

# Phyre2

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Description	RVBD3581c_ (ispF)_4024047_4024526
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3f0gA_</a>	Alignment		100.0	41	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; <b>PDBTitle:</b> co-crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase with cmp
2	<a href="#">c2pmpA_</a>	Alignment		100.0	37	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; <b>PDBTitle:</b> structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate synthase from2 the isoprenoid biosynthetic pathway of arabidopsis thaliana
3	<a href="#">d1gx1a_</a>	Alignment		100.0	42	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> !psF-like <b>Family:</b> !psF-like
4	<a href="#">d1t0aa_</a>	Alignment		100.0	41	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> !psF-like <b>Family:</b> !psF-like
5	<a href="#">c1w57A_</a>	Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ispd/ispf bifunctional enzyme; <b>PDBTitle:</b> structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
6	<a href="#">d1w55a2</a>	Alignment		100.0	32	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> !psF-like <b>Family:</b> !psF-like
7	<a href="#">c2uzhB_</a>	Alignment		100.0	75	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2c-methyl-d-erythritol 2,4-cyclodiphosphate <b>PDBTitle:</b> mycobacterium smegmatis 2c-methyl-d-erythritol-2,4-2 cyclodiphosphate synthase (ispf)
8	<a href="#">d1iv3a_</a>	Alignment		100.0	43	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> !psF-like <b>Family:</b> !psF-like
9	<a href="#">d1vh8a_</a>	Alignment		100.0	42	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> !psF-like <b>Family:</b> !psF-like
10	<a href="#">c5iwvD_</a>	Alignment		100.0	41	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; <b>PDBTitle:</b> crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from bacillus subtilis complexed with cmp and mg2+
11	<a href="#">c4c82A_</a>	Alignment		100.0	33	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; <b>PDBTitle:</b> ispf (plasmodium falciparum) unliganded structure

12	<a href="#">c3re3B_</a>	Alignment		100.0	36	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; <b>PDBTitle:</b> crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from francisella tularensis
13	<a href="#">c3b6nA_</a>	Alignment		100.0	31	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; <b>PDBTitle:</b> crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase pv003920 from plasmodium vivax
14	<a href="#">c5eszG_</a>	Alignment		100.0	32	<b>PDB header:</b> immune system <b>Chain:</b> G: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase, <b>PDBTitle:</b> crystal structure of broadly neutralizing antibody ch04, isolated from2 donor ch0219, in complex with scaffolded trimeric hiv-1 env v1v23 domain from the clade ae strain a244
15	<a href="#">c3nbmA_</a>	Alignment		45.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pts system, lactose-specific iibc components; <b>PDBTitle:</b> the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
16	<a href="#">c6epzA_</a>	Alignment		40.6	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic alpha-galactoside-binding protein; <b>PDBTitle:</b> structure of the periplasmic binding protein melb (atu4661) in complex2 with melibiose from agrobacterium fabrum c58
17	<a href="#">c6i3gA_</a>	Alignment		40.2	9	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, substrate-binding protein, family 5; <b>PDBTitle:</b> crystal structure of a putative peptide binding protein appa from2 clostridium difficile
18	<a href="#">c1w25B_</a>	Alignment		38.1	11	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> stalked-cell differentiation controlling protein; <b>PDBTitle:</b> response regulator pled in complex with c-digmp
19	<a href="#">c4onyB_</a>	Alignment		35.5	21	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> extracellular solute-binding protein family 5; <b>PDBTitle:</b> crystal structure of a abc transporter, periplasmic substrate-binding2 protein from brucella melitensis
20	<a href="#">d1r57a_</a>	Alignment		35.4	18	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
21	<a href="#">c4mgeB_</a>	Alignment	not modelled	34.9	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pts system, cellobiose-specific iib component; <b>PDBTitle:</b> 1.85 angstrom resolution crystal structure of pts system cellobiose-2 specific transporter subunit iib from bacillus anthracis.
22	<a href="#">c6hlxA_</a>	Alignment	not modelled	32.6	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> agaa; <b>PDBTitle:</b> structure of the pbp agaa in complex with agropinic acid from2 a.tumefacien r10
23	<a href="#">c3bbIA_</a>	Alignment	not modelled	31.8	19	<b>PDB header:</b> regulatory protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein of lacI family; <b>PDBTitle:</b> crystal structure of a regulatory protein of lacI family from2 chloroflexus aggregans
24	<a href="#">d2cc0a1</a>	Alignment	not modelled	28.5	9	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> NodB-like polysaccharide deacetylase
25	<a href="#">c4f54A_</a>	Alignment	not modelled	27.6	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf4136 family protein (bt2437) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution
26	<a href="#">c2l2qA_</a>	Alignment	not modelled	27.5	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pts system, cellobiose-specific iib component (cela); <b>PDBTitle:</b> solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
27	<a href="#">c5k9nB_</a>	Alignment	not modelled	26.8	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> polyamine n acetyltransferase; <b>PDBTitle:</b> structural and mechanistic analysis of drosophila melanogaster2 polyamine n acetyltransferase, an enzyme that catalyzes the formation3 of n acetylglmatine
28	<a href="#">d1s5ja2</a>	Alignment	not modelled	26.4	10	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases

						Family:DNA polymerase I
29	<a href="#">c5u4oA</a>	Alignment	not modelled	25.4	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter substrate-binding protein; <b>PDBTitle:</b> a 2.05a x-ray structure of a bacterial extracellular solute-binding2 protein, family 5 for bacillus anthracis str. ames
30	<a href="#">c5nocA</a>	Alignment	not modelled	24.9	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> stage 0 sporulation protein j; <b>PDBTitle:</b> solution nmr structure of the c-terminal domain of parb (spo0j)
31	<a href="#">c2mdpA</a>	Alignment	not modelled	24.5	33	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gene 1.2 protein; <b>PDBTitle:</b> the bacteriophage t7 encoded inhibitor (gp1.2) of e. coli dgtp2 triphosphohydrolase
32	<a href="#">c6dyrA</a>	Alignment	not modelled	24.0	6	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> ebony; <b>PDBTitle:</b> c-terminal condensation domain of ebony in complex with carcinine
33	<a href="#">c4fd5A</a>	Alignment	not modelled	23.4	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arylalkylamine n-acetyltransferase 2; <b>PDBTitle:</b> crystal structure of arylalkylamine n-acetyltransferase 2 from aedes2 aegypti
34	<a href="#">c5a29A</a>	Alignment	not modelled	21.2	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> exopolygalacturonate lyase; <b>PDBTitle:</b> family 2 pectate lyase from vibrio vulnificus
35	<a href="#">d1iiba</a>	Alignment	not modelled	21.0	35	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> PTS system IIB component-like <b>Family:</b> PTS system, Lactose/Cellobiose specific IIB subunit
36	<a href="#">c4l1gB</a>	Alignment	not modelled	19.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidoglycan n-acetylglucosamine deacetylase; <b>PDBTitle:</b> crystal structure of the bc1960 peptidoglycan n-acetylglucosamine2 deacetylase from bacillus cereus
37	<a href="#">c4ij9A</a>	Alignment	not modelled	19.8	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-carboxymethyl-2-hydroxyuconate delta-isomerase; <b>PDBTitle:</b> crystal structure of 5-carboxymethyl-2-hydroxyuconate delta-isomerase
38	<a href="#">c3te4A</a>	Alignment	not modelled	19.4	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dopamine n acetyltransferase, isoform a; <b>PDBTitle:</b> crystal structure of dopamine n acetyltransferase in complex with2 acetyl-coa from drosophila melanogaster
39	<a href="#">c4m1bA</a>	Alignment	not modelled	19.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> polysaccharide deacetylase; <b>PDBTitle:</b> structural determination of ba0150, a polysaccharide deacetylase from2 bacillus anthracis
40	<a href="#">d1h4ra2</a>	Alignment	not modelled	19.3	32	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Third domain of FERM
41	<a href="#">c5icqA</a>	Alignment	not modelled	19.1	19	<b>PDB header:</b> periplasmic binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> methylocystis parvus obbp mbne; <b>PDBTitle:</b> methanobactin periplasmic binding protein
42	<a href="#">d1q8ia2</a>	Alignment	not modelled	18.6	19	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> DNA polymerase I
43	<a href="#">c3qb8A</a>	Alignment	not modelled	18.2	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> a654l protein; <b>PDBTitle:</b> paramecium chlorella bursaria virus1 putative orf a654l is a polyamine2 acetyltransferase
44	<a href="#">c5ipwA</a>	Alignment	not modelled	18.1	7	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptide abc transporter, periplasmic oligopeptide- <b>PDBTitle:</b> oligopeptide-binding protein oppa
45	<a href="#">c5i0cA</a>	Alignment	not modelled	18.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yjdj; <b>PDBTitle:</b> crystal structure of predicted acyltransferase yjdj with acyl-coa n-2 acyltransferase domain from escherichia coli str. k-12
46	<a href="#">d1d5aa2</a>	Alignment	not modelled	15.5	11	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> DNA polymerase I
47	<a href="#">c4fd7A</a>	Alignment	not modelled	15.4	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative arylalkylamine n-acetyltransferase 7; <b>PDBTitle:</b> crystal structure of insect putative arylalkylamine n-2 acetyltransferase 7 from the yellow fever mosquito aedes aegypt
48	<a href="#">d1tgoa2</a>	Alignment	not modelled	15.0	12	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> DNA polymerase I
49	<a href="#">d2j13a1</a>	Alignment	not modelled	14.9	17	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> NodB-like polysaccharide deacetylase
50	<a href="#">c1xaxA</a>	Alignment	not modelled	14.5	5	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical upf0054 protein hi0004; <b>PDBTitle:</b> nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
51	<a href="#">d1f0la1</a>	Alignment	not modelled	14.3	29	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Diphtheria toxin, C-terminal domain <b>Family:</b> Diphtheria toxin, C-terminal domain
52	<a href="#">c4fd4B</a>	Alignment	not modelled	14.3	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> arylalkylamine n-acetyltransferase like 5b; <b>PDBTitle:</b> crystal structure of mosquito arylalkylamine n-acetyltransferase like2 5b
53	<a href="#">c6gr8B</a>	Alignment	not modelled	14.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> inner centromere protein; <b>PDBTitle:</b> human aurkc incenp complex bound to brd-7880
						<b>PDB header:</b> transferase

54	<a href="#">c5mdnB_</a>	Alignment	not modelled	13.4	14	<b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase; <b>PDBTitle:</b> structure of the family b dna polymerase from the hyperthermophilic2 archaeon pyrobaculum caldifontis
55	<a href="#">d1qhta2</a>	Alignment	not modelled	13.2	14	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> DNA polymerase I
56	<a href="#">c2vfjA_</a>	Alignment	not modelled	12.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor; <b>PDBTitle:</b> structure of the a20 ovarian tumour (otu) domain
57	<a href="#">d1wn7a2</a>	Alignment	not modelled	12.5	12	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> DNA polymerase I
58	<a href="#">c5gpoB_</a>	Alignment	not modelled	12.3	33	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sensor protein czcs; <b>PDBTitle:</b> the sensor domain structure of the zinc-responsive histidine kinase2 czcs from pseudomonas aeruginosa
59	<a href="#">d2fi0a1</a>	Alignment	not modelled	12.1	21	<b>Fold:</b> SP0561-like <b>Superfamily:</b> SP0561-like <b>Family:</b> SP0561-like
60	<a href="#">c5ncdA_</a>	Alignment	not modelled	12.1	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan n-acetylglucosamine deacetylase; <b>PDBTitle:</b> crystal structure of the polysaccharide deacetylase bc1974 from2 bacillus cereus in complex with (2s)-2-amino-5-3 (diaminomethylideneamino)-n-hydroxypentanamide
61	<a href="#">c4zebA_</a>	Alignment	not modelled	12.1	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, substrate binding protein (agrocinopines a <b>PDBTitle:</b> pbp acca from a. tumefaciens c58 in complex with agrocinopine a
62	<a href="#">d1ny1a_</a>	Alignment	not modelled	11.6	17	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> NodB-like polysaccharide deacetylase
63	<a href="#">d2c1ia1</a>	Alignment	not modelled	11.6	17	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> NodB-like polysaccharide deacetylase
64	<a href="#">c1s5jA_</a>	Alignment	not modelled	11.4	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase i; <b>PDBTitle:</b> insight in dna replication: the crystal structure of dna2 polymerase b1 from the archaeon sulfolobus solfataricus
65	<a href="#">c5ve9C_</a>	Alignment	not modelled	11.3	33	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> microtubule-actin cross-linking factor 1, isoforms 1/2/3/5; <b>PDBTitle:</b> structure of hacf7 ef1-ef2-gar domains
66	<a href="#">c5lqcA_</a>	Alignment	not modelled	10.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> arce4a; <b>PDBTitle:</b> t48 deacetylase with substrate
67	<a href="#">c6e20B_</a>	Alignment	not modelled	10.8	28	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> galectin; <b>PDBTitle:</b> crystal structure of the dario rerio galectin-1-I2
68	<a href="#">c3dkbA_</a>	Alignment	not modelled	10.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor, alpha-induced protein 3; <b>PDBTitle:</b> crystal structure of a20, 2.5 angstrom
69	<a href="#">c5us5B_</a>	Alignment	not modelled	10.6	18	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> upf0297 protein ef_1202; <b>PDBTitle:</b> solution structure of the ireb homodimer
70	<a href="#">c4bopA_</a>	Alignment	not modelled	10.3	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> otu domain-containing protein 1; <b>PDBTitle:</b> structure of otud1 otu domain
71	<a href="#">d1vr5a1</a>	Alignment	not modelled	10.2	10	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
72	<a href="#">c6dx1A_</a>	Alignment	not modelled	9.9	19	<b>PDB header:</b> hydrolase, protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> rna-dependent rna polymerase; <b>PDBTitle:</b> crystal structure of the viral otu domain protease from galyub virus
73	<a href="#">c2bg5C_</a>	Alignment	not modelled	9.6	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoenolpyruvate-protein kinase; <b>PDBTitle:</b> crystal structure of the phosphoenolpyruvate-binding enzyme i-domain2 from the thermoanaerobacter tengcongensis pep: sugar3 phosphotransferase system (pts)
74	<a href="#">c2c7yB_</a>	Alignment	not modelled	9.6	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase 2; <b>PDBTitle:</b> plant enzyme
75	<a href="#">c1w17A_</a>	Alignment	not modelled	9.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable polysaccharide deacetylase pdaa; <b>PDBTitle:</b> structure of bacillus subtilis pdaa, a family 4 carbohydrate esterase.
76	<a href="#">c6dx3B_</a>	Alignment	not modelled	9.1	20	<b>PDB header:</b> hydrolase, protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> rna-dependent rna polymerase; <b>PDBTitle:</b> crystal structure of the viral otu domain protease from taggart virus
77	<a href="#">c3pfyA_</a>	Alignment	not modelled	9.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> otu domain-containing protein 5; <b>PDBTitle:</b> the catalytic domain of human otud5
78	<a href="#">c4bouA_</a>	Alignment	not modelled	8.9	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> otu domain-containing protein 3; <b>PDBTitle:</b> structure of otud3 otu domain
79	<a href="#">c2ohiB_</a>	Alignment	not modelled	8.6	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> type a flavoprotein fpra; <b>PDBTitle:</b> crystal structure of coenzyme f420h2 oxidase (fpra), a

						diiron2 flavoprotein, reduced state
80	<a href="#">c1ztyA_</a>	Alignment	not modelled	8.6	16	<b>PDB header:</b> sugar binding protein, signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chitin oligosaccharide binding protein; <b>PDBTitle:</b> crystal structure of the chitin oligasaccharide binding2 protein
81	<a href="#">d1hlca_</a>	Alignment	not modelled	8.5	22	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Galectin (animal S-lectin)
82	<a href="#">c2grvC_</a>	Alignment	not modelled	8.5	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> lpqw; <b>PDBTitle:</b> crystal structure of lpqw
83	<a href="#">c3iwgB_</a>	Alignment	not modelled	8.3	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyltransferase, gnat family; <b>PDBTitle:</b> acetyltransferase from gnat family from colwellia psychrerythraea.
84	<a href="#">d1otga_</a>	Alignment	not modelled	8.3	16	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> 5-carboxymethyl-2-hydroxyuconate isomerase (CHMI)
85	<a href="#">c3lkzB_</a>	Alignment	not modelled	8.3	19	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> non-structural protein 5; <b>PDBTitle:</b> structural and functional analyses of a conserved hydrophobic pocket2 of flavivirus methyltransferase
86	<a href="#">c3b0vD_</a>	Alignment	not modelled	8.1	22	<b>PDB header:</b> oxidoreductase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> trna-dihydrouridine synthase; <b>PDBTitle:</b> trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
87	<a href="#">d1v5ra1</a>	Alignment	not modelled	7.9	33	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> GAS2 domain-like <b>Family:</b> GAS2 domain
88	<a href="#">d2pw9a1</a>	Alignment	not modelled	7.8	26	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> FdhD/NarQ
89	<a href="#">c4fm4C_</a>	Alignment	not modelled	7.8	24	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> nitrile hydratase alpha subunit; <b>PDBTitle:</b> wild type fe-type nitrile hydratase from comamonas testosteroni ni1
90	<a href="#">c2mm0A_</a>	Alignment	not modelled	7.8	40	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> host-selective toxin protein; <b>PDBTitle:</b> solution structures of active ptr toxb and its inactive homolog2 highlight protein dynamics as a modulator of toxin activity
91	<a href="#">c5jp6A_</a>	Alignment	not modelled	7.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative polysaccharide deacetylase; <b>PDBTitle:</b> bdellovibrio bacteriovorus peptidoglycan deacetylase bd3279
92	<a href="#">c2wuaA_</a>	Alignment	not modelled	7.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetoacetyl coa thiolase; <b>PDBTitle:</b> structure of the peroxisomal 3-ketoacyl-coa thiolase from sunflower
93	<a href="#">d1wf3a2</a>	Alignment	not modelled	7.6	27	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Prokaryotic type KH domain (KH-domain type II) <b>Family:</b> Prokaryotic type KH domain (KH-domain type II)
94	<a href="#">d1is3a_</a>	Alignment	not modelled	7.6	25	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Galectin (animal S-lectin)
95	<a href="#">d1ef1a2</a>	Alignment	not modelled	7.6	28	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Third domain of FERM
96	<a href="#">d1cmca_</a>	Alignment	not modelled	7.5	23	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Met repressor, Metj (MetR)
97	<a href="#">c3huuC_</a>	Alignment	not modelled	7.5	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcription regulator like protein; <b>PDBTitle:</b> crystal structure of transcription regulator like protein from2 staphylococcus haemolyticus
98	<a href="#">c2oq2B_</a>	Alignment	not modelled	7.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoadenosine phosphosulfate reductase; <b>PDBTitle:</b> crystal structure of yeast paps reductase with pap, a product complex
99	<a href="#">d1xmta_</a>	Alignment	not modelled	7.3	7	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT