutase mutant m27v from2 trichoderma reesei
30	<a href="#">c2a03A_</a>	Alignment	not modelled	100.0	35	<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
31	<a href="#">c1unfX_</a>	Alignment	not modelled	100.0	36	<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
32	<a href="#">c3dc5C_</a>	Alignment	not modelled	100.0	43	<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
33	<a href="#">c1y67D_</a>	Alignment	not modelled	100.0	44	<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 from deinococcus2 radiodurans
34	<a href="#">c1en4C_</a>	Alignment	not modelled	100.0	43	<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 manganese superoxide2 dismutase q146h mutant
35	<a href="#">c5n57B_</a>	Alignment	not modelled	100.0	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> staphylococcus aureus cambialistic superoxide dismutase sodm
36	<a href="#">c2nybC_</a>	Alignment	not modelled	100.0	39	<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 q69e at 1.12 angstrom resolution
37	<a href="#">c1qnnD_</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> cambialistic superoxide dismutase from porphyromonas gingivalis
38	<a href="#">c1my6A_</a>	Alignment	not modelled	100.0	40	<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
39	<a href="#">c4k2wA_</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> x-ray crystal structure of superoxide dismutase from babesia bovis2 solved by sulfur/zinc sad
40	<a href="#">c3lj9A_</a>	Alignment	not modelled	100.0	38	<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
41	<a href="#">c6j55j_</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> crystal structure of an iron superoxide dismutate (fesod) from a2 pathogenic acanthamoeba castellanii
42	<a href="#">c3bfrA_</a>	Alignment	not modelled	100.0	48	<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
43	<a href="#">c2cw3A_</a>	Alignment	not modelled	100.0	28	<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 from perkinsus marinus
44	<a href="#">c2gpcB_</a>	Alignment	not modelled	100.0	37	<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
45	<a href="#">c1cojA_</a>	Alignment	not modelled	100.0	30	<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
46	<a href="#">d1idsa2</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
47	<a href="#">d1b06a2</a>	Alignment	not modelled	100.0	40	<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="#">d1p7ga2</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
49	<a href="#">d1wb8a2</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
50	<a href="#">d2p4ka2</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
51	<a href="#">d1bsma2</a>	Alignment	not modelled	100.0	61	<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="#">d1gv3a2</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
53	<a href="#">d1ma1a2</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
54	<a href="#">d1unfx2</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
						<b>Fold:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain



83	<a href="#">d1my6a1</a>	Alignment	not modelled	99.9	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
84	<a href="#">d1y67a1</a>	Alignment	not modelled	99.9	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
85	<a href="#">d3sdpa1</a>	Alignment	not modelled	99.9	38	<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
86	<a href="#">d1coja1</a>	Alignment	not modelled	99.8	30	<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
87	<a href="#">d2gykb1</a>	Alignment	not modelled	64.0	24	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> HNNH-motif
88	<a href="#">d2jb0b1</a>	Alignment	not modelled	58.5	32	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> HNNH-motif
89	<a href="#">c7ceiB_</a>	Alignment	not modelled	56.9	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
90	<a href="#">c4uhpA_</a>	Alignment	not modelled	53.9	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> large component of pyocin ap41; <b>PDBTitle:</b> crystal structure of the pyocin ap41 dnase-immunity complex
91	<a href="#">c4qkoH_</a>	Alignment	not modelled	52.2	28	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> H: <b>PDB Molecule:</b> pyocin-s2; <b>PDBTitle:</b> the crystal structure of the pyocin s2 nuclease domain, immunity2 protein complex at 1.8 angstroms
92	<a href="#">c4wfcF_</a>	Alignment	not modelled	47.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> exosome complex protein lrp1; <b>PDBTitle:</b> structure of the rrp6-rrp47 interaction
93	<a href="#">c1wqsA_</a>	Alignment	not modelled	46.8	25	<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
94	<a href="#">c6b6iD_</a>	Alignment	not modelled	40.3	32	<b>PDB header:</b> viral protein,protease <b>Chain:</b> D: <b>PDB Molecule:</b> 3c-like protease; <b>PDBTitle:</b> 2.4a resolution structure of human norovirus gii.4 protease
95	<a href="#">c2b5bA_</a>	Alignment	not modelled	30.7	18	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> defensin; <b>PDBTitle:</b> a reptilian defensin with anti-bacterial and anti-viral2 activity
96	<a href="#">c5ew5C_</a>	Alignment	not modelled	29.1	26	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> colicin-e9; <b>PDBTitle:</b> crystal structure of colicin e9 in complex with its immunity protein2 im9
97	<a href="#">d1kfta_</a>	Alignment	not modelled	26.8	12	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Excinuclease UvrC C-terminal domain
98	<a href="#">c1kftA_</a>	Alignment	not modelled	26.8	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
99	<a href="#">d1xlya_</a>	Alignment	not modelled	26.4	11	<b>Fold:</b> RNA-binding protein She2p <b>Superfamily:</b> RNA-binding protein She2p <b>Family:</b> RNA-binding protein She2p
100	<a href="#">c5tw9D_</a>	Alignment	not modelled	26.2	21	<b>PDB header:</b> lipid-binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> iron uptake system component efeo; <b>PDBTitle:</b> 1.50 angstrom crystal structure of c-terminal fragment (residues 322-2 384) of iron uptake system component efeo from yersinia pestis.
101	<a href="#">c3r1fO_</a>	Alignment	not modelled	22.3	27	<b>PDB header:</b> transcription <b>Chain:</b> O: <b>PDB Molecule:</b> esx-1 secretion-associated regulator espr; <b>PDBTitle:</b> crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
102	<a href="#">d3cjsb1</a>	Alignment	not modelled	21.3	21	<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
103	<a href="#">d1xl7a1</a>	Alignment	not modelled	21.0	22	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
104	<a href="#">d1ndba1</a>	Alignment	not modelled	20.7	41	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
105	<a href="#">c4c2mK_</a>	Alignment	not modelled	20.4	13	<b>PDB header:</b> transcription <b>Chain:</b> K: <b>PDB Molecule:</b> dna-directed rna polymerases i and iii subunit rpac2; <b>PDBTitle:</b> structure of rna polymerase i at 2.8 a resolution