Phyre^2

Email	l.a.kelley@imperial.ac.uk
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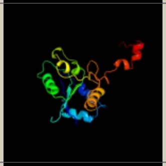
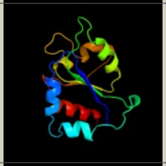
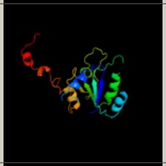
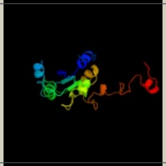
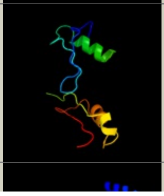
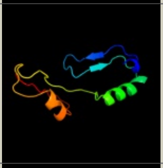
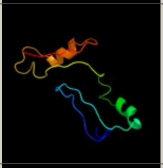
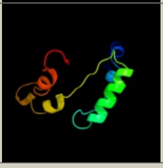
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fug61	Alignment		100.0	51	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nq06-like
2	d1frfs_	Alignment		99.9	20	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
3	d1e3da_	Alignment		99.9	19	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
4	d1wuis1	Alignment		99.9	19	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
5	c1h2aS_	Alignment		99.9	20	**PDB header:**oxidoreductase **Chain:** S: **PDB Molecule:**hydrogenase; **PDBTitle:** single crystals of hydrogenase from desulfovibrio vulgaris
6	c3rgwS_	Alignment		99.8	25	**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		99.8	17	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
8	c3myrE_	Alignment		99.8	21	**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
9	d1cc1s_	Alignment		99.8	22	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
10	c2wpnA_	Alignment		99.8	21	**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		87.7	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	c2z1dA_	Alignment		74.9	16	**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
13	c1zj8B_	Alignment		72.7	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable ferredoxin-dependent nitrite reductase nira; **PDBTitle:** structure of mycobacterium tuberculosis nira protein
14	c3c7bA_	Alignment		69.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
15	d2dlda2	Alignment		68.7	12	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
16	d1ygya2	Alignment		52.4	17	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
17	c2akjA_	Alignment		49.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nitrite reductase, chloroplast; **PDBTitle:** structure of spinach nitrite reductase
18	c3rl4A_	Alignment		48.0	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallophosphoesterase mpped2; **PDBTitle:** rat metallophosphodiesterase mpped2 g252h mutant
19	d1j4aa2	Alignment		41.4	11	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
20	c3trhI_	Alignment		36.9	18	**PDB header:**lyase **Chain:** I: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase **PDBTitle:** structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
21	c3ca8B_	Alignment	not modelled	35.7	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
22	c2d0iC_	Alignment	not modelled	35.3	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure ph0520 protein from pyrococcus horikoshii ot3
23	d1mx3a2	Alignment	not modelled	34.2	16	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
24	c3fhcB_	Alignment	not modelled	33.8	12	**PDB header:**transport protein/hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase ddx19b; **PDBTitle:** crystal structure of human dbp5 in complex with nup214
25	c3c7bE_	Alignment	not modelled	31.8	18	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit beta; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
26	c5aopA_	Alignment	not modelled	29.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase hemoprotein; **PDBTitle:** sulfite reductase structure reduced with crii edta, 5-coordinate2 siroheme, siroheme feii, [4fe-4s] +1
27	c2d3yA_	Alignment	not modelled	28.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** crystal structure of uracil-dna glycosylase from thermus thermophilus2 hb8
28	c2v4jE_	Alignment	not modelled	28.4	14	**PDB header:**oxidoreductase **Chain:** E: **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
29	d1e5da1	Alignment	not modelled	28.0	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
30	d2naca2	Alignment	not modelled	26.6	17	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
31	d1m1la_	Alignment	not modelled	23.8	29	**Fold:**Suppressor of Fused, N-terminal domain **Superfamily:**Suppressor of Fused, N-terminal domain **Family:**Suppressor of Fused, N-terminal domain
32	c1ychD_	Alignment	not modelled	23.8	18	**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
33	c3mglA_	Alignment	not modelled	23.5	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sulfate permease family protein; **PDBTitle:** crystal structure of permease family protein from vibrio2 cholerae
34	d2cv4a1	Alignment	not modelled	22.3	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
35	d1sqsa_	Alignment	not modelled	20.7	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein SP1951
36	c2d16B_	Alignment	not modelled	20.1	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ph1918; **PDBTitle:** crystal structure of ph1918 protein from pyrococcus horikoshii ot3
37	d2dlda1	Alignment	not modelled	19.9	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
38	c2pi1C_	Alignment	not modelled	19.6	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-lactate dehydrogenase; **PDBTitle:** crystal structure of d-lactate dehydrogenase from aquifex2 aeolicus complexed with nad and lactic acid
39	c2gn0A_	Alignment	not modelled	19.1	10	**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)
40	d1fmfa_	Alignment	not modelled	17.7	16	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
41	c1m46B_	Alignment	not modelled	16.3	33	**PDB header:**cell cycle protein **Chain:** B: **PDB Molecule:**iq4 motif from myo2p, a class v myosin; **PDBTitle:** crystal structure of mlc1p bound to iq4 of myo2p, a class v2 myosin
42	c3ikbB_	Alignment	not modelled	15.8	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the structure of a conserved protein from streptococcus2 mutans ua159.
43	d1j4aa1	Alignment	not modelled	15.6	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
44	c2afvB_	Alignment	not modelled	14.5	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**cobalamin biosynthesis precorrin isomerase; **PDBTitle:** the crystal structure of putative precorrin isomerase cbic2 in cobalamin biosynthesis
45	c2gewA_	Alignment	not modelled	14.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cholesterol oxidase; **PDBTitle:** atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo)
46	c2r47C_	Alignment	not modelled	13.2	25	**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
47	d1xm7a_	Alignment	not modelled	12.8	12	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Hypothetical protein aq 1666
48	c3nm5B_	Alignment	not modelled	12.4	6	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mta/sah nucleosidase; **PDBTitle:** helicobacter pylori mtan complexed with formycin a
49	c2nacA_	Alignment	not modelled	12.3	14	**PDB header:**oxidoreductase(aldehyde(d),nad+(a)) **Chain:** A: **PDB Molecule:**nad-dependent formate dehydrogenase; **PDBTitle:** high resolution structures of holo and apo formate dehydrogenase
50	c3rggD_	Alignment	not modelled	12.3	28	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, pure protein; **PDBTitle:** crystal structure of treponema denticola pure bound to air
51	c1e5dA_	Alignment	not modelled	12.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
52	d2fug71	Alignment	not modelled	12.0	71	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Nqo15-like
53	d2ac7a1	Alignment	not modelled	11.3	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases

						Family: Purine and uridine phosphorylases
54	d2fcla1	Alignment	not modelled	10.9	33	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**TM1012-like
55	d2f7wa1	Alignment	not modelled	10.7	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
56	d1f2va_	Alignment	not modelled	10.5	20	**Fold:**Flavodoxin-like **Superfamily:**Precorrin-8X methylmutase CbiC/CobH **Family:**Precorrin-8X methylmutase CbiC/CobH
57	d2zcta1	Alignment	not modelled	10.4	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
58	c3oetF_	Alignment	not modelled	10.4	23	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**erythronate-4-phosphate dehydrogenase; **PDBTitle:** d-erythronate-4-phosphate dehydrogenase complexed with nad
59	c3aerC_	Alignment	not modelled	10.4	13	**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
60	c3bsfB_	Alignment	not modelled	10.4	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**at4g34840; **PDBTitle:** crystal structure of the mta/sah nucleosidase
61	c1geaA_	Alignment	not modelled	10.4	56	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**pituitary adenylate cyclase activating **PDBTitle:** receptor-bound conformation of pacap21
62	c3bl6A_	Alignment	not modelled	10.3	17	**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
63	d1jysa_	Alignment	not modelled	10.3	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
64	c1coyA_	Alignment	not modelled	9.8	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
65	d1fyja_	Alignment	not modelled	9.7	71	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**a tRNA synthase domain
66	d1zj8a3	Alignment	not modelled	9.6	24	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
67	d1k9sa_	Alignment	not modelled	9.6	12	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
68	c3eeiA_	Alignment	not modelled	9.3	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
69	d1ycga1	Alignment	not modelled	9.3	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
70	c3orsD_	Alignment	not modelled	9.1	19	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
71	c1q14A_	Alignment	not modelled	9.0	45	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hst2 protein; **PDBTitle:** structure and autoregulation of the yeast hst2 homolog of sir2
72	c3k1yE_	Alignment	not modelled	9.0	13	**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
73	c3e7dC_	Alignment	not modelled	8.8	12	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**cobh, precorrin-8x methylmutase; **PDBTitle:** crystal structure of precorrin-8x methyl mutase cbic/cobh from2 brucella melitensis
74	d1j8fa_	Alignment	not modelled	8.7	45	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
75	d2i9be3	Alignment	not modelled	8.6	83	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Extracellular domain of cell surface receptors
76	d2fd6u3	Alignment	not modelled	8.6	83	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Extracellular domain of cell surface receptors
77	c3dkbA_	Alignment	not modelled	8.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tumor necrosis factor, alpha-induced protein 3; **PDBTitle:** crystal structure of a20, 2.5 angstrom
78	c2dg2D_	Alignment	not modelled	8.4	24	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**apolipoprotein a-i binding protein; **PDBTitle:** crystal structure of mouse apolipoprotein a-i binding2 protein

79	c2ipiD_	Alignment	not modelled	8.4	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aclacinomycin oxidoreductase (aknox); **PDBTitle:** crystal structure of aclacinomycin oxidoreductase
80	d1qwra_	Alignment	not modelled	8.3	24	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
81	c3tl6B_	Alignment	not modelled	8.1	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase from entamoeba2 histolytica
82	d3cxeb1	Alignment	not modelled	8.1	83	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
83	d1sc6a2	Alignment	not modelled	7.6	12	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
84	d1914a2	Alignment	not modelled	7.5	17	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
85	c2rmzA_	Alignment	not modelled	7.5	43	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin beta-3; **PDBTitle:** bicelle-embedded integrin beta3 transmembrane segment
86	d1qmva_	Alignment	not modelled	7.3	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
87	d1vhwa_	Alignment	not modelled	7.2	10	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
88	c3oj0A_	Alignment	not modelled	7.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** crystal structure of glutamyl-trna reductase from thermoplasma2 volcanium (nucleotide binding domain)
89	c3klbA_	Alignment	not modelled	7.1	18	**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
90	c3iauA_	Alignment	not modelled	7.1	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**threonine deaminase; **PDBTitle:** the structure of the processed form of threonine deaminase isoform 22 from solanum lycopersicum
91	d1pwha_	Alignment	not modelled	7.1	17	**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
92	d1ygya1	Alignment	not modelled	7.1	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
93	c3edoA_	Alignment	not modelled	7.1	23	**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
94	c2j6iC_	Alignment	not modelled	7.0	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
95	c3ibqA_	Alignment	not modelled	7.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxal kinase; **PDBTitle:** crystal structure of pyridoxal kinase from lactobacillus2 plantarum in complex with atp
96	c1zosE_	Alignment	not modelled	7.0	19	**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
97	c3l3bA_	Alignment	not modelled	7.0	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**es1 family protein; **PDBTitle:** crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
98	c3iz6E_	Alignment	not modelled	6.9	10	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**40s ribosomal protein s2 (s5p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
99	d1rutx2	Alignment	not modelled	6.8	19	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain