Phyre^2

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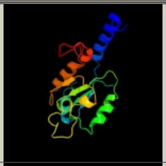
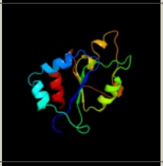
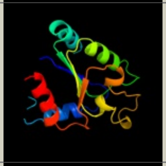
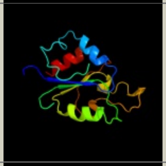
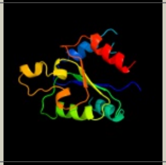
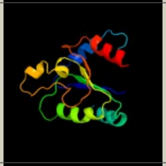
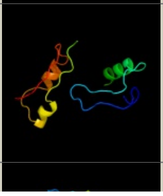
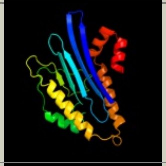
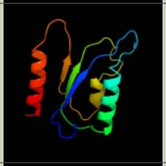
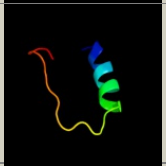
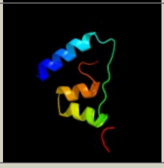
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fug61	Alignment		100.0	36	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nq06-like
2	d1frfs_	Alignment		99.9	22	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
3	d1e3da_	Alignment		99.9	22	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
4	d1wuis1	Alignment		99.9	21	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
5	c1h2aS_	Alignment		99.9	21	**PDB header:**oxidoreductase **Chain:** S: **PDB Molecule:**hydrogenase; **PDBTitle:** single crystals of hydrogenase from desulfovibrio vulgaris
6	c3rgwS_	Alignment		99.9	24	**PDB header:**oxidoreductase/oxidoreductase **Chain:** S: **PDB Molecule:**membrane-bound hydrogenase (nife) small subunit hoxk; **PDBTitle:** crystal structure at 1.5 a resolution of an h2-reduced, o2-tolerant2 hydrogenase from ralstonia eutropha unmasks a novel iron-sulfur3 cluster
7	d1yq9a1	Alignment		99.9	21	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
8	d1cc1s_	Alignment		99.9	26	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
9	c3myrE_	Alignment		99.9	22	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**hydrogenase (nife) small subunit hyda; **PDBTitle:** crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
10	c2wpnA_	Alignment		99.8	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic [nifese] hydrogenase, small subunit; **PDBTitle:** structure of the oxidised, as-isolated nifese hydrogenase2 from d. vulgaris hildenborough
11	c2v4jA_	Alignment		69.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit **PDBTitle:** the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration

12	d2dlda2	Alignment		66.9	14	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
13	d1e5da1	Alignment		65.7	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
14	c2d1eA_	Alignment		56.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phycocyanobilin:ferredoxin oxidoreductase; **PDBTitle:** crystal structure of pcya-biliverdin complex
15	c3rl4A_	Alignment		54.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallophosphoesterase mpped2; **PDBTitle:** rat metallophosphodiesterase mpped2 g252h mutant
16	d1vmea1	Alignment		50.0	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
17	c2d3yA_	Alignment		43.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** crystal structure of uracil-dna glycosylase from thermus thermophilus2 hb8
18	c2r47C_	Alignment		41.3	17	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein mth_862; **PDBTitle:** crystal structure of mth_862 protein of unknown function from2 methanothermobacter thermautotrophicus
19	d1sqsa_	Alignment		39.3	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein SP1951
20	c2z1dA_	Alignment		38.1	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hypd; **PDBTitle:** crystal structure of [nife] hydrogenase maturation protein, hypd from2 thermococcus kodakaraensis
21	c3trhI_	Alignment	not modelled	31.9	25	**PDB header:**lyase **Chain:** I: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase **PDBTitle:** structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
22	c3klbA_	Alignment	not modelled	28.6	19	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative flavoprotein; **PDBTitle:** crystal structure of putative flavoprotein in complex with fmn2 (yp_213683.1) from bacteroides fragilis nctc 9343 at 1.75 a3 resolution
23	c1coyA_	Alignment	not modelled	27.9	15	**PDB header:**oxidoreductase(oxygen receptor) **Chain:** A: **PDB Molecule:**cholesterol oxidase; **PDBTitle:** crystal structure of cholesterol oxidase complexed with a2 steroid substrate. implications for fad dependent alcohol3 oxidases
24	c3ca8B_	Alignment	not modelled	27.2	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydcf; **PDBTitle:** crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
25	c3na7A_	Alignment	not modelled	26.8	13	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
26	c2q9uB_	Alignment	not modelled	25.3	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
27	d2dlda1	Alignment	not modelled	25.2	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
28	c3ikbB_	Alignment	not modelled	23.7	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the structure of a conserved protein from streptococcus2

