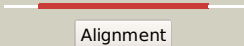

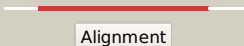

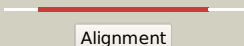







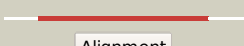













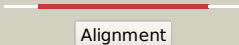





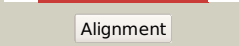

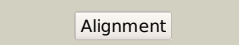











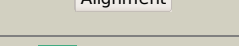
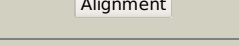


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1001_(arcA)_1117189_1118397
Date	Wed Jul 31 22:05:07 BST 2019
Unique Job ID	178f5ac734d3d895

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1rxxa_</a>	 Alignment		100.0	39	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Arginine deiminase
2	<a href="#">c4bofA_</a>	 Alignment		100.0	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> arginine deiminase; <b>PDBTitle:</b> crystal structure of arginine deiminase from group a streptococcus
3	<a href="#">d1s9ra_</a>	 Alignment		100.0	30	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Arginine deiminase
4	<a href="#">c4e4jl_</a>	 Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> arginine deiminase; <b>PDBTitle:</b> crystal structure of arginine deiminase from mycoplasma penetrans
5	<a href="#">c5wpiB_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hsva; <b>PDBTitle:</b> the virulence-associated protein hsva from the fire blight pathogen2 erwinia amylovora is a polyamine amidinotransferase
6	<a href="#">d1bwda_</a>	 Alignment		100.0	18	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Amidinotransferase
7	<a href="#">c8jdwA_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (l-arginine:glycine amidinotransferase); <b>PDBTitle:</b> crystal structure of human l-arginine:glycine amidinotransferase in2 complex with l-alanine
8	<a href="#">c1jdwA_</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> l-arginine\glycine amidinotransferase; <b>PDBTitle:</b> crystal structure and mechanism of l-arginine: glycine2 amidinotransferase: a mitochondrial enzyme involved in3 creatine biosynthesis
9	<a href="#">d1jdwa_</a>	 Alignment		100.0	17	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Amidinotransferase
10	<a href="#">c3i4aA_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n(g),n(g)-dimethylarginine dimethylaminohydrolase 1; <b>PDBTitle:</b> crystal structure of dimethylarginine dimethylaminohydrolase-1 (ddah-2 1) in complex with n5-(1-iminopropyl)-l-ornithine
11	<a href="#">c2ci6A_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ng, ng-dimethylarginine dimethylaminohydrolase 1; <b>PDBTitle:</b> crystal structure of dimethylarginine2 dimethylaminohydrolase i bound with zinc low ph

12	<a href="#">d1h70a_</a>			100.0	23	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Dimethylarginine dimethylaminohydrolase DDAH
13	<a href="#">c6b2wB_</a>			99.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative peptidyl-arginine deiminase family protein; <b>PDBTitle:</b> c. jejuni c315s agmatine deiminase with substrate bound
14	<a href="#">d2ewoa1</a>			99.6	18	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Porphyromonas-type peptidylarginine deiminase
15	<a href="#">d1xkna_</a>			99.6	19	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Porphyromonas-type peptidylarginine deiminase
16	<a href="#">d1zbra1</a>			99.5	19	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Porphyromonas-type peptidylarginine deiminase
17	<a href="#">c2jerG_</a>			99.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> agmatine deiminase; <b>PDBTitle:</b> agmatine deiminase of enterococcus faecalis catalyzing its2 reaction.
18	<a href="#">d2jera1</a>			99.5	19	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Porphyromonas-type peptidylarginine deiminase
19	<a href="#">d1vkpa_</a>			99.5	18	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Porphyromonas-type peptidylarginine deiminase
20	<a href="#">d2cmua1</a>			99.5	14	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Porphyromonas-type peptidylarginine deiminase
21	<a href="#">c4ytgA_</a>		not modelled	99.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidylarginine deiminase; <b>PDBTitle:</b> crystal structure of porphyromonas gingivalis peptidylarginine2 deiminase (ppad) mutant c351a in complex with dipeptide met-arg.
22	<a href="#">d2dexx3</a>		not modelled	94.2	12	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Peptidylarginine deiminase Pad4, catalytic C-terminal domain
23	<a href="#">c4n2gA_</a>		not modelled	94.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-arginine deiminase type-2; <b>PDBTitle:</b> crystal structure of protein arginine deiminase 2 (d169a, 10 mm ca2+)
24	<a href="#">c4n2kA_</a>		not modelled	93.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-arginine deiminase type-2; <b>PDBTitle:</b> crystal structure of protein arginine deiminase 2 (q350a, 0 mm ca2+)
25	<a href="#">c5hp5A_</a>		not modelled	93.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-arginine deiminase type-1; <b>PDBTitle:</b> srtructure of human peptidylarginine deiminase type i (pad1)
26	<a href="#">c2dexX_</a>		not modelled	92.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> protein-arginine deiminase type iv; <b>PDBTitle:</b> crystal structure of human peptidylarginine deiminase 4 in complex2 with histone h3 n-terminal peptide including arg17
27	<a href="#">d2ebfx2</a>		not modelled	46.3	17	<b>Fold:</b> EreA/ChaN-like <b>Superfamily:</b> EreA/ChaN-like <b>Family:</b> PMT domain-like
28	<a href="#">c6rdu2_</a>		not modelled	43.8	13	<b>PDB header:</b> proton transport <b>Chain:</b> 2: <b>PDB Molecule:</b> asa-2: polytomella f-atp synthase associated subunit 2; <b>PDBTitle:</b> cryo-em structure of polytomella f-atp synthase, rotary

						substate 1e,2 monomer-masked refinement
29	<a href="#">c4o9uB_</a>	Alignment	not modelled	42.9	46	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit beta; <b>PDBTitle:</b> mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
30	<a href="#">d1d4oa_</a>	Alignment	not modelled	40.7	21	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Transhydrogenase domain III (dIII)
31	<a href="#">d1pnoa_</a>	Alignment	not modelled	40.7	38	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Transhydrogenase domain III (dIII)
32	<a href="#">c4rrfD_</a>	Alignment	not modelled	39.6	22	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> threonine--trna ligase; <b>PDBTitle:</b> editing domain of threonyl-trna synthetase from methanococcus2 jannaschii with l-ser3aa
33	<a href="#">c1pt9B_</a>	Alignment	not modelled	38.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase, mitochondrial; <b>PDBTitle:</b> crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
34	<a href="#">c2bruC_</a>	Alignment	not modelled	37.9	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit beta; <b>PDBTitle:</b> complex of the domain i and domain iii of escherichia coli2 transhydrogenase
35	<a href="#">c2hl2A_</a>	Alignment	not modelled	37.7	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> threonyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the editing domain of threonyl-trna2 synthetase from pyrococcus abyssi in complex with an3 analog of seryladenylate
36	<a href="#">d1iuKa_</a>	Alignment	not modelled	37.1	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
37	<a href="#">c4k2bA_</a>	Alignment	not modelled	32.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ntd biosynthesis operon protein ntda; <b>PDBTitle:</b> crystal structure of ntda from bacillus subtilis in complex with the2 internal aldimine
38	<a href="#">c3zs7A_</a>	Alignment	not modelled	30.1	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxal kinase; <b>PDBTitle:</b> crystal structure of pyridoxal kinase from trypanosoma brucei
39	<a href="#">d1daaa_</a>	Alignment	not modelled	29.5	11	<b>Fold:</b> D-aminoacid aminotransferase-like PLP-dependent enzymes <b>Superfamily:</b> D-aminoacid aminotransferase-like PLP-dependent enzymes <b>Family:</b> D-aminoacid aminotransferase-like PLP-dependent enzymes
40	<a href="#">c3ff4A_</a>	Alignment	not modelled	26.9	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 uncharacterized protein chu_1412
41	<a href="#">c4ovkA_</a>	Alignment	not modelled	26.7	24	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein; <b>PDBTitle:</b> crystal structure of periplasmic solute binding protein from2 veillonella parvula dsm 2008
42	<a href="#">c1xtzA_</a>	Alignment	not modelled	26.4	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase; <b>PDBTitle:</b> crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
43	<a href="#">c4lhdB_</a>	Alignment	not modelled	24.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glycine dehydrogenase [decarboxylating]; <b>PDBTitle:</b> crystal structure of synechocystis sp. pcc 6803 glycine decarboxylase2 (p-protein), holo form with pyridoxal-5'-phosphate and glycine,3 closed flexible loop
44	<a href="#">d1u6ma_</a>	Alignment	not modelled	23.9	10	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
45	<a href="#">d1ynha1</a>	Alignment	not modelled	23.5	20	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Succinylarginine dihydrolase-like
46	<a href="#">d2itba1</a>	Alignment	not modelled	23.4	25	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> MiaE-like
47	<a href="#">c3u7jA_</a>	Alignment	not modelled	23.1	35	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
48	<a href="#">c4inpA_</a>	Alignment	not modelled	22.5	24	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> iron (iii) abc transporter, periplasmic iron-binding <b>PDBTitle:</b> the crystal structure of helicobacter pylori ceue (hp1561) with ni(ii)2 bound
49	<a href="#">c4hn9B_</a>	Alignment	not modelled	22.4	24	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> iron complex transport system substrate-binding protein; <b>PDBTitle:</b> crystal structure of iron abc transporter solute-binding protein from2 eubacterium eligens
50	<a href="#">c4x84C_</a>	Alignment	not modelled	21.5	30	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase a from pseudomonas2 aeruginosa
51	<a href="#">c4yajA_</a>	Alignment	not modelled	21.4	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha subunit of acetyl-coenzyme a synthetase <b>PDBTitle:</b> ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form)
52	<a href="#">c4ce5A_</a>	Alignment	not modelled	20.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> at-omegata; <b>PDBTitle:</b> first crystal structure of an (r)-selective omega-transaminase2 from aspergillus terreus
53	<a href="#">c5ux1D_</a>	Alignment	not modelled	20.5	28	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> trna-(ms2)io(6)a-hydroxylase-like; <b>PDBTitle:</b> protein 43 with aldehyde deformylating oxygenase

						activity from2 synechococcus
54	<a href="#">c4nmIA</a>	Alignment	not modelled	19.4	32	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribulose 5-phosphate isomerase; <b>PDBTitle:</b> 2.60 angstrom resolution crystal structure of putative ribose 5-2 phosphate isomerase from toxoplasma gondii me49 in complex with dl-3 malic acid
55	<a href="#">c3wwjE</a>	Alignment	not modelled	19.3	23	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> (r)-amine transaminase; <b>PDBTitle:</b> crystal structure of an engineered sitagliptin-producing transaminase,2 ata-117-rd11
56	<a href="#">c4rrcA</a>	Alignment	not modelled	18.1	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> probable threonine--trna ligase 2; <b>PDBTitle:</b> n-terminal editing domain of threonyl-trna synthetase from aeropyrum2 pernix with l-thr3aa (snapshot 3)
57	<a href="#">c2e58D</a>	Alignment	not modelled	15.4	29	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> mnmc2; <b>PDBTitle:</b> crystal structure of mnmc2 from aquifex aeolicus
58	<a href="#">c5cm0A</a>	Alignment	not modelled	14.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> branched-chain transaminase; <b>PDBTitle:</b> crystal structure of branched-chain aminotransferase from thermophilic2 archaea geoglobus acetivorans
59	<a href="#">c5dlcC</a>	Alignment	not modelled	14.6	26	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pyridoxine 5'-phosphate synthase; <b>PDBTitle:</b> x-ray crystal structure of a pyridoxine 5-prime-phosphate synthase2 from pseudomonas aeruginosa
60	<a href="#">c6eddB</a>	Alignment	not modelled	14.2	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyltransferase pa3944; <b>PDBTitle:</b> crystal structure of a gnat superfamily pa3944 acetyltransferase in2 complex with coa (p1 space group)
61	<a href="#">d1qwga</a>	Alignment	not modelled	13.6	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (2r)-phospho-3-sulfolactate synthase ComA <b>Family:</b> (2r)-phospho-3-sulfolactate synthase ComA
62	<a href="#">d2aeaa1</a>	Alignment	not modelled	13.4	22	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
63	<a href="#">c4d6yA</a>	Alignment	not modelled	13.4	24	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacterial regulatory, fis family protein; <b>PDBTitle:</b> crystal structure of the receiver domain of ntrx from2 brucella abortus in complex with beryll fluoride and3 magnesium
64	<a href="#">c1r0ID</a>	Alignment	not modelled	13.3	15	<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
65	<a href="#">c5ix3A</a>	Alignment	not modelled	13.2	6	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> diamine n-acetyltransferase; <b>PDBTitle:</b> crystal structure of n-acetyltransferase from staphylococcus aureus.
66	<a href="#">d1m5wa</a>	Alignment	not modelled	13.2	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Pyridoxine 5'-phosphate synthase <b>Family:</b> Pyridoxine 5'-phosphate synthase
67	<a href="#">c2z14A</a>	Alignment	not modelled	13.1	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ef-hand domain-containing family member c2; <b>PDBTitle:</b> crystal structure of the n-terminal duf1126 in human ef-2 hand domain containing 2 protein
68	<a href="#">d1f52a1</a>	Alignment	not modelled	12.8	11	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Glutamine synthetase, N-terminal domain <b>Family:</b> Glutamine synthetase, N-terminal domain
69	<a href="#">c5b6aA</a>	Alignment	not modelled	12.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxal kinase pdxy; <b>PDBTitle:</b> structure of pyridoxal kinasefrom pseudomonas aeruginosa
70	<a href="#">c1wv9B</a>	Alignment	not modelled	12.3	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> rhodanese homolog tt1651; <b>PDBTitle:</b> crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
71	<a href="#">d1liua2</a>	Alignment	not modelled	12.3	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate kinase
72	<a href="#">d1xhfa1</a>	Alignment	not modelled	12.1	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
73	<a href="#">d1jkea</a>	Alignment	not modelled	11.9	21	<b>Fold:</b> DTD-like <b>Superfamily:</b> DTD-like <b>Family:</b> DTD-like
74	<a href="#">c1nl0G</a>	Alignment	not modelled	11.6	58	<b>PDB header:</b> immune system <b>Chain:</b> G: <b>PDB Molecule:</b> factor ix; <b>PDBTitle:</b> crystal structure of human factor ix gla domain in complex2 of an inhibitory antibody, 10c12
75	<a href="#">d1gr0a2</a>	Alignment	not modelled	11.5	31	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
76	<a href="#">d1tjna</a>	Alignment	not modelled	11.4	17	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> Chelatase <b>Family:</b> CbiX-like
77	<a href="#">c1tjnA</a>	Alignment	not modelled	11.4	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> sirohydrochlorin cobaltochelataase; <b>PDBTitle:</b> crystal structure of hypothetical protein af0721 from archaeoglobus2 fulgidus
78	<a href="#">c3u0gA</a>	Alignment	not modelled	11.1	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative branched-chain amino acid aminotransferase ilve; <b>PDBTitle:</b> crystal structure of branched-chain amino acid aminotransferase from2 burkholderia pseudomallei

79	<a href="#">c4s1hA_</a>	Alignment	not modelled	11.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxal kinase; <b>PDBTitle:</b> pyridoxal kinase of entamoeba histolytica with adp
80	<a href="#">c3a14B_</a>	Alignment	not modelled	10.9	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase; <b>PDBTitle:</b> crystal structure of dxr from thermotoga maritima, in complex with2 nadph
81	<a href="#">c5uidC_</a>	Alignment	not modelled	10.8	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> aminotransferase tlmj; <b>PDBTitle:</b> the crystal structure of an aminotransferase tlmj from2 streptoaloteichus hindustanus
82	<a href="#">c2zu8A_</a>	Alignment	not modelled	10.6	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mannosyl-3-phosphoglycerate synthase; <b>PDBTitle:</b> crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
83	<a href="#">c2x4bA_</a>	Alignment	not modelled	10.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> limit dextrinase; <b>PDBTitle:</b> barley limit dextrinase in complex with beta-cyclodextrin
84	<a href="#">c4m0jA_</a>	Alignment	not modelled	10.3	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> d-amino acid aminotransferase; <b>PDBTitle:</b> crystal structure of a d-amino acid aminotransferase from burkholderia2 thailandensis e264
85	<a href="#">d1dcfa_</a>	Alignment	not modelled	10.2	31	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> Receiver domain of the ethylene receptor
86	<a href="#">c4rkmK_</a>	Alignment	not modelled	10.1	24	<b>PDB header:</b> unknown function <b>Chain:</b> K: <b>PDB Molecule:</b> mcca; <b>PDBTitle:</b> wolinella succinogenes octaheme sulfite reductase mcca, form i
87	<a href="#">c2rdmB_</a>	Alignment	not modelled	10.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of response regulator receiver protein from2 sinorhizobium medicae wsm419
88	<a href="#">c3qb8A_</a>	Alignment	not modelled	9.9	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
89	<a href="#">c5jqoA_</a>	Alignment	not modelled	9.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lmo2184 protein; <b>PDBTitle:</b> crystal structure of an abc transporter substrate-binding protein from2 listeria monocytogenes egd-e
90	<a href="#">d1p0sl2</a>	Alignment	not modelled	9.6	58	<b>Fold:</b> GLA-domain <b>Superfamily:</b> GLA-domain <b>Family:</b> GLA-domain
91	<a href="#">d1zh2a1</a>	Alignment	not modelled	9.5	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
92	<a href="#">c3otrC_</a>	Alignment	not modelled	9.5	16	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> 2.75 angstrom crystal structure of enolase 1 from toxoplasma gondii
93	<a href="#">c5khbB_</a>	Alignment	not modelled	9.4	24	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> hemin abc transporter, periplasmic hemin-binding protein <b>PDBTitle:</b> crystal structure of periplasmic heme binding protein htb of vibrio2 cholerae
94	<a href="#">d2fiaa1</a>	Alignment	not modelled	9.3	7	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
95	<a href="#">d1gmua2</a>	Alignment	not modelled	9.3	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Urease metallochaperone UreE, C-terminal domain <b>Family:</b> Urease metallochaperone UreE, C-terminal domain
96	<a href="#">c2wnsB_</a>	Alignment	not modelled	9.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> human orotate phosphoribosyltransferase (oprta) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
97	<a href="#">c3hdoB_</a>	Alignment	not modelled	8.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
98	<a href="#">d1xlqa1</a>	Alignment	not modelled	8.8	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
99	<a href="#">c4p9eA_</a>	Alignment	not modelled	8.8	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> deoxycytidylate deaminase; <b>PDBTitle:</b> crystal structure of dcmp deaminase from the cyanophage s-tim5 in apo2 form