







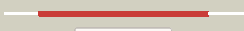















# Phyre2

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Description	RVBD2028c (-) _2274577_2275416
Date	Mon Aug 5 13:25:13 BST 2019
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3loqA_</a>	 Alignment		100.0	15	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> the crystal structure of a universal stress protein from archaeoglobus2 fulgidus dsm 4304
2	<a href="#">c2jaxA_</a>	 Alignment		100.0	28	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein tb31.7; <b>PDBTitle:</b> universal stress protein rv2623 from mycobaterium2 tuberculosis
3	<a href="#">c3ab8B_</a>	 Alignment		100.0	22	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> putative uncharacterized protein ttha0350; <b>PDBTitle:</b> crystal structure of the hypothetical tandem-type universal stress2 protein ttha0350 complexed with atps.
4	<a href="#">c3mt0A_</a>	 Alignment		100.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein pa1789; <b>PDBTitle:</b> the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
5	<a href="#">c3olqA_</a>	 Alignment		100.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> universal stress protein e; <b>PDBTitle:</b> the crystal structure of a universal stress protein e from proteus2 mirabilis hi4320
6	<a href="#">c4r2jA_</a>	 Alignment		100.0	13	<b>PDB header:</b> metal binding protein, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> universal stress protein e; <b>PDBTitle:</b> crystal structure of ydaa (universal stress protein e) from salmonella2 typhimurium
7	<a href="#">c3s3tD_</a>	 Alignment		99.9	35	<b>PDB header:</b> chaperone <b>Chain:</b> D; <b>PDB Molecule:</b> nucleotide-binding protein, universal stress protein uspa <b>PDBTitle:</b> universal stress protein uspa from lactobacillus plantarum
8	<a href="#">c3dloC_</a>	 Alignment		99.8	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C; <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> structure of universal stress protein from archaeoglobus fulgidus
9	<a href="#">c5ahwC_</a>	 Alignment		99.8	17	<b>PDB header:</b> signaling protein <b>Chain:</b> C; <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> crystal structure of universal stress protein msmeq_3811 in2 complex with camp
10	<a href="#">d2z3va1</a>	 Alignment		99.8	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
11	<a href="#">d1mjha_</a>	 Alignment		99.8	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like

12	<a href="#">c3hgmD_</a>	Alignment		99.8	19	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> universal stress protein tead; <b>PDBTitle:</b> universal stress protein tead from the trap transporter teaabc of2 halomonas elongata
13	<a href="#">d1tq8a_</a>	Alignment		99.8	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
14	<a href="#">c3fh0A_</a>	Alignment		99.8	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative universal stress protein kpn_01444; <b>PDBTitle:</b> crystal structure of putative universal stress protein kpn_01444 -2 atpase
15	<a href="#">c3fg9B_</a>	Alignment		99.7	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein of universal stress protein uspa family; <b>PDBTitle:</b> the crystal structure of an universal stress protein uspa2 family protein from lactobacillus plantarum wcf51
16	<a href="#">c4r2B_</a>	Alignment		99.7	27	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> universal stress protein f; <b>PDBTitle:</b> crystal structure of ynaf (universal stress protein f) from salmonella2 typhimurium
17	<a href="#">c4wnyA_</a>	Alignment		99.7	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> crystal structure of a protein from the universal stress protein2 family from burkholderia pseudomallei
18	<a href="#">d1jmva_</a>	Alignment		99.7	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
19	<a href="#">d2gm3a1</a>	Alignment		99.7	12	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
20	<a href="#">c2pfsA_</a>	Alignment		99.7	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> crystal structure of universal stress protein from nitrosomonas2 europaea
21	<a href="#">c2dumD_</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein ph0823; <b>PDBTitle:</b> crystal structure of hypothetical protein, ph0823
22	<a href="#">c3idfA_</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> usp-like protein; <b>PDBTitle:</b> the crystal structure of a usp-like protein from wolinnella2 succinogenes to 2.0a
23	<a href="#">d1q77a_</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
24	<a href="#">c3zquA_</a>	Alignment	not modelled	84.2	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> probable aromatic acid decarboxylase; <b>PDBTitle:</b> structure of a probable aromatic acid decarboxylase
25	<a href="#">c3a2kB_</a>	Alignment	not modelled	84.0	8	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> trna(ile)-lysidine synthase; <b>PDBTitle:</b> crystal structure of tils complexed with trna
26	<a href="#">c6qlgD_</a>	Alignment	not modelled	84.0	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> flavin prenyltransferase pada1, mitochondrial; <b>PDBTitle:</b> crystal structure of anubix (pada1) in complex with fm and2 dimethylallyl pyrophosphate
27	<a href="#">c1ni5A_</a>	Alignment	not modelled	81.8	15	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell cycle protein mesj; <b>PDBTitle:</b> structure of the mesj pp-atpase from escherichia coli
28	<a href="#">c5gafi_</a>	Alignment	not modelled	77.9	14	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 50s ribosomal protein l10; <b>PDBTitle:</b> rnc in complex with srp
						<b>PDB header:</b> lyase/dna

29	<a href="#">c2xrzA</a>	Alignment	not modelled	77.5	15	<b>Chain:</b> A: <b>PDB Molecule:</b> deoxyribodipyrimidine photolyase; <b>PDBTitle:</b> x-ray structure of archaeal class ii cpd photolyase from2 methanosarcina mazeri in complex with intact cpd-lesion
30	<a href="#">c5h75B</a>	Alignment	not modelled	75.4	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> mersacidin decarboxylase,immunoglobulin g-binding protein <b>PDBTitle:</b> crystal structure of the mrsd-protein a fusion protein
31	<a href="#">c3g40A</a>	Alignment	not modelled	71.6	8	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> na-k-cl cotransporter; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of a2 prokaryotic cation chloride cotransporter
32	<a href="#">c4hqnb</a>	Alignment	not modelled	68.7	17	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> sporozoite surface protein 2; <b>PDBTitle:</b> crystal structure of manganese-loaded plasmodium vivax trap protein
33	<a href="#">c3i3wB</a>	Alignment	not modelled	67.5	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoglucosamine mutase; <b>PDBTitle:</b> structure of a phosphoglucosamine mutase from francisella tularensis
34	<a href="#">c2e21A</a>	Alignment	not modelled	67.1	8	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> trna(ile)-lysine synthase; <b>PDBTitle:</b> crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
35	<a href="#">c4kpuB</a>	Alignment	not modelled	67.1	7	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> electron transfer flavoprotein alpha/beta-subunit; <b>PDBTitle:</b> electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
36	<a href="#">c4qg5D</a>	Alignment	not modelled	64.2	23	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> putative phosphoglucomutase; <b>PDBTitle:</b> crystal structure of phosphoglucomutase from leishmania major at 3.52 angstrom resolution
37	<a href="#">c6eoaA</a>	Alignment	not modelled	63.2	17	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphopantothenoilcysteine decarboxylase; <b>PDBTitle:</b> crystal structure of hal3 from cryptococcus neoformans
38	<a href="#">c2ejbA</a>	Alignment	not modelled	59.8	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> probable aromatic acid decarboxylase; <b>PDBTitle:</b> crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
39	<a href="#">c2yxbA</a>	Alignment	not modelled	59.6	9	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme b12-dependent mutase; <b>PDBTitle:</b> crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
40	<a href="#">c4nzpA</a>	Alignment	not modelled	58.1	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> the crystal structure of argininosuccinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
41	<a href="#">c5ol2E</a>	Alignment	not modelled	57.6	4	<b>PDB header:</b> flavoprotein <b>Chain:</b> E: <b>PDB Molecule:</b> electron transfer flavoprotein small subunit; <b>PDBTitle:</b> the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
42	<a href="#">c3dm5A</a>	Alignment	not modelled	57.3	15	<b>PDB header:</b> rna binding protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
43	<a href="#">c4okuA</a>	Alignment	not modelled	56.2	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> micronemal protein mic2; <b>PDBTitle:</b> structure of toxoplasma gondii promic2
44	<a href="#">c4rheB</a>	Alignment	not modelled	54.6	24	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-octaprenyl-4-hydroxybenzoate carboxylase; <b>PDBTitle:</b> crystal structure of ubix, an aromatic acid decarboxylase from the2 colwellia psychrerythraea 34h
45	<a href="#">d2j07a2</a>	Alignment	not modelled	54.0	16	<b>Fold:</b> Cryptochrome/photolyase, N-terminal domain <b>Superfamily:</b> Cryptochrome/photolyase, N-terminal domain <b>Family:</b> Cryptochrome/photolyase, N-terminal domain
46	<a href="#">d1sbza</a>	Alignment	not modelled	52.8	15	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
47	<a href="#">d1ni5a1</a>	Alignment	not modelled	51.2	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PP-loop ATPase
48	<a href="#">c2qy9A</a>	Alignment	not modelled	48.9	12	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the ng+1 construct of the e. coli srp receptor2 ftsy
49	<a href="#">d1p5dx1</a>	Alignment	not modelled	48.6	12	<b>Fold:</b> Phosphoglucomutase, first 3 domains <b>Superfamily:</b> Phosphoglucomutase, first 3 domains <b>Family:</b> Phosphoglucomutase, first 3 domains
50	<a href="#">c2j289</a>	Alignment	not modelled	47.8	14	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> signal recognition particle 54; <b>PDBTitle:</b> model of e. coli srp bound to 70s rncs
51	<a href="#">c4hjhA</a>	Alignment	not modelled	47.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphomannomutase; <b>PDBTitle:</b> iodide sad phased crystal structure of a phosphoglucomutase from2 brucella melitensis complexed with glucose-6-phosphate
52	<a href="#">c4hqfA</a>	Alignment	not modelled	46.4	17	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> thrombospondin-related anonymous protein, trap; <b>PDBTitle:</b> crystal structure of plasmodium falciparum trap, i4 form
53	<a href="#">c3ginD</a>	Alignment	not modelled	45.5	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> epidermin biosynthesis protein epid;

53	<a href="#">c3qjgB_</a>	Alignment	not modelled	43.5	9	<b>PDBTitle:</b> epidermin biosynthesis protein epid from staphylococcus aureus
54	<a href="#">d3pmaG1</a>	Alignment	not modelled	44.8	22	<b>Fold:</b> Phosphoglucomutase, first 3 domains <b>Superfamily:</b> Phosphoglucomutase, first 3 domains <b>Family:</b> Phosphoglucomutase, first 3 domains
55	<a href="#">c6esvA_</a>	Alignment	not modelled	44.1	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative periplasmic phosphite-binding-like protein (pbl) <b>PDBTitle:</b> structure of the phosphate-bound form of aixx from rhizobium sp. str.2 nt-26
56	<a href="#">c3mcuF_</a>	Alignment	not modelled	43.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> dipicolinate synthase, b chain; <b>PDBTitle:</b> crystal structure of the dipicolinate synthase chain b from bacillus2 cereus. northeast structural genomics consortium target bcr215.
