







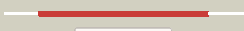















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2549c_(-)_2869737_2870132
Date	Wed Aug 7 12:50:18 BST 2019
Unique Job ID	07ff7aaa0849e412

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5wzfB_</a>	 Alignment		100.0	92	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 23s rrna-specific endonuclease vapc20; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis vapc20 (rv2549c),2 sarcin-ricin loop cleaving toxin
2	<a href="#">d1w8ia_</a>	 Alignment		99.9	23	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
3	<a href="#">c5x3tD_</a>	 Alignment		99.9	20	<b>PDB header:</b> antitoxin/toxin <b>Chain:</b> D: <b>PDB Molecule:</b> ribonuclease vapc26; <b>PDBTitle:</b> vapbc from mycobacterium tuberculosis
4	<a href="#">c4xgrG_</a>	 Alignment		99.9	16	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> G: <b>PDB Molecule:</b> ribonuclease vapc30; <b>PDBTitle:</b> crystal structure of addition module from mycobacterial species
5	<a href="#">d2h1ca1</a>	 Alignment		99.8	14	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
6	<a href="#">c3zvkc_</a>	 Alignment		99.7	11	<b>PDB header:</b> antitoxin/toxin/dna <b>Chain:</b> C: <b>PDB Molecule:</b> toxin of toxin-antitoxin system; <b>PDBTitle:</b> crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
7	<a href="#">c5l6mC_</a>	 Alignment		99.7	12	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ribonuclease vapc; <b>PDBTitle:</b> structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
8	<a href="#">c6a7vG_</a>	 Alignment		99.7	17	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> G: <b>PDB Molecule:</b> ribonuclease vapc11; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
9	<a href="#">c6nklA_</a>	 Alignment		99.7	10	<b>PDB header:</b> antitoxin <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease vapc; <b>PDBTitle:</b> 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
10	<a href="#">c3tndC_</a>	 Alignment		99.6	13	<b>PDB header:</b> translation, toxin <b>Chain:</b> C: <b>PDB Molecule:</b> trna(fmet)-specific endonuclease vapc; <b>PDBTitle:</b> crystal structure of shigella flexneri vapbc toxin-antitoxin complex
11	<a href="#">d2fe1a1</a>	 Alignment		99.5	21	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain

12	<a href="#">c2fe1A_</a>	Alignment		99.5	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein pae0151; <b>PDBTitle:</b> crystal structure of pae0151 from pyrobaculum aerophilum
13	<a href="#">c3h87B_</a>	Alignment		99.5	19	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
14	<a href="#">d1v96a1</a>	Alignment		99.5	11	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
15	<a href="#">c4chgC_</a>	Alignment		99.5	15	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> C: <b>PDB Molecule:</b> probable ribonuclease vapc15; <b>PDBTitle:</b> crystal structure of vapc15 complex from mycobacterium tuberculosis
16	<a href="#">c3dboB_</a>	Alignment		99.4	20	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a member of the vapbc family of toxin-antitoxin2 systems, vapbc-5, from mycobacterium tuberculosis
17	<a href="#">c5sv2A_</a>	Alignment		99.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease vapc21; <b>PDBTitle:</b> toxin vapc21 from mycobacterium tuberculosis
18	<a href="#">d1y82a1</a>	Alignment		99.4	9	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
19	<a href="#">d1v8pa_</a>	Alignment		98.7	20	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
20	<a href="#">c1v8pK_</a>	Alignment		98.6	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> K: <b>PDB Molecule:</b> hypothetical protein pae2754; <b>PDBTitle:</b> crystal structure of pae2754 from pyrobaculum aerophilum
21	<a href="#">c3ix7A_</a>	Alignment	not modelled	97.6	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ttha0540; <b>PDBTitle:</b> crystal structure of a domain of functionally unknown protein from2 thermus thermophilus hb8
22	<a href="#">d1o4wa_</a>	Alignment	not modelled	97.6	16	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
23	<a href="#">c3i8oA_</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> kh domain-containing protein mj1533; <b>PDBTitle:</b> a domain of a functionally unknown protein from methanocaldococcus2 jannaschii dsm 2661.
24	<a href="#">c2lcqA_</a>	Alignment	not modelled	96.8	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative toxin vapc6; <b>PDBTitle:</b> solution structure of the endonuclease nob1 from p.horikoshii
25	<a href="#">c5yz4A_</a>	Alignment	not modelled	95.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rrna-processing protein fcf1; <b>PDBTitle:</b> structure of the pin domain endonuclease utp24
26	<a href="#">c5jpd_</a>	Alignment	not modelled	95.6	19	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> wd40 domain proteins; <b>PDBTitle:</b> cryo-em structure of the 90s pre-ribosome
27	<a href="#">c5ywwA_</a>	Alignment	not modelled	95.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotide binding protein pinc; <b>PDBTitle:</b> archael ruvb-like holiday junction helicase
28	<a href="#">c2hwwC_</a>	Alignment	not modelled	95.3	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> telomerase-binding protein est1a; <b>PDBTitle:</b> structure of pin domain of human smg6
						<b>PDB header:</b> hydrolase

29	<a href="#">c5f4hF_</a>	Alignment	not modelled	95.2	17	<b>Chain:</b> F; <b>PDB Molecule:</b> nucleotide binding protein pinc; <b>PDBTitle:</b> archaeal ruvb-like holiday junction helicase
30	<a href="#">c2hwyB_</a>	Alignment	not modelled	90.2	13	<b>PDB header:</b> rna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> protein smg5; <b>PDBTitle:</b> structure of pin domain of human smg5.
31	<a href="#">c4mj7B_</a>	Alignment	not modelled	82.0	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> rrna-processing protein utp23; <b>PDBTitle:</b> crystal structure of the pin domain of saccharomyces cerevisiae utp23
32	<a href="#">c6g5iy_</a>	Alignment	not modelled	79.6	16	<b>PDB header:</b> ribosome <b>Chain:</b> Y; <b>PDB Molecule:</b> 40s ribosomal protein s24; <b>PDBTitle:</b> cryo-em structure of a late human pre-40s ribosomal subunit - state r
33	<a href="#">d1a77a2</a>	Alignment	not modelled	72.4	19	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
34	<a href="#">c1ul1Y_</a>	Alignment	not modelled	71.4	11	<b>PDB header:</b> hydrolase/dna binding protein <b>Chain:</b> Y; <b>PDB Molecule:</b> flap endonuclease-1; <b>PDBTitle:</b> crystal structure of the human fen1-pcna complex
35	<a href="#">d1ul1x2</a>	Alignment	not modelled	65.1	19	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
36	<a href="#">d1rxwa2</a>	Alignment	not modelled	57.9	16	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
37	<a href="#">c3q8lA_</a>	Alignment	not modelled	55.8	19	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> flap endonuclease 1; <b>PDBTitle:</b> crystal structure of human flap endonuclease fen1 (wt) in complex with2 substrate 5'-flap dna, sm3+, and k+
38	<a href="#">c1a77A_</a>	Alignment	not modelled	55.6	19	<b>PDB header:</b> 5'-3' exo/endo nuclease <b>Chain:</b> A; <b>PDB Molecule:</b> flap endonuclease-1 protein; <b>PDBTitle:</b> flap endonuclease-1 from methanococcus jannaschii
39	<a href="#">c2izoA_</a>	Alignment	not modelled	53.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> flap structure-specific endonuclease; <b>PDBTitle:</b> structure of an archaeal pcna1-pcna2-fen1 complex
40	<a href="#">c1b43A_</a>	Alignment	not modelled	51.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> protein (fen-1); <b>PDBTitle:</b> fen-1 from p. furiosus
41	<a href="#">d1mc8a2</a>	Alignment	not modelled	51.6	16	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
42	<a href="#">c3v32B_</a>	Alignment	not modelled	49.0	8	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> ribonuclease zc3h12a; <b>PDBTitle:</b> crystal structure of mcpip1 n-terminal conserved domain
43	<a href="#">c1rxvA_</a>	Alignment	not modelled	48.0	16	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> flap structure-specific endonuclease; <b>PDBTitle:</b> crystal structure of a. fulgidus fen-1 bound to dna
44	<a href="#">c3v33A_</a>	Alignment	not modelled	47.7	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> ribonuclease zc3h12a; <b>PDBTitle:</b> crystal structure of mcpip1 conserved domain with zinc-finger motif
45	<a href="#">c3qeaZ_</a>	Alignment	not modelled	44.5	25	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> Z; <b>PDB Molecule:</b> exonuclease 1; <b>PDBTitle:</b> crystal structure of human exonuclease 1 exo1 (wt) in complex with dna2 (complex ii)
46	<a href="#">c5t9jB_</a>	Alignment	not modelled	44.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> flap endonuclease gen homolog 1; <b>PDBTitle:</b> crystal structure of human gen1 in complex with holliday junction dna2 in the upper interface
47	<a href="#">c3zddA_</a>	Alignment	not modelled	44.3	11	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> protein xni; <b>PDBTitle:</b> structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium
48	<a href="#">d1b43a2</a>	Alignment	not modelled	42.7	16	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
49	<a href="#">d1zcca2</a>	Alignment	not modelled	40.8	23	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
50	<a href="#">c3oryA_</a>	Alignment	not modelled	40.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> flap endonuclease 1; <b>PDBTitle:</b> crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus
51	<a href="#">c1thzA_</a>	Alignment	not modelled	40.1	16	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> crystal structure of avian aicar transformylase in complex2 with a novel inhibitor identified by virtual ligand3 screening
52	<a href="#">d1pkxa2</a>	Alignment	not modelled	39.8	19	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
53	<a href="#">d1cmwa2</a>	Alignment	not modelled	39.2	15	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
54	<a href="#">d1g8ma2</a>	Alignment	not modelled	39.1	16	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
						<b>PDB header:</b> transferase/hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh;

55	<a href="#">c1zcza_</a>	Alignment	not modelled	36.5	23	<b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazolecarboxamide2 formyltransferase / imp cyclohydrolase (tm1249) from thermotoga3 maritima at 1.88 a resolution
56	<a href="#">c4ehiB_</a>	Alignment	not modelled	31.9	16	<b>PDB header:</b> hydrolase,transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> an x-ray crystal structure of a putative bifunctional2 phosphoribosylaminoimidazolecarboxamide formyltransferase/imp3 cyclohydrolase
57	<a href="#">c4a1oB_</a>	Alignment	not modelled	30.6	16	<b>PDB header:</b> transferase-hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
58	<a href="#">c1ut8B_</a>	Alignment	not modelled	26.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> exodeoxyribonuclease; <b>PDBTitle:</b> divalent metal ions (zinc) bound to t5 5'-exonuclease
59	<a href="#">c4q0rB_</a>	Alignment	not modelled	21.3	13	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair protein rad2; <b>PDBTitle:</b> the catalytic core of rad2 (complex i)
60	<a href="#">d1tfra2</a>	Alignment	not modelled	19.7	23	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
61	<a href="#">c4wa8A_</a>	Alignment	not modelled	16.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flap endonuclease 1; <b>PDBTitle:</b> methanopyrus kandleri fen-1 nuclease
62	<a href="#">c6c34A_</a>	Alignment	not modelled	15.8	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> 5'-3' exonuclease; <b>PDBTitle:</b> mycobacterium smegmatis dna flap endonuclease mutant d125n
63	<a href="#">d1s1da_</a>	Alignment	not modelled	13.8	19	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Apyrase <b>Family:</b> Apyrase
64	<a href="#">c3e0ka_</a>	Alignment	not modelled	10.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> amino-acid acetyltransferase; <b>PDBTitle:</b> crystal structure of c-termianl domain of n-acetylglutamate synthase2 from vibrio parahaemolyticus
65	<a href="#">d3claa_</a>	Alignment	not modelled	8.5	12	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
66	<a href="#">c4gx9A_</a>	Alignment	not modelled	8.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit epsilon,dna polymerase iii <b>PDBTitle:</b> crystal structure of a dna polymerase iii alpha-epsilon chimera
67	<a href="#">d1u9ya1</a>	Alignment	not modelled	8.0	5	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
68	<a href="#">d1oy0a_</a>	Alignment	not modelled	7.8	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Ketopantoate hydroxymethyltransferase PanB
69	<a href="#">d1xo1a2</a>	Alignment	not modelled	7.4	13	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
70	<a href="#">c1qdul_</a>	Alignment	not modelled	7.2	19	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> I: <b>PDB Molecule:</b> caspase-8 alpha-chain; <b>PDBTitle:</b> crystal structure of the complex of caspase-8 with the tripeptide2 ketone inhibitor zevd-dcbmk
71	<a href="#">c3p45l_</a>	Alignment	not modelled	7.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> caspase-6; <b>PDBTitle:</b> crystal structure of apo-caspase-6 at physiological ph
72	<a href="#">d1m3ua_</a>	Alignment	not modelled	6.8	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Ketopantoate hydroxymethyltransferase PanB
73	<a href="#">c3wq4A_</a>	Alignment	not modelled	6.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-primeverosidase; <b>PDBTitle:</b> crystal structure of beta-primeverosidase
74	<a href="#">c3gnoA_</a>	Alignment	not modelled	6.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> os03g0212800 protein; <b>PDBTitle:</b> crystal structure of a rice os3bglu6 beta-glucosidase
75	<a href="#">c3sipC_</a>	Alignment	not modelled	6.1	12	<b>PDB header:</b> hydrolase/ligase/hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> caspase; <b>PDBTitle:</b> crystal structure of drice and diap1-bir1 complex
76	<a href="#">c2i9dC_</a>	Alignment	not modelled	6.1	26	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> chloramphenicol acetyltransferase; <b>PDBTitle:</b> chloramphenicol acetyltransferase
77	<a href="#">c3edqC_</a>	Alignment	not modelled	6.1	9	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> caspase-3; <b>PDBTitle:</b> crystal structure of caspase-3 with inhibitor ac-ldesd-cho
78	<a href="#">d1z4ra1</a>	Alignment	not modelled	5.9	19	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
79	<a href="#">d1tueb_</a>	Alignment	not modelled	5.8	27	<b>Fold:</b> E2 regulatory, transactivation domain <b>Superfamily:</b> E2 regulatory, transactivation domain <b>Family:</b> E2 regulatory, transactivation domain
80	<a href="#">c4ixoB_</a>	Alignment	not modelled	5.8	32	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> nifs-like protein; <b>PDBTitle:</b> x-ray structure of nifs-like protein from rickettsia africae

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81	<a href="#">c4a5uA_</a>	Alignment	not modelled	5.8	14 <b>PDB header:</b> transferase/rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna replicase polyprotein; <b>PDBTitle:</b> turnip yellow mosaic virus proteinase and escherichia coli 30s2 ribosomal s15
82	<a href="#">c3ez4B_</a>	Alignment	not modelled	5.7	18 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-methyl-2-oxobutanoate hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of 3-methyl-2-oxobutanoate hydroxymethyltransferase2 from burkholderia pseudomallei
83	<a href="#">c5ygeA_</a>	Alignment	not modelled	5.7	23 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> amino-acid acetyltransferase; <b>PDBTitle:</b> arga complexed with acecoa and glutamate
84	<a href="#">d2nnua1</a>	Alignment	not modelled	5.6	14 <b>Fold:</b> E2 regulatory, transactivation domain <b>Superfamily:</b> E2 regulatory, transactivation domain <b>Family:</b> E2 regulatory, transactivation domain
85	<a href="#">c1tueG_</a>	Alignment	not modelled	5.3	27 <b>PDB header:</b> replication <b>Chain:</b> G: <b>PDB Molecule:</b> regulatory protein e2; <b>PDBTitle:</b> the x-ray structure of the papillomavirus helicase in2 complex with its molecular matchmaker e2
86	<a href="#">d3pmga2</a>	Alignment	not modelled	5.3	23 <b>Fold:</b> Phosphoglucomutase, first 3 domains <b>Superfamily:</b> Phosphoglucomutase, first 3 domains <b>Family:</b> Phosphoglucomutase, first 3 domains
87	<a href="#">c5cnqA_</a>	Alignment	not modelled	5.2	13 <b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> nuclease-like protein; <b>PDBTitle:</b> crystal structure of the holliday junction-resolving enzyme gen1 (wt)2 in complex with product dna, mg2+ and mn2+ ions
88	<a href="#">c2jeuA_</a>	Alignment	not modelled	5.1	32 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein e2; <b>PDBTitle:</b> transcription activator structure reveals redox control of a2 replication initiation reaction
89	<a href="#">c5jboA_</a>	Alignment	not modelled	5.1	17 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> trichoderma harzianum gh1 beta-glucosidase thbg12