

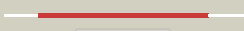






















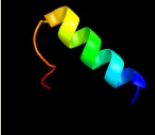


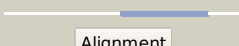

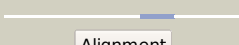

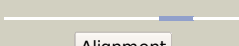

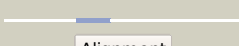






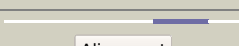

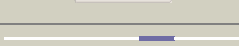
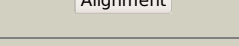
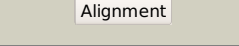
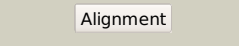




# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD0780\_(hemH)\_873346\_874239  
 Date Fri Jul 26 01:50:36 BST 2019  
 Unique Job ID 6946e57a4dcebb7e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3r9rA_</a>	 Alignment		100.0	76	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole-succinocarboxamide synthase; <b>PDBTitle:</b> structure of a phosphoribosylaminoimidazole-succinocarboxamide2 synthase from mycobacterium abscessus atcc 19977 / dsm 44196
2	<a href="#">d2cnqa1</a>	 Alignment		100.0	44	<b>Fold:</b> SAICAR synthase-like <b>Superfamily:</b> SAICAR synthase-like <b>Family:</b> SAICAR synthase
3	<a href="#">c2z02A_</a>	 Alignment		100.0	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole-succinocarboxamide <b>PDBTitle:</b> crystal structure of f2 phosphoribosylaminoimidazolesuccinocarboxamide synthase3 wit atp from methanocaldococcus jannaschii
4	<a href="#">c2yvvB_</a>	 Alignment		100.0	29	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole succinocarboxamide synthetase; <b>PDBTitle:</b> crystal structure of saicar synthetase from geobacillus kaustophilus
5	<a href="#">c3kreA_</a>	 Alignment		100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole-succinocarboxamide synthase; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole-succinocarboxamide2 synthase from ehrlichia chaffeensis at 1.8a resolution
6	<a href="#">c2gqsA_</a>	 Alignment		100.0	28	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole-succinocarboxamide synthase; <b>PDBTitle:</b> saicar synthetase complexed with cair-mg2+ and adp
7	<a href="#">c3nuaB_</a>	 Alignment		100.0	25	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole-succinocarboxamide synthase; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole-succinocarboxamide2 synthase from clostridium perfringens
8	<a href="#">c3u54B_</a>	 Alignment		100.0	30	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole-succinocarboxamide synthase; <b>PDBTitle:</b> crystal structure (type-1) of saicar synthetase from pyrococcus2 horikoshii ot3
9	<a href="#">c4fe2B_</a>	 Alignment		100.0	30	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole-succinocarboxamide synthase; <b>PDBTitle:</b> x-ray structure of saicar synthetase (purc) from streptococcus2 pneumoniae complexed with air, adp, asp and mg2+
10	<a href="#">c4ja0A_</a>	 Alignment		100.0	27	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase; <b>PDBTitle:</b> crystal structure of the invertebrate bi-functional purine2 biosynthesis enzyme paics at 2.8 a resolution
11	<a href="#">d1kuta_</a>	 Alignment		100.0	29	<b>Fold:</b> SAICAR synthase-like <b>Superfamily:</b> SAICAR synthase-like <b>Family:</b> SAICAR synthase

12	<a href="#">c2h31A_</a>		Alignment		100.0	26	<b>PDB header:</b> ligase, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> multifunctional protein ade2; <b>PDBTitle:</b> crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
13	<a href="#">d2bcgg2</a>		Alignment		57.9	14	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GDI-like N domain
14	<a href="#">c6g51v_</a>		Alignment		32.2	12	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> 40s ribosomal protein s21; <b>PDBTitle:</b> cryo-em structure of a late human pre-40s ribosomal subunit - state d
15	<a href="#">c4im2A_</a>		Alignment		29.2	12	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase tkb1; <b>PDBTitle:</b> structure of tank-binding kinase 1
16	<a href="#">c1zp9A_</a>		Alignment		27.7	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rio1 kinase; <b>PDBTitle:</b> crystal structure of full-length a.fulgidus rio1 serine kinase bound2 to atp and mn2+ ions.
17	<a href="#">c4l8nA_</a>		Alignment		25.4	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pdz domain protein; <b>PDBTitle:</b> crystal structure of a pdz domain protein (bdi_1242) from2 parabacteroides distasonis atcc 8503 at 2.50 a resolution
18	<a href="#">c5hb8B_</a>		Alignment		24.8	46	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoporin nup53; <b>PDBTitle:</b> crystal structure of chaetomium thermophilum nup53 rrm (space group2 p3121)
19	<a href="#">d2r7ka2</a>		Alignment		23.5	10	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> PurP ATP-binding domain-like
20	<a href="#">c5c4iC_</a>		Alignment		21.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxalate oxidoreductase subunit beta; <b>PDBTitle:</b> structure of an oxalate oxidoreductase
21	<a href="#">c5aj3k_</a>		Alignment	not modelled	21.4	24	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> mitoribosomal protein us11m, mrps11; <b>PDBTitle:</b> structure of the small subunit of the mammalian mitoribosome
22	<a href="#">c3c0uA_</a>		Alignment	not modelled	18.7	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yaeq; <b>PDBTitle:</b> crystal structure of e.coli yaeq protein
23	<a href="#">d2g3wa1</a>		Alignment	not modelled	18.2	21	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> YaeQ-like
24	<a href="#">c3byvA_</a>		Alignment	not modelled	17.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rhoptry kinase; <b>PDBTitle:</b> crystal structure of toxoplasma gondii specific rhoptry2 antigen kinase domain
25	<a href="#">d1xyqa_</a>		Alignment	not modelled	16.5	25	<b>Fold:</b> Prion-like <b>Superfamily:</b> Prion-like <b>Family:</b> Prion-like
26	<a href="#">c1dx0A_</a>		Alignment	not modelled	15.2	20	<b>PDB header:</b> prion protein <b>Chain:</b> A: <b>PDB Molecule:</b> prion protein; <b>PDBTitle:</b> bovine prion protein residues 23-230
27	<a href="#">d1i4ma_</a>		Alignment	not modelled	15.2	20	<b>Fold:</b> Prion-like <b>Superfamily:</b> Prion-like <b>Family:</b> Prion-like
28	<a href="#">d1dwya_</a>		Alignment	not modelled	15.1	20	<b>Fold:</b> Prion-like <b>Superfamily:</b> Prion-like <b>Family:</b> Prion-like
29	<a href="#">d1nka1</a>		Alignment	not modelled	14.9	42	<b>Fold:</b> Pre-protein crosslinking domain of SecA <b>Superfamily:</b> Pre-protein crosslinking domain of SecA