57	<a href="#">c4u63A_</a>	Alignment	not modelled	42.2	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dna photolyase; <b>PDBTitle:</b> crystal structure of a bacterial class iii photolyase from2 agrobacterium tumefaciens at 1.67a resolution
58	<a href="#">d1mvlA_</a>	Alignment	not modelled	42.0	16	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
59	<a href="#">c1mvlA_</a>	Alignment	not modelled	42.0	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> ppc decarboxylase athal3a; <b>PDBTitle:</b> ppc decarboxylase mutant c175s
60	<a href="#">c3c04A_</a>	Alignment	not modelled	38.2	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphomannomutase/phosphoglucomutase; <b>PDBTitle:</b> structure of the p368g mutant of pmm/pgm from p. aeruginosa
61	<a href="#">c1zu4A_</a>	Alignment	not modelled	38.1	14	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> ftsY; <b>PDBTitle:</b> crystal structure of ftsY from mycoplasma mycoides-space2 group p21212
62	<a href="#">c3vrhA_</a>	Alignment	not modelled	37.7	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ph0300; <b>PDBTitle:</b> crystal structure of ph0300
63	<a href="#">c1vmaA_</a>	Alignment	not modelled	37.4	20	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsY; <b>PDBTitle:</b> crystal structure of cell division protein ftsY (tm0570) from2 thermotoga maritima at 1.60 a resolution
64	<a href="#">c1vl2C_</a>	Alignment	not modelled	37.3	12	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
65	<a href="#">d1efvb_</a>	Alignment	not modelled	36.5	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
66	<a href="#">c3trjC_</a>	Alignment	not modelled	36.3	17	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> structure of a phosphoheptose isomerase from francisella tularensis
67	<a href="#">c3lqkA_</a>	Alignment	not modelled	36.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase subunit b; <b>PDBTitle:</b> crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
68	<a href="#">c5bmpA_</a>	Alignment	not modelled	35.8	7	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglucomutase; <b>PDBTitle:</b> crystal structure of phosphoglucomutase from xanthomonas citri2 complexed with glucose-1-phosphate
69	<a href="#">c6jddA_</a>	Alignment	not modelled	35.7	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> cypemycin cysteine dehydrogenase (decarboxylating); <b>PDBTitle:</b> crystal structure of the cypemycin decarboxylase cypd.
70	<a href="#">c1qzuB_</a>	Alignment	not modelled	35.1	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein mds018; <b>PDBTitle:</b> crystal structure of human phosphopantothenoylcysteine decarboxylase
71	<a href="#">c6jlsA_</a>	Alignment	not modelled	34.5	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative flavoprotein decarboxylase; <b>PDBTitle:</b> crystal structure of fmn-dependent cysteine decarboxylases tvaf from2 thioviridamide biosynthesis
72	<a href="#">c3fxaA_</a>	Alignment	not modelled	34.1	9	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sis domain protein; <b>PDBTitle:</b> crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
73	<a href="#">d1p3y1_</a>	Alignment	not modelled	33.5	21	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
74	<a href="#">d1qzua_</a>	Alignment	not modelled	32.5	18	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
75	<a href="#">c2hjhB_</a>	Alignment	not modelled	32.1	7	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent histone deacetylase sir2; <b>PDBTitle:</b> crystal structure of the sir2 deacetylase
76	<a href="#">c2yvaB_</a>	Alignment	not modelled	31.9	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dnaa initiator-associating protein diaa; <b>PDBTitle:</b> crystal structure of escherichia coli diaa
77	<a href="#">d1ck4a_</a>	Alignment	not modelled	30.2	10	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain

78	<a href="#">d2iela1</a>	Alignment	not modelled	30.2	13	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
79	<a href="#">c5ghaC</a>	Alignment	not modelled	29.7	9	<b>PDB header:</b> transferase/transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> sulfur transferase ttua; <b>PDBTitle:</b> sulfur transferase ttua in complex with sulfur carrier ttub
80	<a href="#">c6fahB</a>	Alignment	not modelled	29.3	7	<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
81	<a href="#">d1jeoa</a>	Alignment	not modelled	29.0	14	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
82	<a href="#">d1m7ja3</a>	Alignment	not modelled	28.9	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> D-aminoacylase, catalytic domain
83	<a href="#">c2x3yA</a>	Alignment	not modelled	28.6	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> crystal structure of gmha from burkholderia pseudomallei
84	<a href="#">d1tk9a</a>	Alignment	not modelled	27.7	14	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
85	<a href="#">d1g5qa</a>	Alignment	not modelled	27.6	9	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
86	<a href="#">c3euaD</a>	Alignment	not modelled	27.5	14	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> putative fructose-aminoacid-6-phosphate deglycase; <b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (bsu32610) from <i>Bacillus subtilis</i> at 1.90 Å resolution
87	<a href="#">c1wqaB</a>	Alignment	not modelled	26.9	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> phospho-sugar mutase; <b>PDBTitle:</b> crystal structure of pyrococcus horikoshii2 phosphomannomutase/phosphoglucomutase complexed with mg2+
88	<a href="#">c3fj1A</a>	Alignment	not modelled	26.7	9	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerase; <b>PDBTitle:</b> crystal structure of putative phosphosugar isomerase (yp_167080.1)2 from <i>Silicibacter pomeroyi</i> dss-3 at 1.75 Å resolution
89	<a href="#">d1x94a</a>	Alignment	not modelled	26.5	11	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
90	<a href="#">c5by2A</a>	Alignment	not modelled	25.6	26	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> sedoheptulose 7-phosphate isomerase from <i>Colwellia psychrerythraea</i> 2 strain 34h
91	<a href="#">c3uw2A</a>	Alignment	not modelled	25.5	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglucomutase/phosphomannomutase family protein; <b>PDBTitle:</b> x-ray crystal structure of phosphoglucomutase/phosphomannomutase2 family protein (bth_11489)from <i>Burkholderia thailandensis</i>
92	<a href="#">c2derA</a>	Alignment	not modelled	25.2	15	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> trna-specific 2-thiouridylase mnma; <b>PDBTitle:</b> cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
93	<a href="#">d1nmpa</a>	Alignment	not modelled	24.9	36	<b>Fold:</b> NIF3 (NGG1p interacting factor 3)-like <b>Superfamily:</b> NIF3 (NGG1p interacting factor 3)-like <b>Family:</b> NIF3 (NGG1p interacting factor 3)-like
94	<a href="#">c1c4gB</a>	Alignment	not modelled	24.5	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (alpha-d-glucose 1-phosphate phosphoglucomutase); <b>PDBTitle:</b> phosphoglucomutase vanadate based transition state analog complex
95	<a href="#">d1v7pc</a>	Alignment	not modelled	24.2	14	<b>Fold:</b> vWA-like <b>Superfamily:</b> vWA-like <b>Family:</b> Integrin A (or I) domain
96	<a href="#">c1kh2D</a>	Alignment	not modelled	23.9	15	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> argininosuccinate synthetase; <b>PDBTitle:</b> crystal structure of thermus thermophilus hb8 argininosuccinate2 synthetase in complex with atp
97	<a href="#">c3w7bB</a>	Alignment	not modelled	23.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
98	<a href="#">c2puwA</a>	Alignment	not modelled	22.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isomerase domain of glutamine-fructose-6-phosphate <b>PDBTitle:</b> the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from <i>Candida albicans</i>
99	<a href="#">c4u7jB</a>	Alignment	not modelled	22.2	9	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of argininosuccinate synthase from <i>Mycobacterium2 thermoresistibile</i>
100	<a href="#">c2f7IA</a>	Alignment	not modelled	21.9	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 455aa long hypothetical phospho-sugar mutase; <b>PDBTitle:</b> crystal structure of <i>Sulfolobus tokodaii</i> 2 phosphomannomutase/phosphoglucomutase
101	<a href="#">d1zuna1</a>	Alignment	not modelled	21.9	11	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PAPS reductase-like
						<b>Fold:</b> NIF3 (NGG1p interacting factor 3)-like

102	<a href="#">d2fywa1</a>	Alignment	not modelled	21.7	18	<b>Superfamily:</b> NIF3 (NGG1p interacting factor 3)-like <b>Family:</b> NIF3 (NGG1p interacting factor 3)-like
103	<a href="#">c3ragA</a>	Alignment	not modelled	21.6	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein aaci_0196 from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
104	<a href="#">d1vl2a1</a>	Alignment	not modelled	21.5	12	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
105	<a href="#">c3cvyA</a>	Alignment	not modelled	21.4	13	<b>PDB header:</b> lyase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> re11660p; <b>PDBTitle:</b> drosophila melanogaster (6-4) photolyase bound to repaired ds dna
106	<a href="#">c2zkiH</a>	Alignment	not modelled	21.0	23	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> 199aa long hypothetical trp repressor binding <b>PDBTitle:</b> crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
107	<a href="#">c2b2xB</a>	Alignment	not modelled	20.8	10	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> integrin alpha-1; <b>PDBTitle:</b> vla1 rdeltah i-domain complexed with a quadruple mutant of the aqc22 fab
108	<a href="#">d1x92a</a>	Alignment	not modelled	20.7	17	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain