


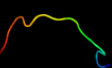













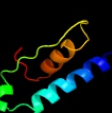




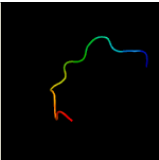
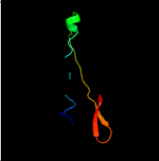
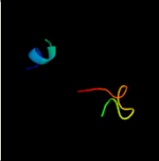

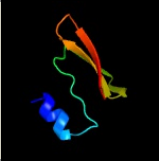


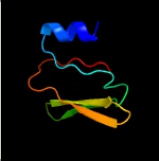
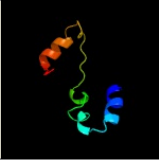


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD1446c\_opcA\_1624460\_1625371  
 Date Fri Aug 2 13:30:02 BST 2019  
 Unique Job ID 42a27cfbecc8b92

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1kl7a_</a>	 Alignment		77.0	16	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
2	<a href="#">d1miau4</a>	 Alignment		24.5	27	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
3	<a href="#">c6ojmB_</a>	 Alignment		22.3	15	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> 1,4-dihydroxy-2-naphthoyl-coa synthase; <b>PDBTitle:</b> crystal structure of 1,4-dihydroxy-2-naphthoyl-coa synthase2 elizabethkingia anophelis nuhp1
4	<a href="#">c3k12F_</a>	 Alignment		21.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F; <b>PDB Molecule:</b> uncharacterized protein a6v7t0; <b>PDBTitle:</b> crystal structure of an uncharacterized protein a6v7t0 from2 pseudomonas aeruginosa
5	<a href="#">c1r0lD_</a>	 Alignment		19.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase; <b>PDBTitle:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase from zymomonas mobilis2 in complex with nadph
6	<a href="#">d1rm6a2</a>	 Alignment		19.0	22	<b>Fold:</b> Molybdenum cofactor-binding domain <b>Superfamily:</b> Molybdenum cofactor-binding domain <b>Family:</b> Molybdenum cofactor-binding domain
7	<a href="#">d1dgja4</a>	 Alignment		17.3	12	<b>Fold:</b> Molybdenum cofactor-binding domain <b>Superfamily:</b> Molybdenum cofactor-binding domain <b>Family:</b> Molybdenum cofactor-binding domain
8	<a href="#">d1ohua_</a>	 Alignment		16.7	8	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death <b>Family:</b> Bcl-2 inhibitors of programmed cell death
9	<a href="#">d1vb3a1</a>	 Alignment		16.0	30	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
10	<a href="#">c4f4fB_</a>	 Alignment		14.7	19	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> x-ray crystal structure of plp bound threonine synthase from brucella2 melitensis
11	<a href="#">d1ffgb_</a>	 Alignment		14.2	26	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> CheY-binding domain of CheA <b>Family:</b> CheY-binding domain of CheA

12	<a href="#">d1iyb4</a>	Alignment		13.5	27	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
13	<a href="#">d1nyed</a>	Alignment		13.5	11	<b>Fold:</b> OsmC-like <b>Superfamily:</b> OsmC-like <b>Family:</b> Ohr/OsmC resistance proteins
14	<a href="#">c5bv1A</a>	Alignment		13.4	37	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> designed tim barrel stim11; <b>PDBTitle:</b> crystal structure of a de novo designed tim-barrel
15	<a href="#">c3ossD</a>	Alignment		12.6	13	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> type 2 secretion system, secretin gspd; <b>PDBTitle:</b> the crystal structure of enterotoxigenic escherichia coli gspc-gspd2 complex from the type ii secretion system
16	<a href="#">d1efpb</a>	Alignment		12.4	21	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
17	<a href="#">c3hrdE</a>	Alignment		11.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> nicotinate dehydrogenase large molybdopterin <b>PDBTitle:</b> crystal structure of nicotinate dehydrogenase
18	<a href="#">c3v7nA</a>	Alignment		11.7	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> crystal structure of threonine synthase (thrc) from from burkholderia2 thailandensis
19	<a href="#">c1o94D</a>	Alignment		11.7	17	<b>PDB header:</b> electron transport <b>Chain:</b> D: <b>PDB Molecule:</b> electron transfer flavoprotein alpha-subunit; <b>PDBTitle:</b> ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
20	<a href="#">c5vldC</a>	Alignment		11.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> histidinol dehydrogenase, chloroplastic; <b>PDBTitle:</b> crystal structure of medicago truncatula l-histidinol dehydrogenase in2 complex with l-histidine and nad+
21	<a href="#">c6jo52</a>	Alignment	not modelled	10.3	38	<b>PDB header:</b> photosynthesis <b>Chain:</b> 2: <b>PDB Molecule:</b> chlorophyll a-b binding protein, chloroplastic; <b>PDBTitle:</b> structure of the green algal photosystem i supercomplex with light-2 harvesting complex i
22	<a href="#">c6fahB</a>	Alignment	not modelled	10.2	12	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> caffeyl-coa reductase-etf complex subunit card; <b>PDBTitle:</b> molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
23	<a href="#">d1o94c</a>	Alignment	not modelled	10.0	20	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
24	<a href="#">c6ijj7</a>	Alignment	not modelled	9.9	24	<b>PDB header:</b> membrane protein <b>Chain:</b> 7: <b>PDB Molecule:</b> lhca7; <b>PDBTitle:</b> photosystem i of chlamydomonas reinhardtii
25	<a href="#">d1yt3a1</a>	Alignment	not modelled	9.8	18	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> HRDC-like <b>Family:</b> RNase D C-terminal domains
26	<a href="#">c2ma1A</a>	Alignment	not modelled	9.4	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna helicase recq; <b>PDBTitle:</b> solution structure of hrdc1 domain of recq helicase from deinococcus2 radiodurans
27	<a href="#">c2yonA</a>	Alignment	not modelled	9.2	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sensory box protein; <b>PDBTitle:</b> solution nmr structure of the c-terminal extension of two bacterial2 light, oxygen, voltage (lov) photoreceptor proteins from3 pseudomonas putida
28	<a href="#">d3clsc1</a>	Alignment	not modelled	9.1	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like

						<b>Family:</b> ETFP subunits
29	<a href="#">d1wuda1</a>	Alignment	not modelled	9.0	11	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> HRDC-like <b>Family:</b> HRDC domain from helicases
30	<a href="#">d2hbka1</a>	Alignment	not modelled	8.8	24	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> HRDC-like <b>Family:</b> EXOSC10 HRDC domain-like
31	<a href="#">c6igz4</a>	Alignment	not modelled	8.6	30	<b>PDB header:</b> plant protein <b>Chain:</b> 4: <b>PDB Molecule:</b> lhca-b; <b>PDBTitle:</b> structure of psi-lhci
32	<a href="#">d7reqb2</a>	Alignment	not modelled	8.5	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
33	<a href="#">c6igz2</a>	Alignment	not modelled	8.3	26	<b>PDB header:</b> plant protein <b>Chain:</b> 2: <b>PDB Molecule:</b> lhca-c; <b>PDBTitle:</b> structure of psi-lhci
34	<a href="#">d1n62b2</a>	Alignment	not modelled	8.1	16	<b>Fold:</b> Molybdenum cofactor-binding domain <b>Superfamily:</b> Molybdenum cofactor-binding domain <b>Family:</b> Molybdenum cofactor-binding domain
35	<a href="#">d1t3qb2</a>	Alignment	not modelled	7.9	24	<b>Fold:</b> Molybdenum cofactor-binding domain <b>Superfamily:</b> Molybdenum cofactor-binding domain <b>Family:</b> Molybdenum cofactor-binding domain
36	<a href="#">d1vm6a2</a>	Alignment	not modelled	7.9	21	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
37	<a href="#">c2z8nB</a>	Alignment	not modelled	7.8	21	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 27.5 kda virulence protein; <b>PDBTitle:</b> structural basis for the catalytic mechanism of phosphothreonine lyase
38	<a href="#">c5f2yF</a>	Alignment	not modelled	7.8	18	<b>PDB header:</b> de novo protein <b>Chain:</b> F: <b>PDB Molecule:</b> ccc-hept-hcys-h-e; <b>PDBTitle:</b> a de novo designed heptameric coiled coil cc-hept-homocys-h-e
39	<a href="#">c5f2yB</a>	Alignment	not modelled	7.7	18	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> ccc-hept-hcys-h-e; <b>PDBTitle:</b> a de novo designed heptameric coiled coil cc-hept-homocys-h-e
40	<a href="#">c6nt5B</a>	Alignment	not modelled	7.6	29	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> stimulator of interferon protein; <b>PDBTitle:</b> cryo-em structure of full-length human sting in the apo state
41	<a href="#">d1vlba4</a>	Alignment	not modelled	7.6	16	<b>Fold:</b> Molybdenum cofactor-binding domain <b>Superfamily:</b> Molybdenum cofactor-binding domain <b>Family:</b> Molybdenum cofactor-binding domain
42	<a href="#">c1t3qB</a>	Alignment	not modelled	7.6	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> quinoline 2-oxidoreductase large subunit; <b>PDBTitle:</b> crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
43	<a href="#">c1vm6B</a>	Alignment	not modelled	7.5	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate reductase (tm1520) from2 thermotoga maritima at 2.27 a resolution
44	<a href="#">c4lvpP</a>	Alignment	not modelled	7.4	31	<b>PDB header:</b> hydrolase/inhibitor/immune system <b>Chain:</b> P: <b>PDB Molecule:</b> subtilisin-like serine protease; <b>PDBTitle:</b> crystal structure of psub1-prodomain-nimp.m7 fab complex
45	<a href="#">d1e8ya2</a>	Alignment	not modelled	7.3	10	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
46	<a href="#">c5ezeB</a>	Alignment	not modelled	7.3	21	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> ccc-hept-bmcys-his-glu; <b>PDBTitle:</b> a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e
47	<a href="#">d1u9pa1</a>	Alignment	not modelled	7.2	32	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
48	<a href="#">c4v1ag</a>	Alignment	not modelled	7.2	9	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 22 of 2
49	<a href="#">d1qbjc</a>	Alignment	not modelled	7.1	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Z-DNA binding domain
50	<a href="#">c2jsxA</a>	Alignment	not modelled	7.0	18	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> protein napd; <b>PDBTitle:</b> solution structure of the e. coli tat proofreading2 chaperone protein napd
51	<a href="#">c3kjlL</a>	Alignment	not modelled	7.0	19	<b>PDB header:</b> unknown function <b>Chain:</b> L: <b>PDB Molecule:</b> nmb1025 protein; <b>PDBTitle:</b> crystal structure of nmb1025, a member of yjgf protein family, from2 neisseria meningitidis (hexagonal crystal form)
52	<a href="#">c3clrD</a>	Alignment	not modelled	6.9	17	<b>PDB header:</b> electron transport <b>Chain:</b> D: <b>PDB Molecule:</b> electron transfer flavoprotein subunit alpha; <b>PDBTitle:</b> crystal structure of the r236a etf mutant from m. methylotrophus
53	<a href="#">d1qu9a</a>	Alignment	not modelled	6.9	13	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> Yjgf-like <b>Family:</b> Yjgf/L-PSP
54	<a href="#">c6igz9</a>	Alignment	not modelled	6.8	19	<b>PDB header:</b> plant protein <b>Chain:</b> 9: <b>PDB Molecule:</b> lhca-i; <b>PDBTitle:</b> structure of psi-lhci

55	<a href="#">c5f2yE</a>	Alignment	not modelled	6.7	21	<b>PDB header:</b> de novo protein <b>Chain:</b> E; <b>PDB Molecule:</b> cc-hept-hcys-h-e; <b>PDBTitle:</b> a de novo designed heptameric coiled coil cc-hept-homocys-h-e
56	<a href="#">c5ezeC</a>	Alignment	not modelled	6.7	21	<b>PDB header:</b> de novo protein <b>Chain:</b> C; <b>PDB Molecule:</b> cc-hept-bmecys-his-glu; <b>PDBTitle:</b> a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e
57	<a href="#">c5ezeE</a>	Alignment	not modelled	6.7	21	<b>PDB header:</b> de novo protein <b>Chain:</b> E; <b>PDB Molecule:</b> cc-hept-bmecys-his-glu; <b>PDBTitle:</b> a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e
58	<a href="#">d1vr8a1</a>	Alignment	not modelled	6.7	18	<b>Fold:</b> TM1622-like <b>Superfamily:</b> TM1622-like <b>Family:</b> TM1622-like
59	<a href="#">c3lf9A</a>	Alignment	not modelled	6.6	21	<b>PDB header:</b> immune system <b>Chain:</b> A; <b>PDB Molecule:</b> 4e10_d0_1is1a_001_c (t161); <b>PDBTitle:</b> crystal structure of hiv epitope-scaffold 4e10_d0_1is1a_001_c
60	<a href="#">c5f2yG</a>	Alignment	not modelled	6.5	21	<b>PDB header:</b> de novo protein <b>Chain:</b> G; <b>PDB Molecule:</b> cc-hept-hcys-h-e; <b>PDBTitle:</b> a de novo designed heptameric coiled coil cc-hept-homocys-h-e
61	<a href="#">c5ezeA</a>	Alignment	not modelled	6.5	21	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> cc-hept-bmecys-his-glu; <b>PDBTitle:</b> a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e
62	<a href="#">c5ezeF</a>	Alignment	not modelled	6.5	21	<b>PDB header:</b> de novo protein <b>Chain:</b> F; <b>PDB Molecule:</b> cc-hept-bmecys-his-glu; <b>PDBTitle:</b> a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e
63	<a href="#">c5f2yA</a>	Alignment	not modelled	6.5	21	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> cc-hept-hcys-h-e; <b>PDBTitle:</b> a de novo designed heptameric coiled coil cc-hept-homocys-h-e
64	<a href="#">d1qgpa</a>	Alignment	not modelled	6.5	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Z-DNA binding domain
65	<a href="#">c3gtzA</a>	Alignment	not modelled	6.4	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative translation initiation inhibitor; <b>PDBTitle:</b> crystal structure of a putative translation initiation inhibitor from2 salmonella typhimurium
66	<a href="#">c1vw44</a>	Alignment	not modelled	6.3	22	<b>PDB header:</b> ribosome <b>Chain:</b> 4; <b>PDB Molecule:</b> 54s ribosomal protein l51, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
67	<a href="#">d2g64a1</a>	Alignment	not modelled	6.2	10	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> 6-pyruvoyl tetrahydropterin synthase
68	<a href="#">c6igz6</a>	Alignment	not modelled	6.0	26	<b>PDB header:</b> plant protein <b>Chain:</b> 6; <b>PDB Molecule:</b> lhca-g; <b>PDBTitle:</b> structure of psi-lhci
69	<a href="#">c5ezeG</a>	Alignment	not modelled	6.0	21	<b>PDB header:</b> de novo protein <b>Chain:</b> G; <b>PDB Molecule:</b> cc-hept-bmecys-his-glu; <b>PDBTitle:</b> a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e
70	<a href="#">c6ijo9</a>	Alignment	not modelled	6.0	26	<b>PDB header:</b> photosynthesis <b>Chain:</b> 9; <b>PDB Molecule:</b> lhca9; <b>PDBTitle:</b> photosystem i of chlamydomonas reinhardtii
71	<a href="#">d2gxba1</a>	Alignment	not modelled	6.0	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Z-DNA binding domain
72	<a href="#">c5f2yC</a>	Alignment	not modelled	5.9	18	<b>PDB header:</b> de novo protein <b>Chain:</b> C; <b>PDB Molecule:</b> cc-hept-hcys-h-e; <b>PDBTitle:</b> a de novo designed heptameric coiled coil cc-hept-homocys-h-e
73	<a href="#">d1rrqa1</a>	Alignment	not modelled	5.9	18	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
74	<a href="#">c3e0zB</a>	Alignment	not modelled	5.8	13	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> protein of unknown function; <b>PDBTitle:</b> crystal structure of a putative imidazole glycerol phosphate synthase2 homolog (eubrec_1070) from eubacterium rectale at 1.75 a resolution
75	<a href="#">d1myka</a>	Alignment	not modelled	5.7	32	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
76	<a href="#">c5f2yD</a>	Alignment	not modelled	5.7	21	<b>PDB header:</b> de novo protein <b>Chain:</b> D; <b>PDB Molecule:</b> cc-hept-hcys-h-e; <b>PDBTitle:</b> a de novo designed heptameric coiled coil cc-hept-homocys-h-e
77	<a href="#">d2ex3b1</a>	Alignment	not modelled	5.7	32	<b>Fold:</b> DNA terminal protein <b>Superfamily:</b> DNA terminal protein <b>Family:</b> DNA terminal protein
78	<a href="#">d1efvb</a>	Alignment	not modelled	5.6	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
79	<a href="#">d1baza</a>	Alignment	not modelled	5.5	32	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
80	<a href="#">c6igz0</a>	Alignment	not modelled	5.5	15	<b>PDB header:</b> plant protein <b>Chain:</b> 0; <b>PDB Molecule:</b> lhca-j; <b>PDBTitle:</b> structure of psi-lhci
						<b>Fold:</b> C2 domain-like

81	<a href="#">d1e7ua2</a>	Alignment	not modelled	5.4	10	<b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
82	<a href="#">c2ex3B_</a>	Alignment	not modelled	5.4	32	<b>PDB header:</b> transferase/replication <b>Chain:</b> B: <b>PDB Molecule:</b> dna terminal protein; <b>PDBTitle:</b> bacteriophage phi29 dna polymerase bound to terminal protein
83	<a href="#">c2ex3D_</a>	Alignment	not modelled	5.4	32	<b>PDB header:</b> transferase/replication <b>Chain:</b> D: <b>PDB Molecule:</b> dna terminal protein; <b>PDBTitle:</b> bacteriophage phi29 dna polymerase bound to terminal protein
84	<a href="#">c2ex3J_</a>	Alignment	not modelled	5.4	32	<b>PDB header:</b> transferase/replication <b>Chain:</b> J: <b>PDB Molecule:</b> dna terminal protein; <b>PDBTitle:</b> bacteriophage phi29 dna polymerase bound to terminal protein
85	<a href="#">c2ex3F_</a>	Alignment	not modelled	5.4	32	<b>PDB header:</b> transferase/replication <b>Chain:</b> F: <b>PDB Molecule:</b> dna terminal protein; <b>PDBTitle:</b> bacteriophage phi29 dna polymerase bound to terminal protein
86	<a href="#">c2ex3L_</a>	Alignment	not modelled	5.4	32	<b>PDB header:</b> transferase/replication <b>Chain:</b> L: <b>PDB Molecule:</b> dna terminal protein; <b>PDBTitle:</b> bacteriophage phi29 dna polymerase bound to terminal protein
87	<a href="#">c2ex3H_</a>	Alignment	not modelled	5.4	32	<b>PDB header:</b> transferase/replication <b>Chain:</b> H: <b>PDB Molecule:</b> dna terminal protein; <b>PDBTitle:</b> bacteriophage phi29 dna polymerase bound to terminal protein
88	<a href="#">d2e1fa1</a>	Alignment	not modelled	5.4	15	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> HRDC-like <b>Family:</b> HRDC domain from helicases
89	<a href="#">c1sb3D_</a>	Alignment	not modelled	5.4	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 4-hydroxybenzoyl-coa reductase alpha subunit; <b>PDBTitle:</b> structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
90	<a href="#">c5ezeD_</a>	Alignment	not modelled	5.3	21	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> cc-hept-bmecys-his-glu; <b>PDBTitle:</b> a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e
91	<a href="#">c2y3yC_</a>	Alignment	not modelled	5.2	8	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> putative nickel-responsive regulator; <b>PDBTitle:</b> holo-ni(ii) hpnikr is a symmetric tetramer containing four canonic2 square-planar ni(ii) ions at physiological ph
92	<a href="#">c3m8yC_</a>	Alignment	not modelled	5.1	16	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphopentomutase; <b>PDBTitle:</b> phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
93	<a href="#">c2bh8B_</a>	Alignment	not modelled	5.1	25	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> 1b11; <b>PDBTitle:</b> combinatorial protein 1b11
94	<a href="#">d1v97a5</a>	Alignment	not modelled	5.0	15	<b>Fold:</b> Molybdenum cofactor-binding domain <b>Superfamily:</b> Molybdenum cofactor-binding domain <b>Family:</b> Molybdenum cofactor-binding domain
95	<a href="#">c3zikA_</a>	Alignment	not modelled	5.0	14	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> wpl1; <b>PDBTitle:</b> structure of the wpl1 protein
96	<a href="#">c5y6qC_</a>	Alignment	not modelled	5.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> aldehyde oxidase large subunit; <b>PDBTitle:</b> crystal structure of an aldehyde oxidase from methylobacillus sp.2 ky4400