


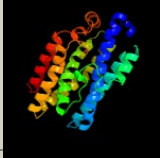



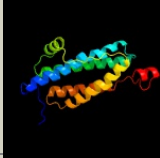

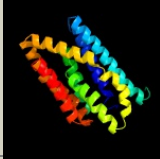



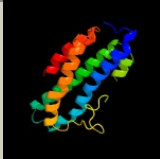

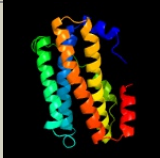

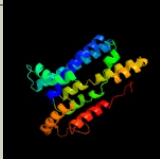

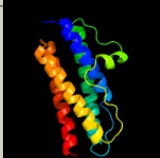

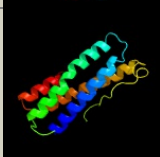
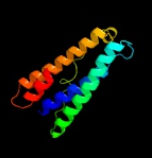
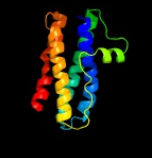
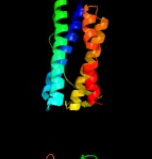
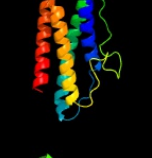
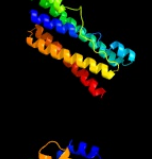


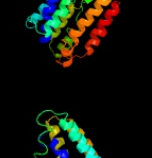
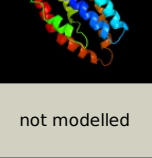


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3210c_(-)_3586840_3587535
Date	Thu Aug 8 16:20:40 BST 2019
Unique Job ID	152c7385d4e02eaa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ez0D_</a>	 Alignment		100.0	35	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein with ferritin-like fold; <b>PDBTitle:</b> crystal structure of protein of unknown function with ferritin-like2 fold (yp_832262.1) from arthrobacter sp. fb24 at 2.33 a resolution
2	<a href="#">c4mudA_</a>	 Alignment		99.9	14	<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
3	<a href="#">d1otka_</a>	 Alignment		99.9	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
4	<a href="#">c3pw1A_</a>	 Alignment		99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylacetic acid degradation protein paaa; <b>PDBTitle:</b> the phenylacetyl-coa monoxygenase paaac subcomplex with phenylacetyl-2 coa
5	<a href="#">c2inpD_</a>	 Alignment		98.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> phenol hydroxylase component phl; <b>PDBTitle:</b> structure of the phenol hydroxylase-regulatory protein2 complex
6	<a href="#">d1mhyb_</a>	 Alignment		97.4	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
7	<a href="#">c3pm5B_</a>	 Alignment		97.4	18	<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
8	<a href="#">d2itba1</a>	 Alignment		96.9	16	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> MiaE-like
9	<a href="#">c6d9fA_</a>	 Alignment		96.7	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative vlmb homolog; <b>PDBTitle:</b> protein 60 with aldehyde deformylating oxidase activity from2 kitasatospora setae
10	<a href="#">c2vzbA_</a>	 Alignment		96.6	15	<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
11	<a href="#">d2fzfa1</a>	 Alignment		96.5	18	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin

12	<a href="#">d2oh3a1</a>	Alignment		96.5	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> AMB4284-like
13	<a href="#">c2clbP</a>	Alignment		96.2	14	<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
14	<a href="#">c3r2rA</a>	Alignment		96.1	18	<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)
15	<a href="#">c2qqyA</a>	Alignment		96.1	11	<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
16	<a href="#">c3fvbB</a>	Alignment		95.8	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> bacterioferritin; <b>PDBTitle:</b> crystal structure of ferritin (bacterioferritin) from brucella2 melitensis
17	<a href="#">c5ux1D</a>	Alignment		95.8	13	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> trna-(ms2)io(6)a)-hydroxylase-like; <b>PDBTitle:</b> protein 43 with aldehyde deformylating oxygenase activity from2 synechococcus
18	<a href="#">c5xx9A</a>	Alignment		95.4	14	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> bacterioferritin; <b>PDBTitle:</b> crystal structure of bacterioferritin
19	<a href="#">c3dhiA</a>	Alignment		95.2	15	<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
20	<a href="#">c3dhgB</a>	Alignment		95.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> toluene 4-monooxygenase hydroxylase beta subunit; <b>PDBTitle:</b> crystal structure of toluene 4-monooxygenase hydroxylase
21	<a href="#">d2inca1</a>	Alignment	not modelled	95.2	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
22	<a href="#">c3bknB</a>	Alignment	not modelled	94.7	11	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> bacterioferritin; <b>PDBTitle:</b> the structure of mycobacterial bacterioferritin
23	<a href="#">c3gvyC</a>	Alignment	not modelled	94.5	17	<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
24	<a href="#">d2fkza1</a>	Alignment	not modelled	94.5	10	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
25	<a href="#">d1mtyb</a>	Alignment	not modelled	94.4	17	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
26	<a href="#">d1j30a</a>	Alignment	not modelled	94.3	16	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
27	<a href="#">c5n5eM</a>	Alignment	not modelled	93.9	20	<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
28	<a href="#">d1jgca</a>	Alignment	not modelled	93.9	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
29	<a href="#">c4am4B</a>	Alignment	not modelled	93.7	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> bacterioferritin;

					<b>PDBTitle:</b> bacterioferritin from blastochloris viridis
30	<a href="#">d1o9ra_</a>	Alignment	not modelled	93.6	13 <b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
31	<a href="#">d2htna1</a>	Alignment	not modelled	93.5	13 <b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
32	<a href="#">c4di0B_</a>	Alignment	not modelled	92.1	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> rubrerythrin; <b>PDBTitle:</b> the structure of rubrerythrin from burkholderia pseudomallei
33	<a href="#">c4r42B_</a>	Alignment	not modelled	91.8	20 <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
34	<a href="#">d2incb1</a>	Alignment	not modelled	91.2	15 <b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
35	<a href="#">d1nf4a_</a>	Alignment	not modelled	91.1	12 <b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
36	<a href="#">c2innA_</a>	Alignment	not modelled	86.7	14 <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
37	<a href="#">c4hr0A_</a>	Alignment	not modelled	82.5	15 <b>PDB header:</b> oxidoreductase <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
38	<a href="#">c5da5R_</a>	Alignment	not modelled	81.4	14 <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
39	<a href="#">d1yuza1</a>	Alignment	not modelled	81.3	15 <b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
40	<a href="#">d1lkoa1</a>	Alignment	not modelled	80.7	18 <b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
41	<a href="#">d1jiga_</a>	Alignment	not modelled	77.7	14 <b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
42	<a href="#">c4cy9A_</a>	Alignment	not modelled	77.5	12 <b>PDB header:</b> iron-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dpsa; <b>PDBTitle:</b> dpsa14 from streptomyces coelicolor
43	<a href="#">c2l9dA_</a>	Alignment	not modelled	77.1	33 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of the protein yp_546394.1, the first structural2 representative of the pfam family pf12112
44	<a href="#">c4etrA_</a>	Alignment	not modelled	76.7	14 <b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> x-ray structure of pa2169 from pseudomonas aeruginosa
45	<a href="#">d1n1qa_</a>	Alignment	not modelled	76.6	10 <b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
46	<a href="#">d1vjxa_</a>	Alignment	not modelled	75.7	17 <b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
47	<a href="#">c1dvbA_</a>	Alignment	not modelled	75.2	19 <b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubrerythrin; <b>PDBTitle:</b> rubrerythrin
48	<a href="#">c1yuzB_</a>	Alignment	not modelled	74.1	14 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nigerythrin; <b>PDBTitle:</b> partially reduced state of nigerythrin
49	<a href="#">c2c6rA_</a>	Alignment	not modelled	73.8	5 <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
50	<a href="#">d1j5a_</a>	Alignment	not modelled	73.7	16 <b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
51	<a href="#">d1dpsa_</a>	Alignment	not modelled	72.4	11 <b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
52	<a href="#">d1vela_</a>	Alignment	not modelled	69.5	14 <b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
53	<a href="#">c2d5kC_</a>	Alignment	not modelled	68.3	10 <b>PDB header:</b> metal binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> dps family protein; <b>PDBTitle:</b> crystal structure of dps from staphylococcus aureus
54	<a href="#">c5ouwA_</a>	Alignment	not modelled	66.1	12 <b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ferritin; <b>PDBTitle:</b> metal free structure of synfntn
55	<a href="#">c2rccC_</a>	Alignment	not modelled	63.5	13 <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