						mutans ua159.
29	c2gn0A_	Alignment	not modelled	22.9	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**threonine dehydratase catabolic; **PDBTitle:** crystal structure of dimeric biodegradative threonine deaminase (tdcb)2 from salmonella typhimurium at 1.7 a resolution (triclinic form with3 one complete subunit built in alternate conformation)
30	c1e5dA_	Alignment	not modelled	22.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
31	d1j4aa1	Alignment	not modelled	22.6	7	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
32	d2ac7a1	Alignment	not modelled	21.8	26	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
33	d2yt9a2	Alignment	not modelled	20.9	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
34	d1ycga1	Alignment	not modelled	20.6	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
35	d2f2ab2	Alignment	not modelled	20.6	27	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**GatB/GatE catalytic domain-like
36	d1w85a_	Alignment	not modelled	19.4	17	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
37	c1xrsB_	Alignment	not modelled	19.3	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**d-lysine 5,6-aminomutase beta subunit; **PDBTitle:** crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
38	c3bsfB_	Alignment	not modelled	19.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**at4g34840; **PDBTitle:** crystal structure of the mta/sah nucleosidase
39	c3nm5B_	Alignment	not modelled	18.7	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mta/sah nucleosidase; **PDBTitle:** helicobacter pylori mtan complexed with formycin a
40	c2g5iB_	Alignment	not modelled	18.1	27	**PDB header:**ligase **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab2 complexed with adp-alf4
41	c1ychD_	Alignment	not modelled	17.7	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitric oxide reductase; **PDBTitle:** x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a scavenging nitric oxide reductase
42	d1jysa_	Alignment	not modelled	17.6	26	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
43	d1xm7a_	Alignment	not modelled	17.2	29	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Hypothetical protein aq 1666
44	d1sc6a1	Alignment	not modelled	17.0	5	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
45	c2is8A_	Alignment	not modelled	16.8	24	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
46	c1geaA_	Alignment	not modelled	16.7	60	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**pituitary adenylate cyclase activating **PDBTitle:** receptor-bound conformation of pacap21
47	c3bl6A_	Alignment	not modelled	16.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-methylthioadenosine nucleosidase/s- **PDBTitle:** crystal structure of staphylococcus aureus 5'-2 methylthioadenosine/s-adenosylhomocysteine nucleosidase in3 complex with formycin a
48	c2wzlA_	Alignment	not modelled	15.8	33	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**phosphoprotein; **PDBTitle:** the structure of the n-rna binding domain of the mokola2 virus phosphoprotein
49	d1pwha_	Alignment	not modelled	15.7	23	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
50	c3d3kD_	Alignment	not modelled	15.6	12	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
51	d2f7wa1	Alignment	not modelled	15.5	18	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
52	c1zosE_	Alignment	not modelled	15.5	14	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**5'-methylthioadenosine / s-adenosylhomocysteine **PDBTitle:** structure of 5'-methylthionadenosine/s-adenosylhomocysteine2 nucleosidase from s. pneumoniae with a transition-state3 inhibitor mt-imma

53	c3eeiA_	Alignment	not modelled	15.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5-methylthioadenosine nucleosidase/s- **PDBTitle:** crystal structure of 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase from neisseria3 meningitidis in complex with methylthio-immucillin-a
54	d1wiwa_	Alignment	not modelled	15.3	25	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
55	c3pdiB_	Alignment	not modelled	14.9	13	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nifn; **PDBTitle:** precursor bound nifen
56	c3k1yE_	Alignment	not modelled	14.7	11	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**oxidoreductase; **PDBTitle:** x-ray structure of oxidoreductase from corynebacterium2 diphtheriae. orthorombic crystal form, northeast structural3 genomics consortium target cdr100d
57	d2h1qa1	Alignment	not modelled	14.4	15	**Fold:**PLP-dependent transferase-like **Superfamily:**Dhaf3308-like **Family:**Dhaf3308-like
58	d2bfda1	Alignment	not modelled	14.4	11	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
59	c2rmzA_	Alignment	not modelled	14.0	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin beta-3; **PDBTitle:** bicelle-embedded integrin beta3 transmembrane segment
60	d1umda_	Alignment	not modelled	14.0	9	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
61	c3c7bA_	Alignment	not modelled	13.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
62	c2qneA_	Alignment	not modelled	13.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase (zp_00558420.1) from2 desulfitobacterium hafniense y51 at 2.30 a resolution
63	d1th5a1	Alignment	not modelled	13.8	14	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
64	c3npgD_	Alignment	not modelled	13.7	12	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**uncharacterized duf364 family protein; **PDBTitle:** crystal structure of a protein with unknown function from duf3642 family (ph1506) from pyrococcus horikoshii at 2.70 a resolution
65	d1xwdb1	Alignment	not modelled	13.5	19	**Fold:**Cystine-knot cytokines **Superfamily:**Cystine-knot cytokines **Family:**Gonadodropin/Follitropin
66	d1fyja_	Alignment	not modelled	13.4	71	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**a tRNA synthase domain
67	c1qfwB_	Alignment	not modelled	13.4	25	**PDB header:**immune system **Chain:** B: **PDB Molecule:**gonadotrophin beta subunit; **PDBTitle:** ternary complex of human chorionic gonadotropin with fv anti alpha2 subunit and fv anti beta subunit
68	c1zj8B_	Alignment	not modelled	13.4	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable ferredoxin-dependent nitrite reductase nira; **PDBTitle:** structure of mycobacterium tuberculosis nira protein
69	d1hcnb_	Alignment	not modelled	13.3	25	**Fold:**Cystine-knot cytokines **Superfamily:**Cystine-knot cytokines **Family:**Gonadodropin/Follitropin
70	c2ax3A_	Alignment	not modelled	13.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein tm0922; **PDBTitle:** crystal structure of a putative carbohydrate kinase (tm0922) from2 thermotoga maritima msb8 at 2.25 a resolution
71	d1nwba_	Alignment	not modelled	13.1	17	**Fold:**HesB-like domain **Superfamily:**HesB-like domain **Family:**HesB-like domain
72	d1fmfa_	Alignment	not modelled	13.0	15	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
73	c3edoA_	Alignment	not modelled	12.9	12	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative trp repressor binding protein; **PDBTitle:** crystal structure of flavoprotein in complex with fmn2 (yp_193882.1) from lactobacillus acidophilus ncfm at 1.203 a resolution
74	c1vmeB_	Alignment	not modelled	12.7	13	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
75	d1m1na_	Alignment	not modelled	12.5	11	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
76	d1ygya1	Alignment	not modelled	12.4	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
77	c3dp9A_	Alignment	not modelled	12.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mta/sah nucleosidase; **PDBTitle:** crystal structure of vibrio cholerae 5'-methylthioadenosine/s-adenosyl2 homocysteine nucleosidase (mtan) complexed with butylthio-dadme-3 immucillin a

78	d1vyia_	 Alignment	not modelled	12.3	33	**Fold:**Phosphoprotein M1, C-terminal domain **Superfamily:**Phosphoprotein M1, C-terminal domain **Family:**Phosphoprotein M1, C-terminal domain
79	c3i4zA_	 Alignment	not modelled	12.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tryptophan dimethylallyltransferase; **PDBTitle:** crystal structure of the dimethylallyl tryptophan synthase fgapt2 from2 aspergillus fumigatus
80	c3tl6B_	 Alignment	not modelled	12.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase from entamoeba2 histolytica
81	c2dmlA_	 Alignment	not modelled	11.9	31	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a6; **PDBTitle:** the solution structure of the first thioredoxin domain of2 mouse protein disulfide-isomerase a6
82	c2dbqA_	 Alignment	not modelled	11.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyoxylate reductase; **PDBTitle:** crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
83	d2b4ya1	 Alignment	not modelled	11.9	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
84	d3cxeb1	 Alignment	not modelled	11.7	83	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
85	c2dg2D_	 Alignment	not modelled	11.7	25	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**apolipoprotein a-i binding protein; **PDBTitle:** crystal structure of mouse apolipoprotein a-i binding2 protein
86	d2fd6u3	 Alignment	not modelled	11.6	83	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Extracellular domain of cell surface receptors
87	d2i9be3	 Alignment	not modelled	11.6	83	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Extracellular domain of cell surface receptors
88	d2naca1	 Alignment	not modelled	11.5	2	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
89	c3oa1B_	 Alignment	not modelled	11.4	30	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**phosphoprotein; **PDBTitle:** crystal structure of phosphoprotein/protein p/protein m1 residues 69-2 297 from rabies virus reveals degradation to c-terminal domain only
90	c3aerC_	 Alignment	not modelled	11.4	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**light-independent protochlorophyllide reductase subunit n; **PDBTitle:** structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
91	c2g76A_	 Alignment	not modelled	11.3	5	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of human 3-phosphoglycerate dehydrogenase
92	d2db7a1	 Alignment	not modelled	11.3	35	**Fold:**Orange domain-like **Superfamily:**Orange domain-like **Family:**Hairy Orange domain
93	c1vddC_	 Alignment	not modelled	11.2	29	**PDB header:**recombination **Chain:** C: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombinational repair protein recr
94	c3orsD_	 Alignment	not modelled	11.2	21	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
95	c2a5yA_	 Alignment	not modelled	11.2	17	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis regulator ced-9; **PDBTitle:** structure of a ced-4/ced-9 complex
96	d2ax3a2	 Alignment	not modelled	11.1	21	**Fold:**YjeF N-terminal domain-like **Superfamily:**YjeF N-terminal domain-like **Family:**YjeF N-terminal domain-like
97	c3rfqC_	 Alignment	not modelled	11.0	26	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase moab2; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
98	d2fug71	 Alignment	not modelled	11.0	71	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Nqo15-like
99	c3pdiG_	 Alignment	not modelled	10.8	18	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nife; **PDBTitle:** precursor bound nifen