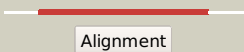

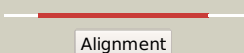

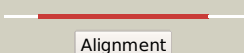

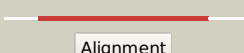





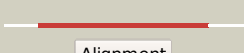

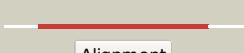




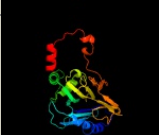


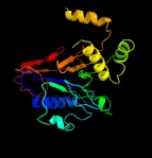

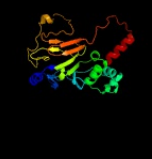



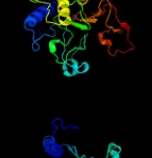

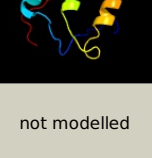




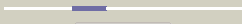
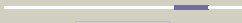


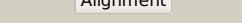
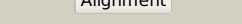
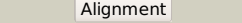
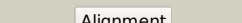
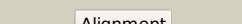
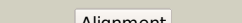



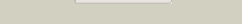
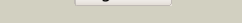
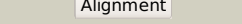
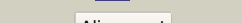




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1061_(-)_1184020_1184883
Date	Wed Jul 31 22:05:13 BST 2019
Unique Job ID	dd16160f9179a52b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">dlte5a_</a>	 Alignment		100.0	23	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
2	<a href="#">c4zfb_</a>	 Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> amidohydrolase egtc; <b>PDBTitle:</b> ergothioneine-biosynthetic ntn hydrolase egtc, apo form
3	<a href="#">clecb_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamine phosphoribosylpyrophosphate <b>PDBTitle:</b> escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
4	<a href="#">dlcfa2</a>	 Alignment		100.0	21	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
5	<a href="#">c3mdnD_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glutamine aminotransferase class-ii domain protein; <b>PDBTitle:</b> structure of glutamine aminotransferase class-ii domain protein2 (spo2029) from silicibacter pomeroyi
6	<a href="#">clgph1_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> 1: <b>PDB Molecule:</b> glutamine phosphoribosyl-pyrophosphate amidotransferase; <b>PDBTitle:</b> structure of the allosteric regulatory enzyme of purine biosynthesis
7	<a href="#">dlgph12</a>	 Alignment		100.0	22	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
8	<a href="#">dlxfA_</a>	 Alignment		100.0	22	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
9	<a href="#">cljxA_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucosamine 6-phosphate synthase; <b>PDBTitle:</b> glucosamine 6-phosphate synthase with glucose 6-phosphate
10	<a href="#">clct9D_</a>	 Alignment		100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> asparagine synthetase b; <b>PDBTitle:</b> crystal structure of asparagine synthetase b from2 escherichia coli
11	<a href="#">dlct9a2</a>	 Alignment		99.9	18	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases

12	<a href="#">d1ofda3</a>	Alignment		99.9	18	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
13	<a href="#">d1ea0a3</a>	Alignment		99.9	19	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
14	<a href="#">c1q15A</a>	Alignment		99.9	12	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> cara; <b>PDBTitle:</b> carbapenam synthetase
15	<a href="#">c1m1zB</a>	Alignment		99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactam synthetase; <b>PDBTitle:</b> beta-lactam synthetase apo enzyme
16	<a href="#">d1jgta2</a>	Alignment		99.8	17	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
17	<a href="#">d1q15a2</a>	Alignment		99.8	12	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
18	<a href="#">c1lm1A</a>	Alignment		99.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin-dependent glutamate synthase; <b>PDBTitle:</b> structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
19	<a href="#">c2vdcF</a>	Alignment		99.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamate synthase [nadh] large chain; <b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
20	<a href="#">c6f1sA</a>	Alignment		29.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cgliir protein; <b>PDBTitle:</b> c-terminal domain of cgli restriction endonuclease h subunit
21	<a href="#">c1y8aA</a>	Alignment	not modelled	18.8	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein af1437; <b>PDBTitle:</b> structure of gene product af1437 from archaeoglobus fulgidus
22	<a href="#">d1zyea1</a>	Alignment	not modelled	17.9	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
23	<a href="#">c2rprA</a>	Alignment	not modelled	17.5	23	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> flywch-type zinc finger-containing protein 1; <b>PDBTitle:</b> solution structure of the fifth flywch domain of flywch-type2 zinc finger-containing protein 1
24	<a href="#">d1kwga1</a>	Alignment	not modelled	16.4	30	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
25	<a href="#">c3sbtB</a>	Alignment	not modelled	14.2	11	<b>PDB header:</b> splicing <b>Chain:</b> B: <b>PDB Molecule:</b> a1 cistron-splicing factor aar2; <b>PDBTitle:</b> crystal structure of a aar2-prp8 complex
26	<a href="#">c2j034</a>	Alignment	not modelled	13.7	30	<b>PDB header:</b> ribosome <b>Chain:</b> 4: <b>PDB Molecule:</b> 50s ribosomal protein l31; <b>PDBTitle:</b> structure of the thermus thermophilus 70s ribosome2 complexed with mrna, trna and paromomycin (part 4 of 4).3 this file contains the 50s subunit from molecule ii.
27	<a href="#">d2j0141</a>	Alignment	not modelled	13.7	30	<b>Fold:</b> L28p-like <b>Superfamily:</b> L28p-like <b>Family:</b> Ribosomal protein L31p
28	<a href="#">c2je2A</a>	Alignment	not modelled	12.3	20	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p460; <b>PDBTitle:</b> cytochrome p460 from nitrosomonas europaea - probable2 nonphysiological oxidized form

29	<a href="#">c2hgi3_</a>	 Alignment	not modelled	12.1	30	<b>PDB header:</b> ribosome <b>Chain:</b> 3: <b>PDB Molecule:</b> 50s ribosomal protein l31; <b>PDBTitle:</b> crystal structure of the 70s thermus thermophilus ribosome showing how2 the 16s 3'-end mimicks mrna e and p codons. this entry 2hgj contains3 50s ribosomal subunit. the 30s ribosomal subunit can be found in pdb4 entry 2hgi.
30	<a href="#">c3bbo1_</a>	 Alignment	not modelled	11.9	33	<b>PDB header:</b> ribosome <b>Chain:</b> 1: <b>PDB Molecule:</b> ribosomal protein l31; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
31	<a href="#">c5o60g_</a>	 Alignment	not modelled	11.7	30	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 50s ribosomal protein l6; <b>PDBTitle:</b> structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
32	<a href="#">c4i43A_</a>	 Alignment	not modelled	11.0	17	<b>PDB header:</b> splicing <b>Chain:</b> A: <b>PDB Molecule:</b> a1 cistron-splicing factor aar2; <b>PDBTitle:</b> crystal structure of prp8:aar2 complex
33	<a href="#">c2b664_</a>	 Alignment	not modelled	10.9	33	<b>PDB header:</b> ribosome <b>Chain:</b> 4: <b>PDB Molecule:</b> 50s ribosomal protein l31; <b>PDBTitle:</b> 50s ribosomal subunit from a crystal structure of release factor rf1,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400
34	<a href="#">c6dzpg_</a>	 Alignment	not modelled	9.8	33	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 50s ribosomal protein l6; <b>PDBTitle:</b> cryo-em structure of mycobacterium smegmatis c(minus) 50s ribosomal2 subunit
35	<a href="#">d1vs6z1</a>	 Alignment	not modelled	9.6	33	<b>Fold:</b> L28p-like <b>Superfamily:</b> L28p-like <b>Family:</b> Ribosomal protein L31p
36	<a href="#">c1zyeL_</a>	 Alignment	not modelled	9.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> thioredoxin-dependent peroxide reductase; <b>PDBTitle:</b> crystal strucutre analysis of bovine mitochondrial peroxidoredoxin iii
37	<a href="#">c2ymvA_</a>	 Alignment	not modelled	9.3	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acg nitroreductase; <b>PDBTitle:</b> structure of reduced m smegmatis 5246, a homologue of m.2 tuberculosis acg
38	<a href="#">c1nh1A_</a>	 Alignment	not modelled	8.3	23	<b>PDB header:</b> avirulence protein <b>Chain:</b> A: <b>PDB Molecule:</b> avirulence b protein; <b>PDBTitle:</b> crystal structure of the type iii effector avrb from2 pseudomonas syringae.
39	<a href="#">d1nh1a_</a>	 Alignment	not modelled	8.3	23	<b>Fold:</b> Antivirulence factor <b>Superfamily:</b> Antivirulence factor <b>Family:</b> Antivirulence factor
40	<a href="#">c2lojA_</a>	 Alignment	not modelled	8.2	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytoplasmic protein; <b>PDBTitle:</b> solution nmr structure of tstm1273 from salmonella typhimurium lt2,2 nesg target stt322, csqid target idp01027 and ocsip target tstm1273
41	<a href="#">c2jraB_</a>	 Alignment	not modelled	7.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein rpa2121; <b>PDBTitle:</b> a novel domain-swapped solution nmr structure of protein rpa2121 from2 rhodospseudomonas palustris. northeast structural genomics target rpt6
42	<a href="#">c1nwdC_</a>	 Alignment	not modelled	7.5	54	<b>PDB header:</b> binding protein/hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamate decarboxylase; <b>PDBTitle:</b> solution structure of ca2+/calmodulin bound to the c-2 terminal domain of petunia glutamate decarboxylase
43	<a href="#">c1nwdB_</a>	 Alignment	not modelled	7.5	54	<b>PDB header:</b> binding protein/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate decarboxylase; <b>PDBTitle:</b> solution structure of ca2+/calmodulin bound to the c-2 terminal domain of petunia glutamate decarboxylase
44	<a href="#">c2hl7A_</a>	 Alignment	not modelled	6.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c-type biogenesis protein ccmh; <b>PDBTitle:</b> crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
45	<a href="#">c2dplA_</a>	 Alignment	not modelled	6.8	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing] subunit b; <b>PDBTitle:</b> crystal structure of the gmp synthase from pyrococcus horikoshii ot3
46	<a href="#">d1ueka2</a>	 Alignment	not modelled	6.8	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> 4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase lspE
47	<a href="#">c4lmiA_</a>	 Alignment	not modelled	6.7	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of putative ketosteroid isomerase from kribbella2 flavida dsm 17836
48	<a href="#">d3en8a1</a>	 Alignment	not modelled	6.5	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rpa4348-like
49	<a href="#">c2oqbA_</a>	 Alignment	not modelled	6.5	16	<b>PDB header:</b> transferase, gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> histone-arginine methyltransferase carm1; <b>PDBTitle:</b> crystal structure of the n-terminal domain of coactivator-associated2 methyltransferase 1 (carm1)
50	<a href="#">c2kq6A_</a>	 Alignment	not modelled	6.5	38	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> polycystin-2; <b>PDBTitle:</b> the structure of the ef-hand domain of polycystin-2 suggests a2 mechanism for ca2+-dependent regulation of polycystin-2 channel3 activity
51	<a href="#">c1vliA_</a>	 Alignment	not modelled	6.3	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> spore coat polysaccharide biosynthesis protein spse; <b>PDBTitle:</b> crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution

52	<a href="#">c2kleA_</a>	Alignment	not modelled	6.3	38	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> polycystin-2; <b>PDBTitle:</b> isic refined solution structure of the calcium binding2 domain of the c-terminal cytosolic domain of polycystin-2
53	<a href="#">c2mhhA_</a>	Alignment	not modelled	6.3	20	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> polycystic kidney disease protein 2; <b>PDBTitle:</b> solution structure of a ef-hand domain from sea urchin polycystin-2
54	<a href="#">c3d3rA_</a>	Alignment	not modelled	5.9	22	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase assembly chaperone hyc/hupf; <b>PDBTitle:</b> crystal structure of the hydrogenase assembly chaperone hyc/hupf2 family protein from shewanella oneidensis mr-1
55	<a href="#">d2z1ca1</a>	Alignment	not modelled	5.8	22	<b>Fold:</b> OB-fold <b>Superfamily:</b> HupF/HypC-like <b>Family:</b> HupF/HypC-like
56	<a href="#">d1vlia2</a>	Alignment	not modelled	5.7	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> NeuB-like
57	<a href="#">d1r0va1</a>	Alignment	not modelled	5.7	26	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> tRNA-intron endonuclease catalytic domain-like <b>Family:</b> tRNA-intron endonuclease catalytic domain-like
58	<a href="#">d3d3ra1</a>	Alignment	not modelled	5.7	22	<b>Fold:</b> OB-fold <b>Superfamily:</b> HupF/HypC-like <b>Family:</b> HupF/HypC-like
59	<a href="#">c3ipwA_</a>	Alignment	not modelled	5.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase tatd family protein; <b>PDBTitle:</b> crystal structure of hydrolase tatd family protein from entamoeba2 histolytica
60	<a href="#">d1f0la1</a>	Alignment	not modelled	5.5	50	<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
61	<a href="#">c1gpmD_</a>	Alignment	not modelled	5.4	18	<b>PDB header:</b> transferase (glutamine amidotransferase) <b>Chain:</b> D: <b>PDB Molecule:</b> gmp synthetase; <b>PDBTitle:</b> escherichia coli gmp synthetase complexed with amp and pyrophosphate
62	<a href="#">c2kw0A_</a>	Alignment	not modelled	5.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ccmh protein; <b>PDBTitle:</b> solution structure of n-terminal domain of ccmh from escherichia.coli
63	<a href="#">d2naca2</a>	Alignment	not modelled	5.3	30	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> Formate/glycerate dehydrogenases, substrate-binding domain
64	<a href="#">c3hshA_</a>	Alignment	not modelled	5.0	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> collagen alpha-1(xviii) chain; <b>PDBTitle:</b> crystal structure of human collagen xviii trimerization domain2 (tetragonal crystal form)