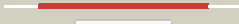


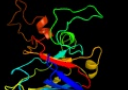
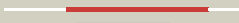
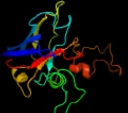



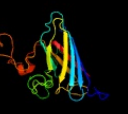














Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0432_(sodC)_519603_520325
Date	Tue Jul 23 14:50:50 BST 2019
Unique Job ID	f4bd993744d4bea46

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6adqZ_	 Alignment		100.0	71	PDB header: electron transport Chain: Z: PDB Molecule: superoxide dismutase [cu-zn]; PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
2	d1pzsa_	 Alignment		100.0	93	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cu,Zn superoxide dismutase-like Family: Cu,Zn superoxide dismutase-like
3	c1pzsa_	 Alignment		100.0	93	PDB header: oxidoreductase, metal binding protein Chain: A: PDB Molecule: superoxide dismutase [cu-zn]; PDBTitle: crystal structure of a cu-zn superoxide dismutase from mycobacterium2 tuberculosis at 1.63 resolution
4	c6dtkA_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: superoxide dismutase c111s/d83s-c111s heterodimer; PDBTitle: heterodimers of fals mutant sod enzyme
5	c6fp6X_	 Alignment		100.0	26	PDB header: metal binding protein Chain: X: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: complex of human cu,zn sod1 with the human copper chaperone for sod12 in a compact conformation
6	d1q0ea_	 Alignment		100.0	30	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cu,Zn superoxide dismutase-like Family: Cu,Zn superoxide dismutase-like
7	c5in2A_	 Alignment		100.0	35	PDB header: oxidoreductase Chain: A: PDB Molecule: extracellular superoxide dismutase [cu-zn]; PDBTitle: crystal structure of extra cellular cu/zn superoxide dismutase from2 onchocerca volvulus at 1.5 angstrom; insight into novel binding site3 and new inhibitors
8	d1srda_	 Alignment		100.0	26	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cu,Zn superoxide dismutase-like Family: Cu,Zn superoxide dismutase-like
9	c3f7IA_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: copper,zinc superoxide dismutase; PDBTitle: x-ray crystal structure of alvinella pompejana cu,zn2 superoxide dismutase
10	d2c9va1	 Alignment		100.0	32	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cu,Zn superoxide dismutase-like Family: Cu,Zn superoxide dismutase-like
11	c2aqmA_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: superoxide dismutase [cu-zn]; PDBTitle: cu/zn superoxide dismutase from brucella abortus

12	c1s4iC_	Alignment		100.0	26	PDB header: oxidoreductase Chain: C: PDB Molecule: superoxide dismutase-like protein yojm; PDBTitle: crystal structure of a sod-like protein from bacillus subtilis
13	d1do5a_	Alignment		100.0	31	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cu,Zn superoxide dismutase-like Family: Cu,Zn superoxide dismutase-like
14	c2q2lB_	Alignment		100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: superoxide dismutase; PDBTitle: crystal structure of superoxide dismutase from p.2 atrosanguina
15	d1eqwa_	Alignment		100.0	28	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cu,Zn superoxide dismutase-like Family: Cu,Zn superoxide dismutase-like
16	d1esoa_	Alignment		100.0	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cu,Zn superoxide dismutase-like Family: Cu,Zn superoxide dismutase-like
17	d1to4a_	Alignment		100.0	26	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cu,Zn superoxide dismutase-like Family: Cu,Zn superoxide dismutase-like
18	d1oala_	Alignment		100.0	34	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cu,Zn superoxide dismutase-like Family: Cu,Zn superoxide dismutase-like
19	c2jlpA_	Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: extracellular superoxide dismutase (cu-zn); PDBTitle: crystal structure of human extracellular copper-zinc superoxide2 dismutase.
20	c2e47A_	Alignment		100.0	27	PDB header: metal binding protein Chain: A: PDB Molecule: time interval measuring enzyme time; PDBTitle: crystal structure analysis of the clock protein ea4 (glycosylation2 form)
21	c3ce1A_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: superoxide dismutase [cu-zn]; PDBTitle: crystal structure of the cu/zn superoxide dismutase from cryptococcus2 liquefaciens strain n6
22	d1xsoa_	Alignment	not modelled	100.0	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cu,Zn superoxide dismutase-like Family: Cu,Zn superoxide dismutase-like
23	c3l9eC_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: C: PDB Molecule: superoxide dismutase [cu-zn]; PDBTitle: crystal structures of holo and cu-deficient cu/znsod from the silkworm2 bombyx mori and the implications in amyotrophic lateral sclerosis
24	c4ojaA_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: superoxide dismutase [cu-zn]; PDBTitle: structure of hydra cu-zn superoxide dismutase
25	d2apsa_	Alignment	not modelled	100.0	32	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cu,Zn superoxide dismutase-like Family: Cu,Zn superoxide dismutase-like
26	d1f1ga_	Alignment	not modelled	100.0	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cu,Zn superoxide dismutase-like Family: Cu,Zn superoxide dismutase-like
27	d1ej8a_	Alignment	not modelled	100.0	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cu,Zn superoxide dismutase-like Family: Cu,Zn superoxide dismutase-like
28	c3kbeA_	Alignment	not modelled	100.0	35	PDB header: oxidoreductase Chain: A: PDB Molecule: superoxide dismutase [cu-zn]; PDBTitle: metal-free c. elegans cu,zn superoxide dismutase
						PDB header: oxidoreductase

29	c3hogA	Alignment	not modelled	100.0	27	Chain: A: PDB Molecule: superoxide dismutase [cu-zn], chloroplatic; PDBTitle: metal-free tomato chloroplast superoxide dismutase
30	c4n3uA	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: potential secreted cu/zn superoxide dismutase; PDBTitle: candida albicans superoxide dismutase 5 (sod5), cu(ii)
31	c1jk9D	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: D: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: heterodimer between h48f-ysod1 and yccs
32	d1jk9b1	Alignment	not modelled	100.0	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cu,Zn superoxide dismutase-like Family: Cu,Zn superoxide dismutase-like
33	c1qupA	Alignment	not modelled	100.0	19	PDB header: chaperone Chain: A: PDB Molecule: superoxide dismutase 1 copper chaperone; PDBTitle: crystal structure of the copper chaperone for superoxide dismutase
34	c4u4iA	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: cu/zn superoxide dismutase; PDBTitle: megavirus chilensis superoxide dismutase
35	c5j0cB	Alignment	not modelled	99.9	42	PDB header: oxidoreductase Chain: B: PDB Molecule: superoxide dismutase [cu-zn],superoxide dismutase [cu-zn], PDBTitle: monomeric human cu,zn superoxide dismutase, loops iv and vii deleted,2 apo form, circular permutant p2/3
36	c4bd4H	Alignment	not modelled	99.9	34	PDB header: oxidoreductase Chain: H: PDB Molecule: superoxide dismutase [cu-zn]; PDBTitle: monomeric human cu,zn superoxide dismutase, loops iv and vii deleted,2 apo form, mutant h43f
37	c5j0fA	Alignment	not modelled	99.7	31	PDB header: oxidoreductase Chain: A: PDB Molecule: superoxide dismutase [cu-zn],oxidoreductase,superoxide PDBTitle: monomeric human cu,zn superoxide dismutase, loops iv and vii deleted,2 apo form, circular permutant p4/5
38	c5icuA	Alignment	not modelled	70.8	11	PDB header: chaperone Chain: A: PDB Molecule: copc; PDBTitle: the crystal structure of copc from methylosinus trichosporium ob3b
39	c1z8rA	Alignment	not modelled	42.0	32	PDB header: hydrolase Chain: A: PDB Molecule: coxsaackievirus b4 polyprotein; PDBTitle: 2a cysteine proteinase from human coxsackievirus b4 (strain2 jyb / benschoten / new york / 51)
40	c2m5tA	Alignment	not modelled	37.1	39	PDB header: viral protein Chain: A: PDB Molecule: human rhinovirus 2a proteinase; PDBTitle: solution structure of the 2a proteinase from a common cold agent,2 human rhinovirus rv-c02, strain w12
41	c1naeA	Alignment	not modelled	32.0	19	PDB header: hydrolase Chain: A: PDB Molecule: putative xylanase; PDBTitle: structure of cscbm6-3 from clostridium stercorarium in2 complex with xylotriose
42	d2hrva	Alignment	not modelled	28.4	29	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
43	d1uy4a	Alignment	not modelled	25.6	20	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 6 carbohydrate binding module, CBM6
44	c2xr4A	Alignment	not modelled	24.3	17	PDB header: sugar binding protein Chain: A: PDB Molecule: lectin; PDBTitle: c-terminal domain of bc2l-c lectin from burkholderia cenocepacia
45	c3osvC	Alignment	not modelled	19.8	15	PDB header: structural protein Chain: C: PDB Molecule: flagellar basal-body rod modification protein flgd; PDBTitle: the crytsal structure of flgd from p. aeruginosa
46	d1gsk3	Alignment	not modelled	18.0	21	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
47	c2vnc	Alignment	not modelled	16.7	14	PDB header: sugar-binding protein Chain: C: PDB Molecule: bcla; PDBTitle: crystal structure of bcla lectin from burkholderia2 cenocepacia in complex with alpha-methyl-mannoside at 1.73 angstrom resolution
48	d1od3a	Alignment	not modelled	16.2	21	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 6 carbohydrate binding module, CBM6
49	d2e9ia1	Alignment	not modelled	15.8	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
50	d1w9sa	Alignment	not modelled	14.8	19	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 6 carbohydrate binding module, CBM6
51	c2k7pA	Alignment	not modelled	14.0	22	PDB header: structural protein Chain: A: PDB Molecule: filamin-a; PDBTitle: filamin a ig-like domains 16-17
52	d2diba1	Alignment	not modelled	13.1	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
53	d1ibya	Alignment	not modelled	12.5	21	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Nitrosocyanin
54	d1gyca3	Alignment	not modelled	11.7	17	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins

55	d1luxx_	Alignment	not modelled	11.5	24	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 6 carbohydrate binding module, CBM6
56	d1sddb2	Alignment	not modelled	11.5	17	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
57	c2mqcA_	Alignment	not modelled	10.6	6	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the protein bvu_0925 from bacteroides vulgatus atcc2 8482
58	c2re3A_	Alignment	not modelled	10.2	33	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf1285 family protein (spo_0140) from2 silicibacter pomeroyi dss-3 at 2.50 a resolution
59	d1bcoa1	Alignment	not modelled	10.2	9	Fold: mu transposase, C-terminal domain Superfamily: mu transposase, C-terminal domain Family: mu transposase, C-terminal domain
60	c1zpuE_	Alignment	not modelled	9.8	26	PDB header: oxidoreductase Chain: E: PDB Molecule: iron transport multicopper oxidase fet3; PDBTitle: crystal structure of fet3p, a multicopper oxidase that functions in2 iron import
61	c3c12A_	Alignment	not modelled	9.8	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: flagellar protein; PDBTitle: crystal structure of flgd from xanthomonas campestris:2 insights into the hook capping essential for flagellar3 assembly
62	d2d7na1	Alignment	not modelled	9.7	22	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
63	d1luxza_	Alignment	not modelled	9.7	17	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 6 carbohydrate binding module, CBM6
64	c3bvcA_	Alignment	not modelled	9.5	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ism_01780; PDBTitle: crystal structure of uncharacterized protein ism_01780 from2 roseovarius nubinhibens ism
65	d1e30a_	Alignment	not modelled	9.2	30	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
66	c2kywA_	Alignment	not modelled	9.1	21	PDB header: cell adhesion Chain: A: PDB Molecule: adhesion exoprotein; PDBTitle: solution nmr structure of a domain of adhesion exoprotein from2 pediococcus pentosaceus, northeast structural genomics consortium3 target ptr410
67	d2j5wa5	Alignment	not modelled	8.6	26	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
68	d1kcwa2	Alignment	not modelled	8.5	22	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
69	c6nfqC_	Alignment	not modelled	8.0	16	PDB header: metal binding protein Chain: C: PDB Molecule: copc; PDBTitle: copc from pseudomonas fluorescens
70	c2mtwA_	Alignment	not modelled	7.2	60	PDB header: protein binding Chain: A: PDB Molecule: erythrocyte-binding antigen 175; PDBTitle: evidence supporting the hypothesis that specifically modifying a2 malaria peptide to fit into hla-dr 1*03 molecules induces antibody3 production and protection
71	c2k3cA_	Alignment	not modelled	7.1	50	PDB header: metal transport Chain: A: PDB Molecule: tmix peptide; PDBTitle: structural and functional characterization of tm ix of the2 nhe1 isoform of the na+/h+ exchanger
72	d1fwxa1	Alignment	not modelled	6.9	24	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Nitrosocyanin
73	d2chha1	Alignment	not modelled	6.8	9	Fold: Calcium-mediated lectin Superfamily: Calcium-mediated lectin Family: Calcium-mediated lectin
74	c3tasC_	Alignment	not modelled	6.5	19	PDB header: oxidoreductase Chain: C: PDB Molecule: small laccase, multi-copper oxidase; PDBTitle: small laccase from streptomyces viridosporus t7a
75	c3biyA_	Alignment	not modelled	6.5	40	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase p300; PDBTitle: crystal structure of p300 histone acetyltransferase domain in complex2 with a bisubstrate inhibitor, lys-coa
76	d2q9oa3	Alignment	not modelled	6.5	16	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
77	c2f2ba_	Alignment	not modelled	6.2	33	PDB header: membrane protein Chain: A: PDB Molecule: aquaporin aqpm; PDBTitle: crystal structure of integral membrane protein aquaporin aqpm at 1.68a2 resolution
78	d1kyaa3	Alignment	not modelled	6.2	19	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
79	c5hqhA_	Alignment	not modelled	6.1	12	PDB header: unknown function Chain: A: PDB Molecule: lmo2119 protein; PDBTitle: 1.32 angstrom crystal structure of ybbr like domain of lmo2119 protein2 from listeria monocytogenes.
80	c4p3wE_	Alignment	not modelled	6.0	20	PDB header: cell adhesion Chain: E: PDB Molecule: filamin-a; PDBTitle: crystal structure of the human filamin a ig-like domains 20-21 in2 complex with migfilin peptide
						PDB header: splicing

81	c3sbtB_	Alignment	not modelled	6.0	29	Chain: B; PDB Molecule: a1 cistron-splicing factor aar2; PDBTitle: crystal structure of a aar2-prp8 complex
82	c2boiA_	Alignment	not modelled	6.0	22	PDB header: lectin Chain: A; PDB Molecule: cv-iii lectin; PDBTitle: 1.1a structure of chromobacterium violaceum lectin cv2i in2 complex with alpha-methyl-fucoside
83	d1mzya2	Alignment	not modelled	5.9	10	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
84	c5lwxA_	Alignment	not modelled	5.8	21	PDB header: oxidoreductase Chain: A; PDB Molecule: multicopper oxidase; PDBTitle: crystal structure of the h253d mutant of mcog from aspergillus niger
85	c5ewoA_	Alignment	not modelled	5.7	19	PDB header: viral protein Chain: A; PDB Molecule: structural protein; PDBTitle: crystal structure of the human astrovirus 1 capsid protein spike2 domain at 0.95-a resolution
86	d1g94a1	Alignment	not modelled	5.7	36	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
87	c4zzkA_	Alignment	not modelled	5.6	13	PDB header: motor protein Chain: A; PDB Molecule: basal-body rod modification protein flgd; PDBTitle: crystal structure of truncated flgd (monoclinic form) from the human2 pathogen helicobacter pylori
88	c6g2dC_	Alignment	not modelled	5.6	25	PDB header: ligase Chain: C; PDB Molecule: acetyl-coa carboxylase 1; PDBTitle: citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution
89	d1uzva_	Alignment	not modelled	5.5	14	Fold: Calcium-mediated lectin Superfamily: Calcium-mediated lectin Family: Calcium-mediated lectin
90	d1qhqa_	Alignment	not modelled	5.5	9	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
91	d1kv7a3	Alignment	not modelled	5.5	27	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
92	d1snra2	Alignment	not modelled	5.4	15	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
93	d1h6ia_	Alignment	not modelled	5.4	33	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
94	d1mzya1	Alignment	not modelled	5.4	13	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
95	d2ysca1	Alignment	not modelled	5.2	60	Fold: WW domain-like Superfamily: WW domain Family: WW domain
96	c2w2eA_	Alignment	not modelled	5.2	33	PDB header: membrane protein Chain: A; PDB Molecule: aquaporin pip2-7 7; PDBTitle: 1.15 angstrom crystal structure of p.pastoris aquaporin, aqy1, in a2 closed conformation at ph 3.5
97	c5i32A_	Alignment	not modelled	5.2	50	PDB header: membrane protein Chain: A; PDB Molecule: aquaporin tip2-1; PDBTitle: ammonia permeable aquaporin attip2;1
98	c1of0A_	Alignment	not modelled	5.2	29	PDB header: oxidoreductase Chain: A; PDB Molecule: spore coat protein a; PDBTitle: crystal structure of bacillus subtilis cota after 1h soaking with abts
99	c2j6gA_	Alignment	not modelled	5.2	20	PDB header: cell adhesion Chain: A; PDB Molecule: faeg; PDBTitle: faeg from f4ac etec strain 5_95, produced in tobacco plant chloroplast