Phyre^2

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Description	P13029
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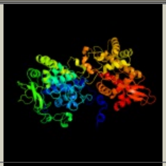
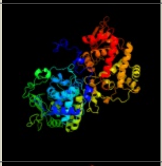
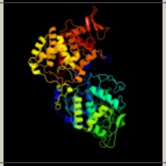
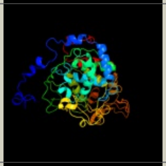
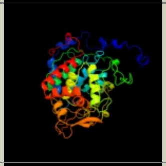
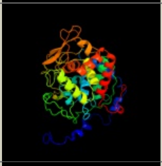
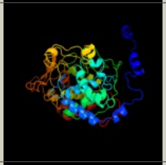
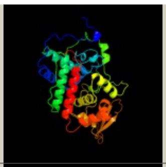
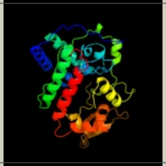
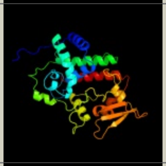
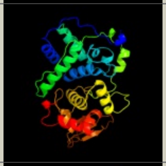
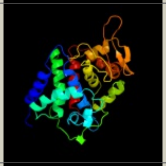
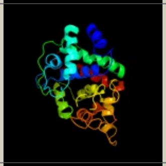
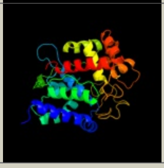
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1itkB_	Alignment		100.0	55	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase-peroxidase; **PDBTitle:** crystal structure of catalase-peroxidase from haloarcula2 marismortui
2	c2b2qB_	Alignment		100.0	66	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase-peroxidase; **PDBTitle:** crystal structure of native catalase-peroxidase katg at2 ph7.5
3	c2fxhB_	Alignment		100.0	66	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase-peroxidase protein; **PDBTitle:** crystal structure of katg at ph 6.5
4	c2ccaA_	Alignment		100.0	59	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxidase/catalase t; **PDBTitle:** crystal structure of the catalase-peroxidase (katg) and2 s315t mutant from mycobacterium tuberculosis
5	c1ub2A_	Alignment		100.0	58	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catalase-peroxidase; **PDBTitle:** crystal structure of catalase-peroxidase from synechococcus pcc 7942
6	d2ccaa1	Alignment		100.0	59	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
7	d1mwva1	Alignment		100.0	70	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
8	d1ub2a1	Alignment		100.0	58	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
9	d1itka1	Alignment		100.0	56	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
10	d1mwva2	Alignment		100.0	61	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
11	d1ub2a2	Alignment		100.0	59	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG

12	d1itka2	Alignment		100.0	53	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
13	c1u2jC_	Alignment		100.0	91	**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)
14	d1u2ka_	Alignment		100.0	91	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
15	d2ccaa2	Alignment		100.0	55	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
16	d2euta1	Alignment		100.0	22	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
17	c3q3uA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lignin peroxidase; **PDBTitle:** trametes cervina lignin peroxidase
18	d1b80a_	Alignment		100.0	17	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
19	d1qpaa_	Alignment		100.0	19	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
20	d1iyna_	Alignment		100.0	34	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
21	d1llpa_	Alignment	not modelled	100.0	18	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
22	c3riwA_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ascorbate peroxidase; **PDBTitle:** the crystal structure of leishmania major peroxidase mutant c197t
23	d2e39a1	Alignment	not modelled	100.0	17	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
24	d1oafa_	Alignment	not modelled	100.0	30	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
25	d1yyda1	Alignment	not modelled	100.0	14	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
26	c2w23A_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**versatile peroxidase vpl2; **PDBTitle:** structure of mutant w169y of pleurotus eryngii versatile2 peroxidase (vp)
27	d1apxa_	Alignment	not modelled	100.0	28	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
28	d1scha_	Alignment	not modelled	100.0	20	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
29	d1pa2a_	Alignment	not modelled	100.0	16	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases

						Family:CCP-like
30	d1qgja_	Alignment	not modelled	100.0	18	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
31	d1bgpa_	Alignment	not modelled	100.0	17	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
32	c3hdlA_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**royal palm tree peroxidase; **PDBTitle:** crystal structure of highly glycosylated peroxidase from royal palm2 tree
33	d1gwua_	Alignment	not modelled	100.0	19	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
34	d1fhfa_	Alignment	not modelled	100.0	19	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
35	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
36	c3ketA_	Alignment	not modelled	61.6	20	**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
37	d1mtyb_	Alignment	not modelled	51.4	21	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
38	c2vcbA_	Alignment	not modelled	44.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylglucosaminidase; **PDBTitle:** family 89 glycoside hydrolase from clostridium perfringens2 in complex with pugnac
39	d1ks8a_	Alignment	not modelled	29.4	11	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
40	d1g87a1	Alignment	not modelled	28.4	20	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
41	c1ga2A_	Alignment	not modelled	26.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase 9g; **PDBTitle:** the crystal structure of endoglucanase 9g from clostridium2 cellulolyticum complexed with cellobiose
42	d1gula1	Alignment	not modelled	25.1	27	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
43	c1js4B_	Alignment	not modelled	22.4	22	**PDB header:**glycosyl hydrolase **Chain:** B: **PDB Molecule:**endo/exocellulase e4; **PDBTitle:** endo/exocellulase:cellobiose from thermomonospora
44	c2dt5A_	Alignment	not modelled	22.1	14	**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
45	c3hjzA_	Alignment	not modelled	21.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transaldolase b; **PDBTitle:** the structure of an aldolase from prochlorococcus marinus
46	d1jnra1	Alignment	not modelled	20.3	19	**Fold:**Spectrin repeat-like **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
47	d1ml6a1	Alignment	not modelled	19.8	14	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
48	c2z8jA_	Alignment	not modelled	19.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gamma-glutamyltranspeptidase; **PDBTitle:** crystal structure of escherichia coli gamma-2 glutamyltranspeptidase in complex with azaserine prepared3 in the dark
49	c2e0wA_	Alignment	not modelled	19.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gamma-glutamyltranspeptidase; **PDBTitle:** t391a precursor mutant protein of gamma-glutamyltranspeptidase from2 escherichia coli
50	d2pfxa1	Alignment	not modelled	19.5	23	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
51	d1gtma2	Alignment	not modelled	18.7	15	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
52	d2i3oa1	Alignment	not modelled	18.5	18	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Gamma-glutamyltranspeptidase-like
53	d1ev4a1	Alignment	not modelled	18.1	16	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
54	d1bgva2	Alignment	not modelled	17.8	18	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
						Fold:GST C-terminal domain-like

55	d1gnwa1	Alignment	not modelled	17.2	18	**Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
56	d1dk5a_	Alignment	not modelled	16.9	21	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
57	d1j3ga_	Alignment	not modelled	16.6	14	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
58	d1tf4a1	Alignment	not modelled	16.1	22	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
59	d1okta1	Alignment	not modelled	15.5	27	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
60	d3e2ba1	Alignment	not modelled	15.4	20	**Fold:**DLC **Superfamily:**DLC **Family:**DLC
61	d1b26a2	Alignment	not modelled	15.2	21	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
62	d1no7a_	Alignment	not modelled	15.1	16	**Fold:**Major capsid protein VP5 **Superfamily:**Major capsid protein VP5 **Family:**Major capsid protein VP5
63	c1no7A_	Alignment	not modelled	15.1	16	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major capsid protein; **PDBTitle:** structure of the large protease resistant upper domain of2 vp5, the major capsid protein of herpes simplex virus-1
64	d1bvua2	Alignment	not modelled	14.6	15	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
65	c2xfgA_	Alignment	not modelled	14.4	32	**PDB header:**hydrolase/sugar binding protein **Chain:** A: **PDB Molecule:**endoglucanase 1; **PDBTitle:** reassembly and co-crystallization of a family 9 processive2 endoglucanase from separately expressed gh9 and cbm3c3 modules
66	d2nlza1	Alignment	not modelled	14.2	21	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Gamma-glutamyltranspeptidase-like
67	d1n00a_	Alignment	not modelled	14.1	20	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
68	c3k8zD_	Alignment	not modelled	13.3	25	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nad-specific glutamate dehydrogenase; **PDBTitle:** crystal structure of gudb1 a decryptified secondary glutamate2 dehydrogenase from b. subtilis
69	d1f3ba1	Alignment	not modelled	13.1	11	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
70	d1v9la2	Alignment	not modelled	13.1	22	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
71	d1b8xa1	Alignment	not modelled	12.8	11	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
72	d1pgja1	Alignment	not modelled	12.6	21	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
73	c2vn2B_	Alignment	not modelled	12.5	26	**PDB header:**replication **Chain:** B: **PDB Molecule:**chromosome replication initiation protein; **PDBTitle:** crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
74	d2e1da1	Alignment	not modelled	12.0	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
75	d1onra_	Alignment	not modelled	11.8	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
76	d1b48a1	Alignment	not modelled	11.6	20	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
77	c3co7C_	Alignment	not modelled	11.5	50	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**forkhead box protein o1; **PDBTitle:** crystal structure of foxo1 dbd bound to dbe2 dna
78	d1k3ya1	Alignment	not modelled	11.2	17	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
79	d1lqgc_	Alignment	not modelled	11.1	25	**Fold:**Cystatin-like **Superfamily:**Uracil-DNA glycosylase inhibitor protein **Family:**Uracil-DNA glycosylase inhibitor protein
80	d1ia6a_	Alignment	not modelled	11.1	27	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
81	d1cmia_	Alignment	not modelled	10.7	20	**Fold:**DLC **Superfamily:**DLC **Family:**DLC

82	c1pgjA_	Alignment	not modelled	10.7	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase; **PDBTitle:** x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
83	d2bgxa2	Alignment	not modelled	10.6	16	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
84	d1gnea1	Alignment	not modelled	10.5	11	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
85	c3h7lC_	Alignment	not modelled	10.2	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase-related protein from vibrio2 parahaemolyticus
86	c2l6pA_	Alignment	not modelled	10.0	31	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**phac1, phac2 and phad genes; **PDBTitle:** nmr solution structure of the protein np_253742.1
87	c2iz2A_	Alignment	not modelled	10.0	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**nuclear hormone receptor ftz-f1; **PDBTitle:** crystal structure of the ligand binding domain of fushi2 tarazu factor 1 from drosophila melanogaster
88	d1ev4c1	Alignment	not modelled	9.7	39	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
89	c2du4B_	Alignment	not modelled	9.7	13	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**o-phosphoseryl-trna synthetase; **PDBTitle:** crystal structure of archaeoglobus fulgidus o-phosphoseryl-2 trna synthetase complexed with trnacys
90	c2v36A_	Alignment	not modelled	9.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gamma-glutamyltranspeptidase large chain; **PDBTitle:** crystal structure of gamma-glutamyl transferase from2 bacillus subtilis
91	c1wcnA_	Alignment	not modelled	9.4	20	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** nmr structure of the carboxyterminal domains of escherichia2 coli nusa
92	d1m0ua1	Alignment	not modelled	9.4	15	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
93	d1pd211	Alignment	not modelled	9.2	14	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
94	d1ugia_	Alignment	not modelled	8.6	25	**Fold:**Cystatin-like **Superfamily:**Uracil-DNA glycosylase inhibitor protein **Family:**Uracil-DNA glycosylase inhibitor protein
95	c1xkmD_	Alignment	not modelled	8.5	29	**PDB header:**antibiotic **Chain:** D: **PDB Molecule:**distinctin chain b; **PDBTitle:** nmr structure of antimicrobial peptide distinctin in water
96	d1ljra1	Alignment	not modelled	8.4	27	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
97	c3cq0B_	Alignment	not modelled	8.4	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative transaldolase ygr043c; **PDBTitle:** crystal structure of tal2_yeast
98	c1clcA_	Alignment	not modelled	8.2	25	**PDB header:**glycosyl hydrolase **Chain:** A: **PDB Molecule:**endoglucanase celd; ec: 3.2.1.4; **PDBTitle:** three-dimensional structure of endoglucanase d at 1.92 angstroms resolution
99	c3m16A_	Alignment	not modelled	8.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transaldolase; **PDBTitle:** structure of a transaldolase from oleispira antarctica