Phyre²

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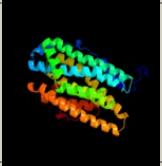
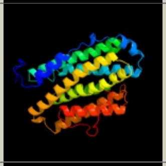
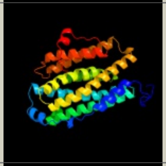
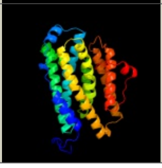
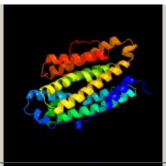
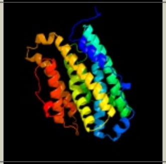
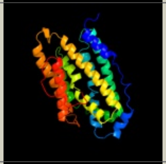
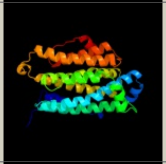
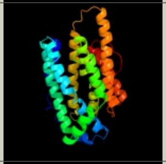
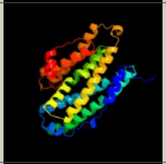
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1oquc_	Alignment		100.0	65	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
2	d1r2fa_	Alignment		100.0	87	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
3	c1r2fB_	Alignment		100.0	86	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**protein (ribonucleotide reductase r2); **PDBTitle:** ribonucleotide reductase r2f protein from salmonella2 typhimurium
4	d1uzra_	Alignment		100.0	70	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
5	d3dhza1	Alignment		100.0	66	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
6	c1yfdA_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase 1 beta **PDBTitle:** crystal structure of the y122h mutant of ribonucleotide2 reductase r2 protein from e. coli
7	c2rccC_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**ribonucleoside-diphosphate reductase subunit beta; **PDBTitle:** crystal structure of putative class i ribonucleotide reductase2 (np_241368.1) from bacillus halodurans at 1.90 a resolution
8	d1smsa_	Alignment		100.0	16	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
9	d1mxra_	Alignment		100.0	24	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
10	c1syyA_	Alignment		100.0	20	**PDB header:**replication,oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase beta chain; **PDBTitle:** crystal structure of the r2 subunit of ribonucleotide reductase from2 chlamydia trachomatis
11	d1syya_	Alignment		100.0	20	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like

12	d1jk0a_	Alignment		100.0	19	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
13	c1h0oA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase; **PDBTitle:** cobalt substitution of mouse r2 ribonucleotide reductase to2 model the reactive diferrous state
14	c1smqD_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**ribonucleoside-diphosphate reductase small chain **PDBTitle:** structure of the ribonucleotide reductase rnr2 homodimer2 from saccharomyces cerevisiae
15	d1w68a_	Alignment		100.0	19	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
16	c3hf1B_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ribonucleoside-diphosphate reductase subunit m2 **PDBTitle:** crystal structure of human p53r2
17	c2o1zA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleotide reductase subunit r2; **PDBTitle:** plasmodium vivax ribonucleotide reductase subunit r22 (pv086155)
18	c2p1iA_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleotide reductase, small chain; **PDBTitle:** plasmodium yoelii ribonucleotide reductase subunit r2 (py03671)
19	c2vuxB_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ribonucleoside-diphosphate reductase subunit m2 b; **PDBTitle:** human ribonucleotide reductase, subunit m2 b
20	d1jk0b_	Alignment		100.0	15	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
21	c3ee4A_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable ribonucleoside-diphosphate reductase; **PDBTitle:** r2-like ligand binding mn/fe oxidase from m. tuberculosis
22	d2inca1	Alignment	not modelled	99.1	12	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
23	d1mhyd_	Alignment	not modelled	99.0	9	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
24	d1mtyd_	Alignment	not modelled	98.9	9	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
25	c3dhiA_	Alignment	not modelled	98.9	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**toluene 4-monooxygenase hydroxylase alpha subunit; **PDBTitle:** crystal structure of reduced toluene 4-monoxygenase hydroxylase2 complexed with effector protein
26	c3chtA_	Alignment	not modelled	98.7	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**p-aminobenzoate n-oxygenase; **PDBTitle:** crystal structure of di-iron aurf with partially bound ligand
27	c3dhgB_	Alignment	not modelled	98.5	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**toluene 4-monooxygenase hydroxylase beta subunit; **PDBTitle:** crystal struture of toluene 4-monoxygenase hydroxylase
28	d1afra_	Alignment	not modelled	98.3	12	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like

29	c2innA_	Alignment	not modelled	98.3	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phenol hydroxylase component phn; **PDBTitle:** structure of the phenol hydroxyalse-regulatory protein2 complex
30	d2incb1	Alignment	not modelled	98.1	14	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
31	d1za0a1	Alignment	not modelled	98.1	14	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
32	c2inpD_	Alignment	not modelled	98.0	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**phenol hydroxylase component phl; **PDBTitle:** structure of the phenol hydroxylase-regulatory protein2 complex
33	c3pw1A_	Alignment	not modelled	97.4	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phenylacetic acid degradation protein paaa; **PDBTitle:** the phenylacetyl-coa monooxygenase paaac subcomplex with phenylacetyl-2 coa
34	d1mhyb_	Alignment	not modelled	96.1	9	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
35	c3pm5B_	Alignment	not modelled	95.8	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**benzoyl-coa oxygenase component b; **PDBTitle:** crystal structure of boxb in mixed valent state with bound benzoyl-coa
36	c3qhbA_	Alignment	not modelled	95.6	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**symerythrin; **PDBTitle:** crystal structure of oxidized symerythrin from cyanophora paradoxa
37	d2fzfa1	Alignment	not modelled	95.1	12	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
38	c2rd3A_	Alignment	not modelled	92.2	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of tena homologue (hp1287) from2 helicobacter pylori
39	c2qcxA_	Alignment	not modelled	91.6	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcriptional activator tena; **PDBTitle:** crystal structure of bacillus subtilis tena y112f mutant complexed2 with formyl aminomethyl pyrimidine
40	d1udda_	Alignment	not modelled	91.4	7	**Fold:**Heme oxygenase-like **Superfamily:**Heme oxygenase-like **Family:**TENA/THI-4
41	d2oc5a1	Alignment	not modelled	90.5	14	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**PMT1231-like
42	c2hr5B_	Alignment	not modelled	90.4	14	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
43	c3ddeB_	Alignment	not modelled	90.2	10	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**tena/thi-4 protein, domain of unknown function with a heme **PDBTitle:** crystal structure of a domain of unknown function with a heme2 oxygenase-like fold (sden_3740) from shewanella denitrificans os2173 at 2.30 a resolution
44	d1rtwa_	Alignment	not modelled	90.1	14	**Fold:**Heme oxygenase-like **Superfamily:**Heme oxygenase-like **Family:**TENA/THI-4
45	c3bjdA_	Alignment	not modelled	88.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative 3-oxoacyl-(acyl-carrier-protein) synthase; **PDBTitle:** crystal structure of putative 3-oxoacyl-(acyl-carrier-protein)2 synthase from pseudomonas aeruginosa
46	d1jkva_	Alignment	not modelled	88.2	9	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Manganese catalase (T-catalase)
47	d1nnqa1	Alignment	not modelled	86.4	13	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
48	d1yv1a1	Alignment	not modelled	85.5	6	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
49	d1mtyb_	Alignment	not modelled	85.3	8	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
50	d1lkoa1	Alignment	not modelled	84.9	10	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
51	d1j30a_	Alignment	not modelled	83.8	10	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
52	c3bknB_	Alignment	not modelled	83.6	15	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**bacterioferritin; **PDBTitle:** the structure of mycobacterial bacterioferritin
53	d1z72a1	Alignment	not modelled	83.3	11	**Fold:**Heme oxygenase-like **Superfamily:**Heme oxygenase-like **Family:**TENA/THI-4
54	c1yuzB_	Alignment	not modelled	80.4	7	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin

55	d2fkza1	Alignment	not modelled	79.4	11	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
56	d2cwla1	Alignment	not modelled	79.2	13	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Manganese catalase (T-catalase)
57	c3oghB_	Alignment	not modelled	79.1	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ycie; **PDBTitle:** crystal structure of ycie protein from e. coli cft073, a member of2 ferritine-like superfamily of diiron-containing four-helix-bundle3 proteins
58	d1rcwa_	Alignment	not modelled	77.7	10	**Fold:**Heme oxygenase-like **Superfamily:**Heme oxygenase-like **Family:**PqqC-like
59	d1otka_	Alignment	not modelled	76.4	14	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
60	d2htna1	Alignment	not modelled	73.6	13	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
61	d1vjxa_	Alignment	not modelled	72.3	13	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
62	c3oqlA_	Alignment	not modelled	71.9	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tena homolog; **PDBTitle:** crystal structure of a tena homolog (pspto1738) from pseudomonas2 syringae pv. tomato str. dc3000 at 2.54 a resolution
63	c3oqlB_	Alignment	not modelled	71.8	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tena homolog; **PDBTitle:** crystal structure of a tena homolog (pspto1738) from pseudomonas2 syringae pv. tomato str. dc3000 at 2.54 a resolution
64	c2qqyA_	Alignment	not modelled	69.8	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sigma b operon; **PDBTitle:** crystal structure of ferritin like, diiron-carboxylate proteins from2 bacillus anthracis str. ames
65	d1nf4a_	Alignment	not modelled	67.7	14	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
66	d2gm8a1	Alignment	not modelled	66.4	6	**Fold:**Heme oxygenase-like **Superfamily:**Heme oxygenase-like **Family:**TENA/THI-4
67	d2oh3a1	Alignment	not modelled	64.4	10	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**AMB4284-like
68	c1dvbA_	Alignment	not modelled	62.9	13	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
69	c3gvyC_	Alignment	not modelled	61.4	13	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**bacterioferritin; **PDBTitle:** crystal structure of bacterioferritin from r.sphaeroides
70	d1jgca_	Alignment	not modelled	60.1	12	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
71	c3r2rA_	Alignment	not modelled	58.4	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**bacterioferritin; **PDBTitle:** 1.65a resolution structure of iron soaked ftna from pseudomonas2 aeruginosa (ph 6.0)
72	c3mvuA_	Alignment	not modelled	53.1	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tena family transcriptional regulator; **PDBTitle:** crystal structure of a tena family transcription regulator2 (tm1040_3656) from silicibacter sp. tm1040 at 1.80 a resolution
73	d1zpya1	Alignment	not modelled	51.8	15	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**half-ferritin
74	c2vzbA_	Alignment	not modelled	51.1	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative bacterioferritin-related protein; **PDBTitle:** a dodecameric thioferritin in the bacterial domain, characterization2 of the bacterioferritin-related protein from bacteroides fragilis
75	d1yuza1	Alignment	not modelled	48.1	8	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
76	c3no6B_	Alignment	not modelled	43.9	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transcriptional activator tena; **PDBTitle:** crystal structure of a putative thiaminase ii (se1693) from2 staphylococcus epidermidis atcc 12228 at 1.65 a resolution
77	c2hz8A_	Alignment	not modelled	41.3	27	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed diiron protein; **PDBTitle:** qm/mm structure refined from nmr-structure of a single2 chain diiron protein
78	c3rm5B_	Alignment	not modelled	36.3	5	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hydroxymethylpyrimidine/phosphomethylpyrimidine kinase **PDBTitle:** structure of trifunctional thi20 from yeast
79	c1to9A_	Alignment	not modelled	29.5	7	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**thi-4 protein; **PDBTitle:** crystal structure of thi-4 protein from bacillus subtilis
80	d1to9a_	Alignment	not modelled	29.5	7	**Fold:**Heme oxygenase-like **Superfamily:**Heme oxygenase-like **Family:**TENA/THI-4
						PDB header:transferase

81	c3ap3A_	Alignment	not modelled	29.0	25	**Chain:** A: **PDB Molecule:**protein-tyrosine sulfotransferase 2; **PDBTitle:** crystal structure of human tyrosylprotein sulfotransferase-2 complexed2 with pap
82	c3fvbB_	Alignment	not modelled	28.5	13	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**bacterioferritin; **PDBTitle:** crystal structure of ferritin (bacterioferritin) from2 brucella melitensis
83	c3bvkC_	Alignment	not modelled	28.1	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**ferritin; **PDBTitle:** structural basis for the iron uptake mechanism of helicobacter pylori2 ferritin
84	d1ee8a1	Alignment	not modelled	27.2	13	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
85	d2za7a1	Alignment	not modelled	26.5	12	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
86	c3qd8M_	Alignment	not modelled	24.9	14	**PDB header:**metal binding protein **Chain:** M: **PDB Molecule:**probable bacterioferritin bfrb; **PDBTitle:** crystal structure of mycobacterium tuberculosis bfrb
87	c3hl1B_	Alignment	not modelled	24.1	12	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**ferritin like protein; **PDBTitle:** crystal structure of a ferritin like protein (cc_0557) from2 caulobacter vibrioides at 1.95 a resolution
88	d1k82a1	Alignment	not modelled	21.6	16	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
89	d1mfra_	Alignment	not modelled	21.2	14	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
90	d1r3ba_	Alignment	not modelled	20.1	24	**Fold:**Bromodomain-like **Superfamily:**Mob1/phocein **Family:**Mob1/phocein
91	d1vk3a4	Alignment	not modelled	19.7	26	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
92	d1r2za1	Alignment	not modelled	18.1	15	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
93	d1pi1a_	Alignment	not modelled	17.7	24	**Fold:**Bromodomain-like **Superfamily:**Mob1/phocein **Family:**Mob1/phocein
94	d1lnla1	Alignment	not modelled	16.8	14	**Fold:**Di-copper centre-containing domain **Superfamily:**Di-copper centre-containing domain **Family:**Hemocyanin middle domain
95	c3q4nA_	Alignment	not modelled	16.8	8	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj0754; **PDBTitle:** crystal structure of hypothetical protein mj0754 from methanococcus2 jannaschii dsm 2661
96	c1wx2A_	Alignment	not modelled	16.5	23	**PDB header:**oxidoreductase/metal transport **Chain:** A: **PDB Molecule:**tyrosinase; **PDBTitle:** crystal structure of the oxy-form of the copper-bound streptomyces2 castaneoglobisporus tyrosinase complexed with a caddie protein3 prepared by the addition of hydrogenperoxide
97	d1uw0a_	Alignment	not modelled	16.2	14	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**PARP-type zinc finger
98	d1r03a_	Alignment	not modelled	16.0	15	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
99	c2zetD_	Alignment	not modelled	15.7	28	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**melanophilin; **PDBTitle:** crystal structure of the small gtpase rab27b complexed with2 the slp homology domain of slac2-a/melanophilin