


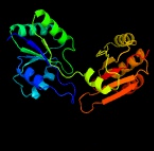





























Phyre2

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Description	RVBD1003_(-)_1120026_1120883
Date	Wed Jul 31 22:05:07 BST 2019
Unique Job ID	d66db9f69890ae93

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5hw4C_	 Alignment		100.0	40	PDB header: transferase Chain: C: PDB Molecule: ribosomal rna small subunit methyltransferase i; PDBTitle: crystal structure of escherichia coli 16s rrna methyltransferase rsmi2 in complex with adomet
2	c3kwpA_	 Alignment		100.0	44	PDB header: transferase Chain: A: PDB Molecule: predicted methyltransferase; PDBTitle: crystal structure of putative methyltransferase from lactobacillus2 brevis
3	d1cbfa_	 Alignment		100.0	19	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
4	c1cbfA_	 Alignment		100.0	19	PDB header: methyltransferase Chain: A: PDB Molecule: cobalt-precorrin-4 transmethylase; PDBTitle: the x-ray structure of a cobalamin biosynthetic enzyme, cobalt2 precorrin-4 methyltransferase, cbif
5	d1wyza1	 Alignment		100.0	21	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
6	c1pjtB_	 Alignment		100.0	19	PDB header: transferase/oxidoreductase/lyase Chain: B: PDB Molecule: siroheme synthase; PDBTitle: the structure of the ser128ala point-mutant variant of cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelataze for3 siroheme synthesis
7	c2yboA_	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: the x-ray structure of the sam-dependent uroporphyrinogen2 iii methyltransferase nire from pseudomonas aeruginosa in3 complex with sah
8	c4e16A_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: precorrin-4 c(11)-methyltransferase; PDBTitle: precorrin-4 c(11)-methyltransferase from clostridium difficile
9	d1s4da_	 Alignment		100.0	17	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
10	c3ncdC_	 Alignment		100.0	15	PDB header: transferase Chain: B: PDB Molecule: precorrin-4 c(11)-methyltransferase; PDBTitle: crystal structure of precorrin-4 c11-methyltransferase from2 rhodobacter capsulatus
11	d1pjqa2	 Alignment		100.0	19	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase

12	d1wdea_	Alignment		100.0	23	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
13	c2zvba_	Alignment		100.0	22	PDB header: transferase Chain: A; PDB Molecule: precorrin-3 c17-methyltransferase; PDBTitle: crystal structure of tt0207 from thermus thermophilus hb8
14	c3nutC_	Alignment		100.0	24	PDB header: transferase Chain: C; PDB Molecule: precorrin-3 methylase; PDBTitle: crystal structure of the methyltransferase cobj
15	d1va0a1	Alignment		100.0	17	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
16	d1ve2a1	Alignment		100.0	19	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
17	c2qbuA_	Alignment		100.0	16	PDB header: transferase Chain: A; PDB Molecule: precorrin-2 methyltransferase; PDBTitle: crystal structure of methanothermobacter thermautotrophicus cbil
18	d1vhva_	Alignment		100.0	18	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
19	d2deka1	Alignment		100.0	16	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
20	c3nd1B_	Alignment		100.0	15	PDB header: transferase Chain: B; PDB Molecule: precorrin-6a synthase/cobf protein; PDBTitle: crystal structure of precorrin-6a synthase from rhodobacter capsulatus
21	c3i4tA_	Alignment	not modelled	100.0	14	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: diphthine synthase; PDBTitle: crystal structure of putative diphthine synthase from entamoeba2 histolytica
22	c2e0kA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A; PDB Molecule: precorrin-2 c20-methyltransferase; PDBTitle: crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
23	c3fq6A_	Alignment	not modelled	100.0	51	PDB header: transferase Chain: A; PDB Molecule: methyltransferase; PDBTitle: the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi
24	c2nnpA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A; PDB Molecule: putative cobalamin synthesis related protein; PDBTitle: crystal structure of putative cobalamin synthesis related protein2 (cobf) from corynebacterium diphtheriae
25	c2bb3B_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B; PDB Molecule: cobalamin biosynthesis precorrin-6y methylase (cbie); PDBTitle: crystal structure of cobalamin biosynthesis precorrin-6y methylase2 (cbie) from archaeoglobus fulgidus
26	d2bb3a1	Alignment	not modelled	100.0	19	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
27	c5n0sA_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A; PDB Molecule: peptide n-methyltransferase; PDBTitle: crystal structure of opha-delta6 mutant y98a in complex with sam
28	c3hh1D_	Alignment	not modelled	99.9	39	PDB header: transferase Chain: D; PDB Molecule: tetrapyrrole methylase family protein; PDBTitle: the structure of a tetrapyrrole methylase family protein

						domain from2 chlorobium tepidum t1s
29	c3q3vA_	Alignment	not modelled	80.6	17	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of phosphoglycerate kinase from campylobacter2 jejuni.
30	c2px0D_	Alignment	not modelled	79.3	11	PDB header: biosynthetic protein Chain: D: PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmppnp/mg(2+)
31	d1phpa_	Alignment	not modelled	79.1	19	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
32	d1vpea_	Alignment	not modelled	79.0	17	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
33	c5b04G_	Alignment	not modelled	62.2	22	PDB header: translation Chain: G: PDB Molecule: probable translation initiation factor eif-2b subunit PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
34	d2ezla_	Alignment	not modelled	61.3	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
35	c4qmkB_	Alignment	not modelled	60.5	38	PDB header: toxin Chain: B: PDB Molecule: type iii secretion system effector protein exou; PDBTitle: crystal structure of type iii effector protein exou (exou)
36	c4akfA_	Alignment	not modelled	59.2	31	PDB header: transferase Chain: A: PDB Molecule: vipd; PDBTitle: crystal structure of vipd from legionella pneumophila
37	c5fyaA_	Alignment	not modelled	59.1	23	PDB header: hydrolase Chain: A: PDB Molecule: patatin-like protein, plpd; PDBTitle: cubic crystal of the native plpd
38	c3tu3B_	Alignment	not modelled	58.5	31	PDB header: toxin/toxin chaperone Chain: B: PDB Molecule: exou; PDBTitle: 1.92 angstrom resolution crystal structure of the full-length spcu in2 complex with full-length exou from the type iii secretion system of3 pseudomonas aeruginosa
39	c4dg5A_	Alignment	not modelled	55.4	11	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of staphylococcal phosphoglycerate kinase
40	d1v6sa_	Alignment	not modelled	51.7	18	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
41	c1keeH_	Alignment	not modelled	51.1	19	PDB header: ligase Chain: H: PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
42	c4ltyD_	Alignment	not modelled	50.4	27	PDB header: hydrolase Chain: D: PDB Molecule: exonuclease subunit sbcd; PDBTitle: crystal structure of e.coli sbcd at 1.8 a resolution
43	c5kinC_	Alignment	not modelled	49.7	15	PDB header: lyase Chain: C: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
44	d1xfia_	Alignment	not modelled	49.6	30	Fold: AF1104-like Superfamily: AF1104-like Family: AF1104-like
45	d1ybha1	Alignment	not modelled	49.4	9	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
46	c3bioB_	Alignment	not modelled	46.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of oxidoreductase (gfo/idh/moca family member) from2 porphyromonas gingivalis w83
47	c4akxB_	Alignment	not modelled	45.5	31	PDB header: transport protein Chain: B: PDB Molecule: exou; PDBTitle: structure of the heterodimeric complex exou-spcu from the type iii2 secretion system (t3s) of pseudomonas aeruginosa
48	c3navB_	Alignment	not modelled	45.2	14	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
49	c5dboA_	Alignment	not modelled	45.2	28	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b-like protein; PDBTitle: crystal structure of the tetrameric eif2b-beta2-delta2 complex from c.2 thermophilum
50	c4da9C_	Alignment	not modelled	43.5	21	PDB header: oxidoreductase Chain: C: PDB Molecule: short-chain dehydrogenase/reductase; PDBTitle: crystal structure of putative short-chain dehydrogenase/reductase from2 sinorhizobium meliloti 1021
51	c6cluC_	Alignment	not modelled	43.2	17	PDB header: antimicrobial protein Chain: C: PDB Molecule: dihydropteroate synthase; PDBTitle: staphylococcus aureus dihydropteroate synthase (sadhps) f171 e208k2 double mutant structure
52	c1cr6A_	Alignment	not modelled	40.6	12	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
53	c2cunA_	Alignment	not modelled	39.4	17	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii ot3
						Fold: NAD(P)-binding Rossmann-fold domains

54	d2d59a1	Alignment	not modelled	38.7	11	Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
55	d1p3y1	Alignment	not modelled	38.5	8	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
56	c2z2uA	Alignment	not modelled	37.8	14	PDB header: metal binding protein Chain: A: PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaeal tyw1
57	c4njka	Alignment	not modelled	37.2	25	PDB header: lyase Chain: A: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from burkholderia multivorans in complex2 with adomet, 7-carboxy-7-deazaguanine, and mg2+
58	d1t9ba1	Alignment	not modelled	37.0	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
59	c5ldgA	Alignment	not modelled	36.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: (-)-isopiperitenone reductase; PDBTitle: isopiperitenone reductase from mentha piperita in complex with2 isopiperitenone and nadp
60	c2qasA	Alignment	not modelled	36.1	20	PDB header: hydrolase activator Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of caulobacter crescentus sspb ortholog
61	d2q4qa1	Alignment	not modelled	36.0	20	Fold: MTH938-like Superfamily: MTH938-like Family: MTH938-like
62	d1q6za1	Alignment	not modelled	35.7	19	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
63	c6i7tB	Alignment	not modelled	35.1	16	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: eif2b:eif2 complex
64	d1iuka	Alignment	not modelled	34.9	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
65	c5o30A	Alignment	not modelled	34.6	19	PDB header: lyase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of the novel halohydrin dehalogenase hheg
66	c3zlbA	Alignment	not modelled	34.3	13	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of phosphoglycerate kinase from streptococcus2 pneumoniae
67	c2a5hC	Alignment	not modelled	33.6	17	PDB header: isomerase Chain: C: PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
68	c5o3zK	Alignment	not modelled	33.0	29	PDB header: oxidoreductase Chain: K: PDB Molecule: sorbitol-6-phosphate dehydrogenase; PDBTitle: crystal structure of sorbitol-6-phosphate 2-dehydrogenase srlid from2 erwinia amylovora
69	c3lqkA	Alignment	not modelled	32.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit b; PDBTitle: crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
70	c3qanB	Alignment	not modelled	32.6	24	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-pyrroline-5-carboxylate dehydrogenase 1; PDBTitle: crystal structure of 1-pyrroline-5-carboxylate dehydrogenase from2 bacillus halodurans
71	c2qazC	Alignment	not modelled	32.5	20	PDB header: hydrolase activator Chain: C: PDB Molecule: sspb protein; PDBTitle: structure of c. crescentus sspb ortholog
72	c2qcnA	Alignment	not modelled	31.6	18	PDB header: lyase Chain: A: PDB Molecule: uridine 5'-monophosphate synthase; PDBTitle: covalent complex of the orotidine-5'-monophosphate decarboxylase2 domain of human ump synthase with 6-iodo-ump
73	c3l7oB	Alignment	not modelled	30.6	14	PDB header: isomerase Chain: B: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
74	d1yl7a1	Alignment	not modelled	30.6	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
75	c5jg7A	Alignment	not modelled	30.4	15	PDB header: metal transport Chain: A: PDB Molecule: fur regulated salmonella iron transporter; PDBTitle: crystal structure of putative periplasmic binding protein from2 salmonella typhimurium lt2
76	c1w59B	Alignment	not modelled	30.3	14	PDB header: cell division Chain: B: PDB Molecule: cell division protein ftsz homolog 1; PDBTitle: ftsz dimer, empty (m. jannaschii)
77	c6gq0A	Alignment	not modelled	30.2	11	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar binding protein; PDBTitle: crystal structure of ganp, a glucose-galactose binding protein from2 geobacillus stearothermophilus
78	c5yaaD	Alignment	not modelled	30.1	11	PDB header: hydrolase Chain: D: PDB Molecule: meiosis regulator and mrna stability factor 1; PDBTitle: crystal structure of marf1 nyn domain from mus musculus
						PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, short chain

79	c4x54A	Alignment	not modelled	29.9	26	dehydrogenase/reductase family; PDBTitle: crystal structure of an oxidoreductase (short chain2 dehydrogenase/reductase) from brucella ovis
80	c3npgD	Alignment	not modelled	29.9	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
81	d1jeyb2	Alignment	not modelled	29.4	6	Fold: vWA-like Superfamily: vWA-like Family: Ku80 subunit N-terminal domain
82	c3vh3A	Alignment	not modelled	29.2	27	PDB header: metal binding protein/protein transport Chain: A: PDB Molecule: ubiquitin-like modifier-activating enzyme atg7; PDBTitle: crystal structure of atg7ctd-atg8 complex
83	c5ijgB	Alignment	not modelled	29.1	19	PDB header: hydrolase Chain: B: PDB Molecule: cys/met metabolism pyridoxal-phosphate-dependent enzyme; PDBTitle: crystal structure of o-acetylhomoserine sulfhydrylase from brucella2 melitensis at 2.0 a resolution
84	c5sxyA	Alignment	not modelled	28.8	10	PDB header: chaperone Chain: A: PDB Molecule: bifunctional coenzyme pqq synthesis protein c/d; PDBTitle: the solution nmr structure for the pqqd truncation of methylobacterium2 extorquens pqqcd representing a functional and stand-alone3 ribosomally synthesized and post-translational modified (ripp)4 recognition element (rre)
85	c2j7pA	Alignment	not modelled	28.7	20	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
86	d16pka	Alignment	not modelled	28.7	20	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
87	c4ak9A	Alignment	not modelled	28.4	16	PDB header: protein transport Chain: A: PDB Molecule: cpftsyl; PDBTitle: structure of chloroplast ftsy from physcomitrella patens
88	c4jenB	Alignment	not modelled	28.4	13	PDB header: hydrolase Chain: B: PDB Molecule: cmp n-glycosidase; PDBTitle: structure of clostridium botulinum cmp n-glycosidase, bcmb
89	c6m9uA	Alignment	not modelled	28.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family PDBTitle: structure of the apo-form of 20beta-hydroxysteroid dehydrogenase from2 bifidobacterium adolescentis strain I2-32
90	d2djia1	Alignment	not modelled	27.8	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
91	c4ldrA	Alignment	not modelled	27.7	18	PDB header: isomerase, cell invasion Chain: A: PDB Molecule: methylthioribose-1-phosphate isomerase; PDBTitle: structure of the s283y mutant of mrdi
92	c6gg0G	Alignment	not modelled	27.6	21	PDB header: translation Chain: G: PDB Molecule: translation initiation factor eif-2b subunit delta; PDBTitle: structure of eif2b-eif2 (phosphorylated at ser51) complex (model 1)
93	c4wt7B	Alignment	not modelled	27.4	11	PDB header: transport protein Chain: B: PDB Molecule: abc transporter substrate binding protein (ribose); PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from agrobacterium vitis (avi_5165, target efi-511223)3 with bound allitol
94	c3gx1A	Alignment	not modelled	27.3	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin1832 protein; PDBTitle: crystal structure of a domain of lin1832 from listeria innocua
95	d2h1qa1	Alignment	not modelled	27.2	19	Fold: PLP-dependent transferase-like Superfamily: Dhaf3308-like Family: Dhaf3308-like
96	c3ecsD	Alignment	not modelled	27.1	21	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of human eif2b alpha
97	c3hl2D	Alignment	not modelled	26.9	15	PDB header: transferase Chain: D: PDB Molecule: o-phosphoseryl-trna(sec) selenium transferase; PDBTitle: the crystal structure of the human sepsecs-trnasec complex
98	d1xw8a	Alignment	not modelled	26.8	19	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
99	c4zeoH	Alignment	not modelled	26.8	27	PDB header: translation Chain: H: PDB Molecule: translation initiation factor eif-2b-like protein; PDBTitle: crystal structure of eif2b delta from chaetomium thermophilum
100	c5hqjA	Alignment	not modelled	26.7	12	PDB header: solute-binding protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of abc transporter solute binding protein b1g1h72 from burkholderia graminis c4d1m, target efi-511179, in complex with3 d-arabinose
101	c4gxtA	Alignment	not modelled	26.7	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: a conserved functionally unknown protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from2 anaerococcus prevotii dsm 20548 PDB header: oxidoreductase

102	c3o26A_	Alignment	not modelled	26.7	23	Chain: A: PDB Molecule: salutaridine reductase; PDBTitle: the structure of salutaridine reductase from papaver somniferum.
103	d1jeva2	Alignment	not modelled	26.3	6	Fold: vWA-like Superfamily: vWA-like Family: Ku70 subunit N-terminal domain
104	c5ux5C_	Alignment	not modelled	26.2	16	PDB header: oxidoreductase/transferase Chain: C: PDB Molecule: bifunctional protein proline utilization a (puta); PDBTitle: structure of proline utilization a (puta) from corynebacterium2 freiburgense
105	c2q5cA_	Alignment	not modelled	26.1	15	PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
106	d2gk3a1	Alignment	not modelled	26.0	10	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: STM3548-like
107	d2dlda2	Alignment	not modelled	25.5	24	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
108	c4ru1C_	Alignment	not modelled	25.4	13	PDB header: transport protein Chain: C: PDB Molecule: monosaccharide abc transporter substrate-binding protein, PDBTitle: crystal structure of carbohydrate transporter acei_1806 from2 acidothermus cellulolyticus 11b, target efi-510965, in complex with3 myo-inositol
109	c3upyB_	Alignment	not modelled	25.4	17	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the brucella abortus enzyme catalyzing the first2 committed step of the methylerythritol 4-phosphate pathway.
110	d1f0ka_	Alignment	not modelled	25.3	24	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Peptidoglycan biosynthesis glycosyltransferase MurG
111	d2dfaa1	Alignment	not modelled	25.2	27	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
112	c4wzza_	Alignment	not modelled	25.2	14	PDB header: transport protein Chain: A: PDB Molecule: putative sugar abc transporter, substrate-binding protein; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from clostridium phytofermentas (cphy_0583, target efi-3 511148) with bound l-rhamnose
113	c2nysA_	Alignment	not modelled	25.1	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: agr_c_3712p; PDBTitle: x-ray crystal structure of protein agr_c_3712 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr88.
114	d2nysa1	Alignment	not modelled	25.1	18	Fold: SspB-like Superfamily: SspB-like Family: AGR C 3712p-like
115	c2vpiA_	Alignment	not modelled	25.1	23	PDB header: ligase Chain: A: PDB Molecule: gmp synthase; PDBTitle: human gmp synthetase - glutaminase domain
116	d2ozlb2	Alignment	not modelled	25.0	25	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
117	d1ptma_	Alignment	not modelled	24.7	25	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: PdxA-like
118	c4f9iA_	Alignment	not modelled	24.7	23	PDB header: oxidoreductase Chain: A: PDB Molecule: proline dehydrogenase/delta-1-pyrroline-5-carboxylate PDBTitle: crystal structure of proline utilization a (puta) from geobacter2 sulfurreducens pca
119	c3bmrA_	Alignment	not modelled	24.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: pteridine reductase; PDBTitle: structure of pteridine reductase 1 (ptr1) from trypanosoma2 brucei in ternary complex with cofactor (nadp+) and3 inhibitor (compound ax6)
120	c5I53A_	Alignment	not modelled	24.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: (-)-menthone:(+)-neomenthol reductase; PDBTitle: menthone neomenthol reductase from mentha piperita in complex with2 nadp