56	<a href="#">c5n5fC_</a>	Alignment	not modelled	62.8	16	<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
57	<a href="#">d1nnga1</a>	Alignment	not modelled	62.2	16	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
58	<a href="#">c3bvKc_</a>	Alignment	not modelled	61.6	16	<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
59	<a href="#">c2z90D_</a>	Alignment	not modelled	60.6	5	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> starvation-inducible dna-binding protein or fine <b>PDBTitle:</b> crystal structure of the second dps from mycobacterium2 smegmatis
60	<a href="#">c2hr5B_</a>	Alignment	not modelled	59.7	17	<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
61	<a href="#">c2c41K_</a>	Alignment	not modelled	59.2	11	<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
62	<a href="#">d1mtyd_</a>	Alignment	not modelled	58.6	10	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
63	<a href="#">d1yv1a1</a>	Alignment	not modelled	57.4	11	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
64	<a href="#">d3dhza1</a>	Alignment	not modelled	54.5	10	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
65	<a href="#">c4a25A_</a>	Alignment	not modelled	54.3	10	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ferritin dps family protein; <b>PDBTitle:</b> x-ray structure dps from kineococcus radiotolerans in2 complex with mn (ii) ions.
66	<a href="#">c2chpC_</a>	Alignment	not modelled	53.0	13	<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
67	<a href="#">c2f7nA_</a>	Alignment	not modelled	52.5	11	<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> structure of d. radiodurans dps-1
68	<a href="#">d1m6ex_</a>	Alignment	not modelled	52.0	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Salicylic acid carboxyl methyltransferase (SAMT)
69	<a href="#">c5uxqB_</a>	Alignment	not modelled	51.3	14	<b>PDB header:</b> lyase <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)
70	<a href="#">c2vxXB_</a>	Alignment	not modelled	51.0	13	<b>PDB header:</b> dna-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> starvation induced dna binding protein; <b>PDBTitle:</b> x-ray structure of dpsa from thermosynechococcus elongatus
71	<a href="#">c5hjhB_</a>	Alignment	not modelled	50.2	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> ferritin, dps family protein; <b>PDBTitle:</b> dps4 from nostoc punctiforme in complex with fe ions
72	<a href="#">c3kwoA_</a>	Alignment	not modelled	49.4	8	<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
73	<a href="#">c3e6sD_</a>	Alignment	not modelled	49.3	15	<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
74	<a href="#">c2rlwA_</a>	Alignment	not modelled	48.1	20	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> plnf; <b>PDBTitle:</b> three-dimensional structure of the two peptides that2 constitute the two-peptide bacteriocin plantaricin ef
75	<a href="#">d1u5ta1</a>	Alignment	not modelled	43.3	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Vacuolar sorting protein domain
76	<a href="#">d1vlga_</a>	Alignment	not modelled	42.2	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
77	<a href="#">c3iq1A_</a>	Alignment	not modelled	41.8	9	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> dps family protein; <b>PDBTitle:</b> crystal structure of dps protein from vibrio cholerae o1, a member of2 a broad superfamily of ferritin-like diiron-carboxylate proteins
78	<a href="#">c2pliA_</a>	Alignment	not modelled	41.3	10	<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)
79	<a href="#">c4cybl_</a>	Alignment	not modelled	40.7	8	<b>PDB header:</b> iron binding protein <b>Chain:</b> I: <b>PDB Molecule:</b> putative dna protection protein; <b>PDBTitle:</b> dpSC from streptomyces coelicolor
80	<a href="#">d1brwa2</a>	Alignment	not modelled	40.2	21	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase

						catalytic domain
81	<a href="#">c2eg5C</a>	Alignment	not modelled	40.2	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> xanthosine methyltransferase; <b>PDBTitle:</b> the structure of xanthosine methyltransferase
82	<a href="#">c4mhlA</a>	Alignment	not modelled	38.6	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> interleukin-11; <b>PDBTitle:</b> the crystal structure of human interleukin-11
83	<a href="#">d1tjoa</a>	Alignment	not modelled	38.0	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
84	<a href="#">c2xgwA</a>	Alignment	not modelled	37.9	14	<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
85	<a href="#">d2yw6a1</a>	Alignment	not modelled	37.1	12	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
86	<a href="#">c5wpmA</a>	Alignment	not modelled	35.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferritin; <b>PDBTitle:</b> zn-bound structure of chaetopterus variopedatus ferritin
87	<a href="#">d1zpya1</a>	Alignment	not modelled	34.5	16	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> half-ferritin
88	<a href="#">c1r2fB</a>	Alignment	not modelled	34.2	12	<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
89	<a href="#">d1euma</a>	Alignment	not modelled	34.0	16	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
90	<a href="#">c2ib0A</a>	Alignment	not modelled	33.7	15	<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
91	<a href="#">d2ib0a1</a>	Alignment	not modelled	33.7	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Rv2844-like
92	<a href="#">d1r2fa</a>	Alignment	not modelled	30.7	12	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
93	<a href="#">d1s3qa1</a>	Alignment	not modelled	29.9	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
94	<a href="#">c2jd8C</a>	Alignment	not modelled	29.7	16	<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
95	<a href="#">c6a4uD</a>	Alignment	not modelled	28.5	14	<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
96	<a href="#">c3hf1B</a>	Alignment	not modelled	28.3	15	<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
97	<a href="#">d2cwl1</a>	Alignment	not modelled	28.2	19	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Manganese catalase (T-catalase)
98	<a href="#">c2yjkF</a>	Alignment	not modelled	27.9	9	<b>PDB header:</b> metal-binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> afp; <b>PDBTitle:</b> structure of dps from microbacterium arborescens in the2 high iron form
99	<a href="#">c1syvA</a>	Alignment	not modelled	27.1	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
100	<a href="#">d1syva</a>	Alignment	not modelled	27.1	14	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
101	<a href="#">c1brwB</a>	Alignment	not modelled	27.1	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (pyrimidine nucleoside phosphorylase); <b>PDBTitle:</b> the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
102	<a href="#">d1uoua2</a>	Alignment	not modelled	26.6	17	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
103	<a href="#">c4bmtB</a>	Alignment	not modelled	26.2	12	<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
104	<a href="#">d1mhyd</a>	Alignment	not modelled	25.9	11	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
105	<a href="#">c4cmyN</a>	Alignment	not modelled	25.4	12	<b>PDB header:</b> metal transport <b>Chain:</b> N: <b>PDB Molecule:</b> ferritin; <b>PDBTitle:</b> chlorobium tepidum ferritin

106	<a href="#">d1rcda_</a>	Alignment	not modelled	25.3	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
107	<a href="#">c3b5iB_</a>	Alignment	not modelled	25.3	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> s-adenosyl-l-methionine:salicylic acid carboxyl <b>PDBTitle:</b> crystal structure of indole-3-acetic acid methyltransferase
108	<a href="#">d1lb3a_</a>	Alignment	not modelled	23.9	17	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
109	<a href="#">d1ohua_</a>	Alignment	not modelled	23.7	11	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death <b>Family:</b> Bcl-2 inhibitors of programmed cell death
110	<a href="#">d1krqa_</a>	Alignment	not modelled	23.4	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
111	<a href="#">c5vrdD_</a>	Alignment	not modelled	23.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> bifunctional coenzyme pqq synthesis protein c/d; <b>PDBTitle:</b> crystal structure for methylobacterium extorquens pqqcd (natural2 fusion)
112	<a href="#">c4wwrD_</a>	Alignment	not modelled	23.1	23	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> ubiquitin-like protein 4a; <b>PDBTitle:</b> crystal structure of bag6-ubl4a dimerization domain
113	<a href="#">c4z29B_</a>	Alignment	not modelled	23.0	29	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> magnetotaxis protein mtxa; <b>PDBTitle:</b> crystal structure of the magnetobacterial protein mtxa c-terminal2 domain
114	<a href="#">c6mupK_</a>	Alignment	not modelled	22.2	50	<b>PDB header:</b> nuclear protein <b>Chain:</b> K: <b>PDB Molecule:</b> centromere protein c; <b>PDBTitle:</b> cenp-a nucleosome bound by two copies of cenp-c(cd) and two copies2 cenp-n(nt)
115	<a href="#">c6mupL_</a>	Alignment	not modelled	22.2	50	<b>PDB header:</b> nuclear protein <b>Chain:</b> L: <b>PDB Molecule:</b> centromere protein c; <b>PDBTitle:</b> cenp-a nucleosome bound by two copies of cenp-c(cd) and two copies2 cenp-n(nt)
116	<a href="#">c6muoK_</a>	Alignment	not modelled	22.2	50	<b>PDB header:</b> nuclear protein <b>Chain:</b> K: <b>PDB Molecule:</b> centromere protein c; <b>PDBTitle:</b> cenp-a nucleosome bound by two copies of cenp-c(cd) and one copy cenp-2 n(nt)