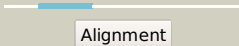


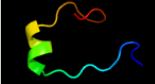

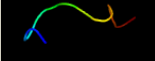
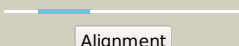
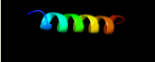
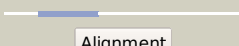

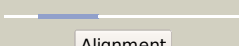

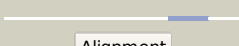

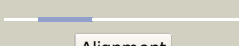
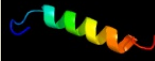

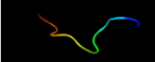






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3047c_(-)_3408033_3408317
Date	Thu Aug 8 16:20:22 BST 2019
Unique Job ID	01dbcf7d812d87b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ub2a2	 Alignment		36.2	33	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
2	c3mxnB_	 Alignment		33.8	38	PDB header: replication Chain: B: PDB Molecule: recq-mediated genome instability protein 2; PDBTitle: crystal structure of the rmi core complex
3	c2l1uA_	 Alignment		31.8	46	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase b2, mitochondrial; PDBTitle: structure-functional analysis of mammalian msrb2 protein
4	d1itka2	 Alignment		30.2	13	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
5	c2b2qB_	 Alignment		24.5	44	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase-peroxidase; PDBTitle: crystal structure of native catalase-peroxidase katg at ph7.5
6	c2fxhB_	 Alignment		24.5	44	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase-peroxidase protein; PDBTitle: crystal structure of katg at ph 6.5
7	c2k8dA_	 Alignment		22.9	24	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase msrb; PDBTitle: solution structure of a zinc-binding methionine sulfoxide reductase
8	c1u2jC_	 Alignment		21.6	29	PDB header: oxidoreductase Chain: C: PDB Molecule: peroxidase/catalase hpi; PDBTitle: crystal structure of the c-terminal domain from the2 catalase-peroxidase katg of escherichia coli (p21 21 21)
9	c2kaoA_	 Alignment		21.3	25	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase b1; PDBTitle: structure of reduced mouse methionine sulfoxide reductase b12 (sec95cys mutant)
10	d2ccaa1	 Alignment		21.0	33	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
11	d1mwva1	 Alignment		20.6	37	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG

12	c3hcjB_	Alignment		20.1	56	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase; PDBTitle: structure of msrb from xanthomonas campestris (oxidized2 form)
13	d1l1da_	Alignment		19.8	67	Fold: Mss4-like Superfamily: Mss4-like Family: SelR domain
14	d1u2ka_	Alignment		19.8	29	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
15	d1mwva2	Alignment		19.4	22	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
16	c3e0mB_	Alignment		18.3	56	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase msra/msrb PDBTitle: crystal structure of fusion protein of msra and msrb
17	d1xm0a1	Alignment		18.2	67	Fold: Mss4-like Superfamily: Mss4-like Family: SelR domain
18	d2hiqa1	Alignment		17.7	23	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Hypothetical protein YdhR
19	c4j80B_	Alignment		17.2	33	PDB header: chaperone Chain: B: PDB Molecule: chaperone protein dnaj 2; PDBTitle: thermus thermophilus dnaj
20	c3cezA_	Alignment		16.7	56	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase; PDBTitle: crystal structure of methionine-r-sulfoxide reductase from2 burkholderia pseudomallei
21	d1ub2a1	Alignment	not modelled	15.8	40	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
22	c1wd6B_	Alignment	not modelled	15.0	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein ydhr; PDBTitle: crystal structure of jw1657 from escherichia coli
23	d1itka1	Alignment	not modelled	14.7	30	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
24	c3ut2B_	Alignment	not modelled	14.3	30	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase-peroxidase 2; PDBTitle: crystal structure of fungal magkatg2
25	d1gwya_	Alignment	not modelled	14.0	25	Fold: Cytolysin/lectin Superfamily: Cytolysin/lectin Family: Anemone pore-forming cytolysin
26	c1itkB_	Alignment	not modelled	12.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase-peroxidase; PDBTitle: crystal structure of catalase-peroxidase from haloarcula2 marismortui
27	c2ccaA_	Alignment	not modelled	12.5	26	PDB header: oxidoreductase Chain: A: PDB Molecule: peroxidase/catalase t; PDBTitle: crystal structure of the catalase-peroxidase (katg) and2 s315t mutant from mycobacterium tuberculosis
28	c5fa9B_	Alignment	not modelled	12.4	56	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase msra; PDBTitle: bifunctional methionine sulfoxide reductase ab (msrab) from treponema2 denticola

