

# Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1afra_</a>	Alignment		100.0	21	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
2	<a href="#">d1za0a1</a>	Alignment		100.0	100	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
3	<a href="#">c5hyhA_</a>	Alignment		98.5	12	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> cmlI (chemically reduced state), arylamine oxygenase of2 chloramphenicol biosynthetic pathway
4	<a href="#">c3hf1B_</a>	Alignment		98.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase subunit m2 b; <b>PDBTitle:</b> crystal structure of human p53r2
5	<a href="#">c1h0oA_</a>	Alignment		98.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase; <b>PDBTitle:</b> cobalt substitution of mouse r2 ribonucleotide reductase to2 model the reactive diferrous state
6	<a href="#">d1w68a_</a>	Alignment		98.4	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
7	<a href="#">c2p1iA_</a>	Alignment		98.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleotide reductase, small chain; <b>PDBTitle:</b> plasmodium yoelii ribonucleotide reductase subunit r2 (py03671)
8	<a href="#">d1uzra_</a>	Alignment		98.4	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
9	<a href="#">c2o1zA_</a>	Alignment		98.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleotide reductase subunit r2; <b>PDBTitle:</b> plasmodium vivax ribonucleotide reductase subunit r2 (pv086155)
10	<a href="#">c3chtA_</a>	Alignment		98.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> p-aminobenzoate n-oxygenase; <b>PDBTitle:</b> crystal structure of di-iron aurf with partially bound ligand
11	<a href="#">d1smsa_</a>	Alignment		98.3	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like

12	<a href="#">d1jk0b_</a>	Alignment		98.3	18	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
13	<a href="#">d1oquc_</a>	Alignment		98.2	14	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
14	<a href="#">c1r2fB_</a>	Alignment		98.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (ribonucleotide reductase r2); <b>PDBTitle:</b> ribonucleotide reductase r2f protein from salmonella2 typhimurium
15	<a href="#">c2rccC_</a>	Alignment		98.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase subunit beta; <b>PDBTitle:</b> crystal structure of putative class i ribonucleotide reductase2 (np_241368.1) from bacillus halodurans at 1.90 a resolution
16	<a href="#">c2vuxB_</a>	Alignment		98.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase subunit m2 b; <b>PDBTitle:</b> human ribonucleotide reductase, subunit m2 b
17	<a href="#">c4bmtB_</a>	Alignment		98.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase subunit beta; <b>PDBTitle:</b> crystal structure of ribonucleotide reductase di-iron nrdf2 from bacillus cereus
18	<a href="#">d3dhza1</a>	Alignment		98.1	14	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
19	<a href="#">c1smqD_</a>	Alignment		98.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase small chain <b>PDBTitle:</b> structure of the ribonucleotide reductase rnr2 homodimer2 from saccharomyces cerevisiae
20	<a href="#">c4n83F_</a>	Alignment		98.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase subunit beta; <b>PDBTitle:</b> x-ray crystal structure of streptococcus sanguinis dimanganese(ii)-2 nrdf
21	<a href="#">d1jk0a_</a>	Alignment	not modelled	98.0	19	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
22	<a href="#">d1r2fa_</a>	Alignment	not modelled	98.0	14	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
23	<a href="#">c4a58B_</a>	Alignment	not modelled	98.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase small chain; <b>PDBTitle:</b> crystal structure of a monometal state of the2 ribonucleotide-reductase small subunit from epstein-barr virus in3 orthorhombic space group
24	<a href="#">c6qzrA_</a>	Alignment	not modelled	98.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase; <b>PDBTitle:</b> crystal structure of r2-like ligand-binding oxidase from sulfolobus2 acidocaldarius solved by 3d micro-crystal electron diffraction
25	<a href="#">d1mxra_</a>	Alignment	not modelled	97.9	17	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
26	<a href="#">c3ee4A_</a>	Alignment	not modelled	97.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable ribonucleoside-diphosphate reductase; <b>PDBTitle:</b> r2-like ligand binding mn/fe oxidase from m. tuberculosis
27	<a href="#">d2oh3a1</a>	Alignment	not modelled	97.9	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> AMB4284-like
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase

28	<a href="#">c6gp2A_</a>	Alignment	not modelled	97.9	14	beta chain; <b>PDBTitle:</b> ribonucleotide reductase class ie r2 from mesoplasma florum, dopa-2 active form <b>PDB header:</b> oxidoreductase
29	<a href="#">c4hr0A_</a>	Alignment	not modelled	97.9	15	<b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleotide reductase small subunit; <b>PDBTitle:</b> r2-like ligand-binding oxidase with aerobically reconstituted metal2 cofactor <b>PDB header:</b> lyase
30	<a href="#">c6d9fA_</a>	Alignment	not modelled	97.8	15	<b>Chain:</b> A: <b>PDB Molecule:</b> putative vlbm homolog; <b>PDBTitle:</b> protein 60 with aldehyde deformylating oxidase activity from2 kitasatospora setae
31	<a href="#">c4r42B_</a>	Alignment	not modelled	97.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alr3090 protein; <b>PDBTitle:</b> crystal structure of katb, a manganese catalase from anabaena pcc7120
32	<a href="#">d2fzfa1</a>	Alignment	not modelled	97.7	14	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
33	<a href="#">c5xx9A_</a>	Alignment	not modelled	97.7	12	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> bacterioferritin; <b>PDBTitle:</b> crystal structure of bacterioferritin
34	<a href="#">c1syyA_</a>	Alignment	not modelled	97.7	14	<b>PDB header:</b> replication, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase beta chain; <b>PDBTitle:</b> crystal structure of the r2 subunit of ribonucleotide reductase from2 chlamydia trachomatis
35	<a href="#">d1syya_</a>	Alignment	not modelled	97.7	14	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
36	<a href="#">d1vjxa_</a>	Alignment	not modelled	97.6	16	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
37	<a href="#">c4dr0A_</a>	Alignment	not modelled	97.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase subunit beta; <b>PDBTitle:</b> crystal structure of bacillus subtilis dimanganese(ii) nrdf <b>PDB header:</b> oxidoreductase
38	<a href="#">c6cwqA_</a>	Alignment	not modelled	97.5	14	<b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleotide reductase; <b>PDBTitle:</b> x-ray crystal structure of flavobacterium johnsoniae dimanganese(ii)2 ribonucleotide reductase beta subunit (as-isolated) <b>PDB header:</b> lyase
39	<a href="#">c5uxgB_</a>	Alignment	not modelled	97.5	18	<b>Chain:</b> B: <b>PDB Molecule:</b> aldehyde deformylating oxygenase; <b>PDBTitle:</b> protein 84 with aldehyde deformylating oxygenase activity from2 sulfobolus tokodaii (monoclinic)
40	<a href="#">d1jgca_</a>	Alignment	not modelled	97.4	14	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
41	<a href="#">c5n5eM_</a>	Alignment	not modelled	97.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> pfc_05175; <b>PDBTitle:</b> crystal structure of encapsulated ferritin domain from pyrococcus2 furiosus pfc_05175
42	<a href="#">c4di0B_</a>	Alignment	not modelled	97.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> rubrerythrin; <b>PDBTitle:</b> the structure of rubrerythrin from burkholderia pseudomallei
43	<a href="#">c3bknB_</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> bacterioferritin; <b>PDBTitle:</b> the structure of mycobacterial bacterioferritin
44	<a href="#">c2vzbA_</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative bacterioferritin-related protein; <b>PDBTitle:</b> a dodecameric thioferritin in the bacterial domain, characterization2 of the bacterioferritin-related protein from bacteroides fragilis
45	<a href="#">c4mudA_</a>	Alignment	not modelled	97.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ring oxydation complex/ phenylacetic acid degradation <b>PDBTitle:</b> crystal structure of a ring oxydation complex/ phenylacetic acid2 degradation-like protein (sso1313) from sulfobolus solfataricus p2 at3 2.43 a resolution
46	<a href="#">c1yfdA_</a>	Alignment	not modelled	97.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase 1 beta chain; <b>PDBTitle:</b> crystal structure of the y122h mutant of ribonucleotide reductase r22 protein from e. coli
47	<a href="#">c5olkD_</a>	Alignment	not modelled	97.1	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase, beta subunit 1; <b>PDBTitle:</b> crystal structure of the atp-cone-containing nrdb from2 leeuwenhoekiella blandensis
48	<a href="#">c3e6sD_</a>	Alignment	not modelled	97.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> ferritin; <b>PDBTitle:</b> crystal structure of ferritin soaked with iron from pseudo-nitzschia2 multiseris
49	<a href="#">c3q4nA_</a>	Alignment	not modelled	97.1	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mj0754; <b>PDBTitle:</b> crystal structure of hypothetical protein mj0754 from methanococcus2 jannaschii dsm 2661
50	<a href="#">c4am4B_</a>	Alignment	not modelled	97.0	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> bacterioferritin; <b>PDBTitle:</b> bacterioferritin from blastochloris viridis
51	<a href="#">c3qhbA_</a>	Alignment	not modelled	97.0	18	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> symerythrin; <b>PDBTitle:</b> crystal structure of oxidized symerythrin from cyanophora paradoxa
52	<a href="#">d2fkza1</a>	Alignment	not modelled	97.0	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin

53	<a href="#">c2clbP</a>	Alignment	not modelled	96.9	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> P: <b>PDB Molecule:</b> dps-like protein; <b>PDBTitle:</b> the structure of the dps-like protein from sulfobolus2 solfataricus reveals a bacterioferritin-like di-metal3 binding site within a dps-like dodecameric assembly
54	<a href="#">d2htna1</a>	Alignment	not modelled	96.9	14	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
55	<a href="#">d2inca1</a>	Alignment	not modelled	96.9	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
56	<a href="#">d1lkoa1</a>	Alignment	not modelled	96.8	21	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
57	<a href="#">d1vlga</a>	Alignment	not modelled	96.7	12	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
58	<a href="#">c3gvyC</a>	Alignment	not modelled	96.7	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> bacterioferritin; <b>PDBTitle:</b> crystal structure of bacterioferritin from r.sphaeroides
59	<a href="#">d1nf4a</a>	Alignment	not modelled	96.7	18	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
60	<a href="#">c3dhiA</a>	Alignment	not modelled	96.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> toluene 4-monooxygenase hydroxylase alpha subunit; <b>PDBTitle:</b> crystal structure of reduced toluene 4-monooxygenase hydroxylase2 complexed with effector protein
61	<a href="#">d1krqa</a>	Alignment	not modelled	96.5	16	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
62	<a href="#">d1j30a</a>	Alignment	not modelled	96.5	17	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
63	<a href="#">c5ouWA</a>	Alignment	not modelled	96.5	11	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ferritin; <b>PDBTitle:</b> metal free structure of synftn
64	<a href="#">d1jkva</a>	Alignment	not modelled	96.4	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Manganese catalase (T-catalase)
65	<a href="#">c3qd8M</a>	Alignment	not modelled	96.4	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> M: <b>PDB Molecule:</b> probable bacterioferritin bfrb; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis bfrb
66	<a href="#">c3r2rA</a>	Alignment	not modelled	96.4	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacterioferritin; <b>PDBTitle:</b> 1.65a resolution structure of iron soaked ftna from pseudomonas2 aeruginosa (ph 6.0)
67	<a href="#">d1nnqa1</a>	Alignment	not modelled	96.3	12	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
68	<a href="#">d1mtyd</a>	Alignment	not modelled	96.3	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
69	<a href="#">c2ib0A</a>	Alignment	not modelled	96.2	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical alanine rich protein; <b>PDBTitle:</b> crystal structure of a conserved hypothetical protein, rv2844, from2 mycobacterium tuberculosis
70	<a href="#">d2ib0a1</a>	Alignment	not modelled	96.2	9	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Rv2844-like
71	<a href="#">d1yv1a1</a>	Alignment	not modelled	96.1	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
72	<a href="#">c5da5R</a>	Alignment	not modelled	95.9	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> R: <b>PDB Molecule:</b> rru_a0973; <b>PDBTitle:</b> crystal structure of rhodospirillum rubrum rru_a0973
73	<a href="#">d1s3qa1</a>	Alignment	not modelled	95.9	14	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
74	<a href="#">c2qqyA</a>	Alignment	not modelled	95.8	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sigma b operon; <b>PDBTitle:</b> crystal structure of ferritin like, diiron-carboxylate proteins from2 bacillus anthracis str. ames
75	<a href="#">c5wpaA</a>	Alignment	not modelled	95.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferritin; <b>PDBTitle:</b> zn-bound structure of chaetopterus variopedatus ferritin
76	<a href="#">c1dvbA</a>	Alignment	not modelled	95.7	19	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubrerythrin; <b>PDBTitle:</b> rubrerythrin
77	<a href="#">c5n5fC</a>	Alignment	not modelled	95.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> encapsulated ferritin; <b>PDBTitle:</b> crystal structure of haliangium ochraceum encapsulated ferritin
78	<a href="#">c3bvkc</a>	Alignment	not modelled	95.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> ferritin; <b>PDBTitle:</b> structural basis for the iron uptake mechanism of helicobacter pylori2 ferritin
79	<a href="#">c3f6bP</a>	Alignment	not modelled	95.6	12	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> bacterioferritin;

79	<a href="#">c3rvub</a>	Alignment	not modelled	93.0	12	<b>PDBTitle:</b> crystal structure of ferritin (bacterioferritin) from brucella2 melitensis
80	<a href="#">d1yuza1</a>	Alignment	not modelled	95.5	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
81	<a href="#">c4cmyN</a>	Alignment	not modelled	95.5	15	<b>PDB header:</b> metal transport <b>Chain:</b> N: <b>PDB Molecule:</b> ferritin; <b>PDBTitle:</b> chlorobium tepidum ferritin
82	<a href="#">d1lb3a</a>	Alignment	not modelled	95.2	18	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
83	<a href="#">d1zpya1</a>	Alignment	not modelled	95.2	9	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> half-ferritin
84	<a href="#">d1rcda</a>	Alignment	not modelled	95.2	17	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
85	<a href="#">d1r03a</a>	Alignment	not modelled	95.1	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
86	<a href="#">d2ceia1</a>	Alignment	not modelled	95.0	14	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
87	<a href="#">d1euma</a>	Alignment	not modelled	94.7	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
88	<a href="#">c3qz3A</a>	Alignment	not modelled	94.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferritin; <b>PDBTitle:</b> the crystal structure of ferritin from vibrio cholerae o1 biovar el2 tor str. n16961
89	<a href="#">c6a4uD</a>	Alignment	not modelled	94.5	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> ferritin; <b>PDBTitle:</b> the first crystal structure of crustacean ferritin that is a hybrid2 type of h and l ferritin
90	<a href="#">d2za7a1</a>	Alignment	not modelled	94.2	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
91	<a href="#">c1yuzB</a>	Alignment	not modelled	94.1	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nigerythrin; <b>PDBTitle:</b> partially reduced state of nigerythrin
92	<a href="#">d1mfra</a>	Alignment	not modelled	94.0	17	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
93	<a href="#">c2jd8C</a>	Alignment	not modelled	93.9	15	<b>PDB header:</b> metal transport <b>Chain:</b> C: <b>PDB Molecule:</b> ferritin homolog; <b>PDBTitle:</b> crystal structure of the zn-soaked ferritin from the2 hyperthermophilic archaeal anaerobe pyrococcus furiosus
94	<a href="#">d1mhyd</a>	Alignment	not modelled	93.7	16	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
95	<a href="#">c3pm5B</a>	Alignment	not modelled	92.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> benzoyl-coa oxygenase component b; <b>PDBTitle:</b> crystal structure of boxb in mixed valent state with bound benzoyl-coa
96	<a href="#">c2hr5B</a>	Alignment	not modelled	92.7	12	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> rubrerythrin; <b>PDBTitle:</b> pf1283- rubrerythrin from pyrococcus furiosus iron bound form
97	<a href="#">c3pw1A</a>	Alignment	not modelled	91.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylacetic acid degradation protein paaa; <b>PDBTitle:</b> the phenylacetyl-coa monooxygenase paaac subcomplex with phenylacetyl-2 coa
98	<a href="#">c3vnxA</a>	Alignment	not modelled	91.2	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferritin; <b>PDBTitle:</b> crystal structure of ferritin from multicellular green algae, ulva2 pertusa.
99	<a href="#">d1z6om1</a>	Alignment	not modelled	89.2	17	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
100	<a href="#">d2cwa1</a>	Alignment	not modelled	87.0	11	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Manganese catalase (T-catalase)
101	<a href="#">d1otka</a>	Alignment	not modelled	85.5	14	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
102	<a href="#">c3oghB</a>	Alignment	not modelled	83.8	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein ycie; <b>PDBTitle:</b> crystal structure of ycie protein from e. coli cft073, a member of2 ferritin-like superfamily of diiron-containing four-helix-bundle3 proteins
103	<a href="#">c2innA</a>	Alignment	not modelled	79.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phenol hydroxylase component phn; <b>PDBTitle:</b> structure of the phenol hydroxylase-regulatory protein complex
104	<a href="#">c3kwoA</a>	Alignment	not modelled	75.3	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative bacterioferritin; <b>PDBTitle:</b> crystal structure of putative bacterioferritin from2 campylobacter jejuni
105	<a href="#">d2incb1</a>	Alignment	not modelled	70.7	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like

106	<a href="#">c3dhgB_</a>	Alignment	not modelled	70.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> toluene 4-monoxygenase hydroxylase beta subunit; <b>PDBTitle:</b> crystal structure of toluene 4-monoxygenase hydroxylase
107	<a href="#">d2fjca1</a>	Alignment	not modelled	69.9	10	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
108	<a href="#">d2itba1</a>	Alignment	not modelled	69.4	20	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> MiaE-like
109	<a href="#">c5ux1D_</a>	Alignment	not modelled	65.2	17	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> trna-(ms(2)io(6)a)-hydroxylase-like; <b>PDBTitle:</b> protein 43 with aldehyde deformylating oxygenase activity from2 synechococcus
110	<a href="#">d1jj5a_</a>	Alignment	not modelled	61.7	9	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
111	<a href="#">c3a9qR_</a>	Alignment	not modelled	59.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> R: <b>PDB Molecule:</b> <b>PDBTitle:</b> crystal structure analysis of e173a variant of the soybean2 ferritin sfer4
112	<a href="#">d1o9ra_</a>	Alignment	not modelled	58.7	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
113	<a href="#">c2c41K_</a>	Alignment	not modelled	58.1	12	<b>PDB header:</b> iron-binding/oxidation protein <b>Chain:</b> K: <b>PDB Molecule:</b> dps family dna-binding stress response protein; <b>PDBTitle:</b> x-ray structure of dps from thermosynechococcus elongatus
114	<a href="#">d1dpsa_</a>	Alignment	not modelled	57.6	12	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
115	<a href="#">c2xgwA_</a>	Alignment	not modelled	55.2	5	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> peroxide resistance protein; <b>PDBTitle:</b> zinc-bound crystal structure of streptococcus pyogenes dpr
116	<a href="#">c2chpC_</a>	Alignment	not modelled	49.6	6	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> metalloregulation dna-binding stress protein; <b>PDBTitle:</b> crystal structure of the dodecameric ferritin mrga from b. subtilis2 168
117	<a href="#">c2wlaA_</a>	Alignment	not modelled	49.2	5	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dps-like peroxide resistance protein; <b>PDBTitle:</b> streptococcus pyogenes dpr
118	<a href="#">d1vela_</a>	Alignment	not modelled	48.0	12	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
119	<a href="#">d2yw6a1</a>	Alignment	not modelled	43.4	10	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
120	<a href="#">c2c6rA_</a>	Alignment	not modelled	43.4	7	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding stress response protein, dps family; <b>PDBTitle:</b> fe-soaked crystal structure of the dps92 from deinococcus2 radiodurans