Phyre2

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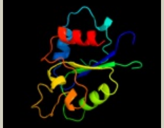
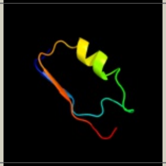
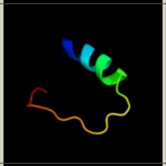
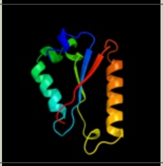
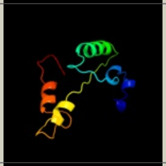
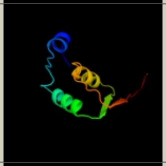
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fug61	Alignment		100.0	32	**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	d1wuis1	Alignment		99.9	21	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
4	d1e3da_	Alignment		99.9	22	**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	17	**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	18	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
8	c3myrE_	Alignment		99.9	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		99.9	28	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
10	c2wpnA_	Alignment		99.8	23	**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		63.5	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		57.2	15	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
13	d1e5da1	Alignment		53.5	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
14	c3rl4A_	Alignment		49.9	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallophosphoesterase mpped2; **PDBTitle:** rat metallophosphodiesterase mpped2 g252h mutant
15	c2d3yA_	Alignment		41.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** crystal structure of uracil-dna glycosylase from thermus thermophilus2 hb8
16	c3aerC_	Alignment		38.6	18	**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
17	c3trhI_	Alignment		36.7	24	**PDB header:**lyase **Chain:** I: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase **PDBTitle:** structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
18	d1sqsa_	Alignment		33.7	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein SP1951
19	d1vmea1	Alignment		33.0	8	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
20	c1zvuA_	Alignment		32.7	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit a; **PDBTitle:** structure of the full-length e. coli parc subunit
21	c2rf4B_	Alignment	not modelled	31.8	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna-directed rna polymerase i subunit rpa4; **PDBTitle:** crystal structure of the rna polymerase i subcomplex a14/43
22	c3ca8B_	Alignment	not modelled	30.0	18	**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
23	c1xrsB_	Alignment	not modelled	30.0	25	**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
24	c2q9uB_	Alignment	not modelled	29.6	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
25	d2hkja2	Alignment	not modelled	29.3	23	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
26	c1coyA_	Alignment	not modelled	27.0	13	**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
27	d2f2ab2	Alignment	not modelled	24.1	31	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**GatB/GatE catalytic domain-like
28	d1nwba_	Alignment	not modelled	22.3	16	**Fold:**HesB-like domain **Superfamily:**HesB-like domain **Family:**HesB-like domain
						PDB header:structural genomics, unknown function

29	c3ikbB_	Alignment	not modelled	22.1	11	**Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the structure of a conserved protein from streptococcus2 mutans ua159.
30	d2ac7a1	Alignment	not modelled	21.4	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
31	c2z1dA_	Alignment	not modelled	21.0	20	**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
32	d2dlda1	Alignment	not modelled	20.6	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
33	c2ax3A_	Alignment	not modelled	19.9	20	**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
34	c2gn0A_	Alignment	not modelled	19.6	17	**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)
35	c3d3kD_	Alignment	not modelled	19.5	12	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
36	d1s98a_	Alignment	not modelled	19.2	22	**Fold:**HesB-like domain **Superfamily:**HesB-like domain **Family:**HesB-like domain
37	d1miob_	Alignment	not modelled	18.8	11	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
38	d1m1la_	Alignment	not modelled	18.3	20	**Fold:**Suppressor of Fused, N-terminal domain **Superfamily:**Suppressor of Fused, N-terminal domain **Family:**Suppressor of Fused, N-terminal domain
39	c2xdqA_	Alignment	not modelled	18.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase subunit n; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-2 chlb)2 complex
40	c3bsfB_	Alignment	not modelled	17.7	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**at4g34840; **PDBTitle:** crystal structure of the mta/sah nucleosidase
41	d2ax3a2	Alignment	not modelled	17.5	20	**Fold:**YjeF N-terminal domain-like **Superfamily:**YjeF N-terminal domain-like **Family:**YjeF N-terminal domain-like
42	c3na7A_	Alignment	not modelled	17.5	12	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
43	d2yt9a2	Alignment	not modelled	17.4	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
44	d1b3qa1	Alignment	not modelled	17.2	19	**Fold:**ROP-like **Superfamily:**Homodimeric domain of signal transducing histidine kinase **Family:**Homodimeric domain of signal transducing histidine kinase
45	c2is8A_	Alignment	not modelled	17.1	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	d1j4aa1	Alignment	not modelled	17.0	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
47	c3nm5B_	Alignment	not modelled	16.9	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mta/sah nucleosidase; **PDBTitle:** helicobacter pylori mtan complexed with formycin a
48	c2dg2D_	Alignment	not modelled	16.2	21	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**apolipoprotein a-i binding protein; **PDBTitle:** crystal structure of mouse apolipoprotein a-i binding2 protein
49	d1jysa_	Alignment	not modelled	15.8	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
50	c2d1eA_	Alignment	not modelled	15.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phycocyanobilin:ferredoxin oxidoreductase; **PDBTitle:** crystal structure of pcya-biliverdin complex
51	d1j4aa2	Alignment	not modelled	15.5	16	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
52	c2wzlA_	Alignment	not modelled	15.2	30	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**phosphoprotein; **PDBTitle:** the structure of the n-rna binding domain of the mokola2 virus phosphoprotein
53	d1pwha_	Alignment	not modelled	15.1	21	**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

54	d2h1qa1	Alignment	not modelled	14.9	18	**Fold:**PLP-dependent transferase-like **Superfamily:**Dhaf3308-like **Family:**Dhaf3308-like
55	c1geaA_	Alignment	not modelled	14.9	60	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**pituitary adenylate cyclase activating **PDBTitle:** receptor-bound conformation of pacap21
56	c2k4zA_	Alignment	not modelled	14.8	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dsrr; **PDBTitle:** solution nmr structure of allochromatium vinosum dsrr:2 northeast structural genomics consortium target op5
57	c3bl6A_	Alignment	not modelled	14.6	9	**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
58	c2q2eB_	Alignment	not modelled	14.6	31	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b; **PDBTitle:** crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei
59	c3eeiA_	Alignment	not modelled	14.5	11	**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
60	d1w85a_	Alignment	not modelled	14.4	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
61	c1zosE_	Alignment	not modelled	14.4	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
62	c3npgD_	Alignment	not modelled	14.3	15	**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
63	c2g5iB_	Alignment	not modelled	14.1	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab2 complexed with adp-alf4
64	c1e5dA_	Alignment	not modelled	14.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
65	d1xwdb1	Alignment	not modelled	13.7	19	**Fold:**Cystine-knot cytokines **Superfamily:**Cystine-knot cytokines **Family:**Gonadodropin/Follitropin
66	c3pdiB_	Alignment	not modelled	13.3	11	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nifn; **PDBTitle:** precursor bound nifen
67	d1hcnb_	Alignment	not modelled	13.3	25	**Fold:**Cystine-knot cytokines **Superfamily:**Cystine-knot cytokines **Family:**Gonadodropin/Follitropin
68	c1qfwB_	Alignment	not modelled	13.1	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
69	c2zbkB_	Alignment	not modelled	12.9	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b; **PDBTitle:** crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
70	c1vmeB_	Alignment	not modelled	12.8	11	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
71	c1ychD_	Alignment	not modelled	12.4	25	**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
72	d1fyja_	Alignment	not modelled	12.0	57	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**a tRNA synthase domain
73	d1fmfa_	Alignment	not modelled	12.0	18	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
74	c2rmzA_	Alignment	not modelled	12.0	24	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin beta-3; **PDBTitle:** bicelle-embedded integrin beta3 transmembrane segment
75	d1vyia_	Alignment	not modelled	11.9	30	**Fold:**Phosphoprotein M1, C-terminal domain **Superfamily:**Phosphoprotein M1, C-terminal domain **Family:**Phosphoprotein M1, C-terminal domain
76	c3k1yE_	Alignment	not modelled	11.8	9	**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
77	c3dp9A_	Alignment	not modelled	11.7	14	**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	d1sc6a1	Alignment	not modelled	11.4	5	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
79	c3tl6B_	Alignment	not modelled	11.4	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase from entamoeba2 histolytica
80	c3oa1B_	Alignment	not modelled	11.2	26	**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
81	d1th5a1	Alignment	not modelled	11.0	14	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
82	d1umda_	Alignment	not modelled	10.9	8	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
83	d2bfda1	Alignment	not modelled	10.8	11	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
84	d3cxeb1	Alignment	not modelled	10.8	83	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
85	d2b0ja2	Alignment	not modelled	10.6	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
86	c2d2aA_	Alignment	not modelled	10.6	21	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**sufa protein; **PDBTitle:** crystal structure of escherichia coli sufa involved in2 biosynthesis of iron-sulfur clusters
87	c3klbA_	Alignment	not modelled	10.5	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
88	c1z34A_	Alignment	not modelled	10.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of trichomonas vaginalis purine nucleoside2 phosphorylase complexed with 2-fluoro-2'-deoxyadenosine
89	c3pdiG_	Alignment	not modelled	10.4	18	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nife; **PDBTitle:** precursor bound nifen
90	d1k9sa_	Alignment	not modelled	10.2	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
91	c3rfqC_	Alignment	not modelled	10.2	24	**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
92	c2apnA_	Alignment	not modelled	10.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein hi1723; **PDBTitle:** hi1723 solution structure
93	c2dmlA_	Alignment	not modelled	10.0	26	**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
94	c3c7bA_	Alignment	not modelled	9.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
95	c3h0mE_	Alignment	not modelled	9.8	23	**PDB header:**ligase **Chain:** E: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
96	d2fug71	Alignment	not modelled	9.8	71	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Nqo15-like
97	c2o2kA_	Alignment	not modelled	9.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionine synthase; **PDBTitle:** crystal structure of the activation domain of human2 methionine synthase isoform/mutant d963e/k1071n
98	c1vddC_	Alignment	not modelled	9.6	33	**PDB header:**recombination **Chain:** C: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombinational repair protein recr
99	d1r0ka3	Alignment	not modelled	9.6	33	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like