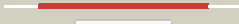



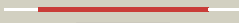

















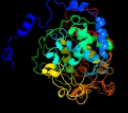





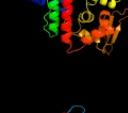

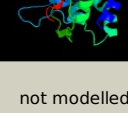


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1908c_(katG)_2153896_2156118
Date	Fri Aug 2 13:30:52 BST 2019
Unique Job ID	55c8689d3730d5e4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ccaA_	 Alignment		100.0	100	PDB header: oxidoreductase Chain: A: PDB Molecule: peroxidase/catalase t; PDBTitle: crystal structure of the catalase-peroxidase (katg) and2 s315t mutant from mycobacterium tuberculosis
2	c3ut2B_	 Alignment		100.0	57	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase-peroxidase 2; PDBTitle: crystal structure of fungal magkatg2
3	c1itkB_	 Alignment		100.0	57	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase-peroxidase; PDBTitle: crystal structure of catalase-peroxidase from haloarcula2 marismortui
4	c2b2qB_	 Alignment		100.0	68	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase-peroxidase; PDBTitle: crystal structure of native catalase-peroxidase katg at ph7.5
5	c2fxhB_	 Alignment		100.0	68	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase-peroxidase protein; PDBTitle: crystal structure of katg at ph 6.5
6	c5whqA_	 Alignment		100.0	58	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase-peroxidase; PDBTitle: crystal structure of the catalase-peroxidase from neurospora crassa at2 2.9 a
7	c1ub2A_	 Alignment		100.0	55	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase-peroxidase; PDBTitle: crystal structure of catalase-peroxidase from synechococcus pcc 7942
8	c3vImB_	 Alignment		100.0	59	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase-peroxidase 2; PDBTitle: crystal structure analysis of the met244ala variant of katg from2 haloarcula marismortui
9	d2ccaa1	 Alignment		100.0	100	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
10	d1mwva1	 Alignment		100.0	68	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
11	d1ub2a1	 Alignment		100.0	58	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG

12	d1itka1	Alignment		100.0	59	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
13	d1mwva2	Alignment		100.0	67	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
14	d1itka2	Alignment		100.0	54	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
15	d2ccaa2	Alignment		100.0	100	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
16	d1ub2a2	Alignment		100.0	52	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
17	c1u2jC	Alignment		100.0	53	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)
18	d1u2ka	Alignment		100.0	53	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
19	d2euta1	Alignment		100.0	33	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
20	d1iyna	Alignment		100.0	32	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
21	d1oafa	Alignment	not modelled	100.0	27	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
22	c3riwA	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: ascorbate peroxidase; PDBTitle: the crystal structure of leishmania major peroxidase mutant c197t
23	d1lpa	Alignment	not modelled	100.0	20	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
24	d1qpaa	Alignment	not modelled	100.0	18	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
25	c3q3uA	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: lignin peroxidase; PDBTitle: trametes cervina lignin peroxidase
26	d1b80a	Alignment	not modelled	100.0	17	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
27	d1apxa	Alignment	not modelled	100.0	31	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
28	c4bm2A	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: manganese peroxidase 4; PDBTitle: crystal structure of manganese peroxidase 4 from pleurotus2 ostreatus - crystal form ii
29	c2w23A	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: versatile peroxidase vpl2;

29	c4wz9A_	Alignment	not modelled	100.0	21	PDBTitle: structure of mutant w169y of pleurotus eryngii versatile2 peroxidase (vp)
30	d2e39a1	Alignment	not modelled	100.0	18	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
31	d1scha_	Alignment	not modelled	100.0	16	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
32	d1yyda1	Alignment	not modelled	100.0	18	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
33	d1bgpa_	Alignment	not modelled	100.0	16	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
34	d1pa2a_	Alignment	not modelled	100.0	17	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
35	c3hdiA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: royal palm tree peroxidase; PDBTitle: crystal structure of highly glycosylated peroxidase from royal palm2 tree
36	d1fhfa_	Alignment	not modelled	100.0	15	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
37	d1qgja_	Alignment	not modelled	100.0	18	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
38	d1gwua_	Alignment	not modelled	100.0	17	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
39	c5viaA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: pseudoperoxidase; PDBTitle: crystal structural of leishmania major pseudoperoxidase
40	c3rrwB_	Alignment	not modelled	100.0	20	PDB header: plant protein Chain: B: PDB Molecule: thylakoid lumenal 29 kda protein, chloroplastic; PDBTitle: crystal structure of the tl29 protein from arabidopsis thaliana
41	d1ljra1	Alignment	not modelled	67.1	16	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
42	d1gula1	Alignment	not modelled	57.4	18	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
43	d1mtyb_	Alignment	not modelled	53.3	25	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
44	d1b8xa1	Alignment	not modelled	50.3	10	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
45	d1ev4c1	Alignment	not modelled	44.9	14	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
46	d1r5aa1	Alignment	not modelled	42.4	17	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
47	d1tw9a1	Alignment	not modelled	39.1	19	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
48	d1ev4a1	Alignment	not modelled	37.1	14	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
49	d2pfxa1	Alignment	not modelled	36.5	19	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
50	c3ketA_	Alignment	not modelled	33.8	17	PDB header: transcription/dna Chain: A: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
51	d1gnea1	Alignment	not modelled	33.2	10	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
52	d1xw6a1	Alignment	not modelled	31.3	17	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
53	d1b48a1	Alignment	not modelled	31.2	19	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
54	d1gnwa1	Alignment	not modelled	29.6	19	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
55	c5mrwG_	Alignment	not modelled	29.3	18	PDB header: hydrolase Chain: G: PDB Molecule: potassium-transporting atpase kdpc subunit; PDBTitle: structure of the kdpcfab complex

56	d1k3ya1	Alignment	not modelled	28.9	16	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
57	c5dqsD_	Alignment	not modelled	28.2	16	PDB header: translation Chain: D: PDB Molecule: elongation factor 1-beta; PDBTitle: complex structure of human elongation factor 1b alpha and gamma gst-2 like domains
58	c3c1IB_	Alignment	not modelled	27.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: putative antioxidant defense protein mlr4105; PDBTitle: crystal structure of an antioxidant defense protein (mlr4105) from2 mesorhizobium loti maff303099 at 2.00 a resolution
59	d1f3ba1	Alignment	not modelled	27.8	12	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
60	c5zz5D_	Alignment	not modelled	27.6	9	PDB header: gene regulation Chain: D: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: redox-sensing transcriptional repressor rex
61	d1ml6a1	Alignment	not modelled	26.1	12	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
62	d1gsua1	Alignment	not modelled	25.3	17	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
63	d1v2aa1	Alignment	not modelled	24.1	24	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
64	d1j1wa1	Alignment	not modelled	24.0	20	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
65	d2cvda1	Alignment	not modelled	23.9	10	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
66	d1bvua2	Alignment	not modelled	23.6	18	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
67	c2ymaB_	Alignment	not modelled	22.8	23	PDB header: carbohydrate binding protein Chain: B: PDB Molecule: protein os-9 homolog; PDBTitle: x-ray structure of the yos9 dimerization domain
68	c2dt5A_	Alignment	not modelled	22.8	19	PDB header: dna binding protein Chain: A: PDB Molecule: at-rich dna-binding protein; PDBTitle: crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
69	d1duga1	Alignment	not modelled	22.6	10	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
70	d1bgva2	Alignment	not modelled	22.6	17	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
71	d1pn9a1	Alignment	not modelled	22.4	24	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
72	d2fhea1	Alignment	not modelled	22.1	17	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
73	c3rxyA_	Alignment	not modelled	21.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nif3 protein; PDBTitle: crystal structure of nif3 superfamily protein from sphaerobacter2 thermophilus
74	d1dk5a_	Alignment	not modelled	21.4	16	Fold: Annexin Superfamily: Annexin Family: Annexin
75	d1gtma2	Alignment	not modelled	21.4	15	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
76	c3wg9D_	Alignment	not modelled	20.1	10	PDB header: transcription Chain: D: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: crystal structure of rsp, a rex-family repressor
77	c5uz9D_	Alignment	not modelled	19.9	17	PDB header: immune system/rna Chain: D: PDB Molecule: crispr-associated protein csy3; PDBTitle: cryo em structure of anti-crisprs, acrf1 and acrf2, bound to type i-f2 crrna-guided crispr surveillance complex
78	d1pd211	Alignment	not modelled	19.8	10	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
79	c6fhjA_	Alignment	not modelled	19.0	20	PDB header: hydrolase Chain: A: PDB Molecule: protein,protein; PDBTitle: structural dynamics and catalytic properties of a multi-modular2 xanthanase, native.
80	d1b4pa1	Alignment	not modelled	18.9	15	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
81	d1v9la2	Alignment	not modelled	18.6	18	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
82	c1zxnB_	Alignment	not modelled	18.1	29	PDB header: isomerase Chain: B: PDB Molecule: dna topoisomerase ii, alpha isozyme; PDBTitle: human dna topoisomerase iia atpase/adp

83	c6fhnA	Alignment	not modelled	17.6	20	PDB header: hydrolase Chain: A: PDB Molecule: protein; PDBTitle: structural dynamics and catalytic properties of a multi-modular2 xanthanase (pt derivative)
84	c4gdxA	Alignment	not modelled	17.6	21	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase 1 heavy chain; PDBTitle: crystal structure of human gamma-glutamyl transpeptidase--glutamate2 complex
85	d1m0ua1	Alignment	not modelled	17.4	16	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
86	d2i3oa1	Alignment	not modelled	17.3	18	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Gamma-glutamyltranspeptidase-like
87	c2e0wA	Alignment	not modelled	17.3	15	PDB header: transferase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: t391a precursor mutant protein of gamma-glutamyltranspeptidase from2 escherichia coli
88	d1hwxa2	Alignment	not modelled	17.1	19	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
89	c5hy0D	Alignment	not modelled	16.7	31	PDB header: hydrolase Chain: D: PDB Molecule: ring-opening amidohydrolase; PDBTitle: orotic acid hydrolase
90	c5f0gB	Alignment	not modelled	16.6	17	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase d2; PDBTitle: structure of the glutathione transferase delta 2 from drosophila2 melanogaster
91	d4gtua1	Alignment	not modelled	16.5	10	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
92	d1oe8a1	Alignment	not modelled	16.3	18	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
93	d1jvra	Alignment	not modelled	16.1	21	Fold: Retroviral matrix proteins Superfamily: Retroviral matrix proteins Family: HTLV-II matrix protein
94	d1f2ea1	Alignment	not modelled	16.0	16	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
95	c4o8wE	Alignment	not modelled	16.0	21	PDB header: structural protein, signaling protein Chain: E: PDB Molecule: spore germination protein; PDBTitle: crystal structure of the gerd spore germination protein
96	d1okta1	Alignment	not modelled	15.9	38	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
97	c6bupC	Alignment	not modelled	15.8	28	PDB header: hydrolase Chain: C: PDB Molecule: cyanuric acid amidohydrolase; PDBTitle: crystal structures of cyanuric acid hydrolase from moorella2 thermoacetica complexed with cyanuric acid
98	d1jnra1	Alignment	not modelled	15.5	18	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
99	c4j94A	Alignment	not modelled	15.2	33	PDB header: hydrolase Chain: A: PDB Molecule: membrane-anchored mycosin mycp1; PDBTitle: crystal structure of mycp1 from the esx-1 type vii secretion system