29	d1lxja_	Alignment	not modelled	12.4	14	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
30	c3vImB_	Alignment	not modelled	11.4	30	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase-peroxidase 2; PDBTitle: crystal structure analysis of the met244ala variant of katg from <i>haloarcula marismortui</i>
31	d1llpa_	Alignment	not modelled	10.9	24	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
32	d1atxa_	Alignment	not modelled	10.3	86	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
33	d1iyna_	Alignment	not modelled	10.1	48	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
34	c1ub2A_	Alignment	not modelled	9.1	39	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase-peroxidase; PDBTitle: crystal structure of catalase-peroxidase from <i>synechococcus pcc 7942</i>
35	d1gmnbl	Alignment	not modelled	9.0	46	Fold: Hairpin loop containing domain-like Superfamily: Hairpin loop containing domain-like Family: Hairpin loop containing domain
36	d1iaza_	Alignment	not modelled	8.9	28	Fold: Cytolysin/lectin Superfamily: Cytolysin/lectin Family: Anemone pore-forming cytolysin
37	d2e39a1	Alignment	not modelled	8.7	20	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
38	d1d0da_	Alignment	not modelled	7.6	67	Fold: BPTI-like Superfamily: BPTI-like Family: Soft tick anticoagulant proteins
39	c6rdu9_	Alignment	not modelled	7.5	67	PDB header: proton transport Chain: 9: PDB Molecule: asa-9: polytomella f-atp synthase associated subunit 9; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 monomer-masked refinement
40	d1vk8a_	Alignment	not modelled	7.5	19	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
41	c5whqA_	Alignment	not modelled	7.3	30	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase-peroxidase; PDBTitle: crystal structure of the catalase-peroxidase from <i>neurospora crassa at2 2.9 a</i>
42	c2xdgB_	Alignment	not modelled	7.2	29	PDB header: signaling protein Chain: B: PDB Molecule: growth hormone-releasing hormone receptor; PDBTitle: crystal structure of the extracellular domain of human growth hormone2 releasing hormone receptor.
43	d1b80a_	Alignment	not modelled	7.2	24	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
44	d2gtad1	Alignment	not modelled	6.9	16	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
45	c1tapA_	Alignment	not modelled	6.7	67	PDB header: proteinase inhibitor Chain: A: PDB Molecule: factor xa inhibitor; PDBTitle: nmr solution structure of recombinant tick anticoagulant2 protein (rtap), a factor xa inhibitor from the tick3 <i>ornithodoros moubata</i>
46	d1ujoa_	Alignment	not modelled	6.6	21	Fold: CH domain-like Superfamily: Calponin-homology domain, CH-domain Family: Calponin-homology domain, CH-domain
47	d1nqka_	Alignment	not modelled	6.3	20	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
48	c4h3zA_	Alignment	not modelled	6.2	33	PDB header: transferase Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of a symmetric dimer of a trna (guanine-(n(1)-)-2 methyltransferase from <i>burkholderia phymatum</i> bound to s-adenosyl3 homocystein in both half-sites
49	c2w23A_	Alignment	not modelled	6.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: versatile peroxidase vpl2; PDBTitle: structure of mutant w169y of <i>pleurotus eryngii</i> versatile2 peroxidase (vp)
50	c5wyrA_	Alignment	not modelled	6.1	47	PDB header: transferase Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure and catalytic mechanism of the essential m1g37 trna2 methyltransferase trmd from <i>pseudomonas aeruginosa</i>
51	c2q9lA_	Alignment	not modelled	5.9	23	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of imazg from <i>vibrio dat 722</i> : ctag-imazg (p43212)
52	c6gboG_	Alignment	not modelled	5.9	30	PDB header: viral protein Chain: G: PDB Molecule: polymerase cofactor vp35; PDBTitle: crystal structure of the oligomerization domain of vp35 from ebola2 virus
53	d1qpaa_	Alignment	not modelled	5.6	16	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
54	c1apfA_	Alianment	not modelled	5.3	56	PDB header: cardiac stimulant Chain: A: PDB Molecule: anthopleurin-b;