						<b>Family:</b> Pre-protein crosslinking domain of SecA
30	<a href="#">c1fo7A_</a>	Alignment	not modelled	14.5	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> prion protein; <b>PDBTitle:</b> human prion protein mutant e200k fragment 90-231
31	<a href="#">d1fo7a_</a>	Alignment	not modelled	14.5	20	<b>Fold:</b> Prion-like <b>Superfamily:</b> Prion-like <b>Family:</b> Prion-like
32	<a href="#">d1xyua_</a>	Alignment	not modelled	13.4	25	<b>Fold:</b> Prion-like <b>Superfamily:</b> Prion-like <b>Family:</b> Prion-like
33	<a href="#">d1tqba_</a>	Alignment	not modelled	13.2	20	<b>Fold:</b> Prion-like <b>Superfamily:</b> Prion-like <b>Family:</b> Prion-like
34	<a href="#">d1tf5a1</a>	Alignment	not modelled	13.1	30	<b>Fold:</b> Pre-protein crosslinking domain of SecA <b>Superfamily:</b> Pre-protein crosslinking domain of SecA <b>Family:</b> Pre-protein crosslinking domain of SecA
35	<a href="#">c3dzoA_</a>	Alignment	not modelled	13.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rhopty kinase domain; <b>PDBTitle:</b> crystal structure of a rhopty kinase from toxoplasma gondii
36	<a href="#">d1b10a_</a>	Alignment	not modelled	12.8	20	<b>Fold:</b> Prion-like <b>Superfamily:</b> Prion-like <b>Family:</b> Prion-like
37	<a href="#">d1pmia_</a>	Alignment	not modelled	12.1	24	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmLC-like cupins <b>Family:</b> Type I phosphomannose isomerase
38	<a href="#">d1xyxa_</a>	Alignment	not modelled	12.0	20	<b>Fold:</b> Prion-like <b>Superfamily:</b> Prion-like <b>Family:</b> Prion-like
39	<a href="#">c1xu0A_</a>	Alignment	not modelled	11.8	40	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> prion protein; <b>PDBTitle:</b> solution structure of xenopus leavis prion protein
40	<a href="#">d1xu0a_</a>	Alignment	not modelled	11.8	40	<b>Fold:</b> Prion-like <b>Superfamily:</b> Prion-like <b>Family:</b> Prion-like
41	<a href="#">d1u3ma_</a>	Alignment	not modelled	11.3	40	<b>Fold:</b> Prion-like <b>Superfamily:</b> Prion-like <b>Family:</b> Prion-like
42	<a href="#">c6c87A_</a>	Alignment	not modelled	10.8	40	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> rab gdp dissociation inhibitor alpha; <b>PDBTitle:</b> crystal structure of rab gdp dissociation inhibitor alpha from2 naegleria fowleri
43	<a href="#">c6m7zE_</a>	Alignment	not modelled	9.9	10	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> bradyzoite pseudokinase 1; <b>PDBTitle:</b> a divergent kinase lacking the glycine-rich loop regulates membrane2 ultrastructure of the toxoplasma parasitophorous vacuole
44	<a href="#">c1ehiB_</a>	Alignment	not modelled	9.7	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine:d-lactate ligase; <b>PDBTitle:</b> d-alanine:d-lactate ligase (Imddl2) of vancomycin-resistant2 leuconostoc mesenteroides
45	<a href="#">d2ot9a1</a>	Alignment	not modelled	9.6	13	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> YaeQ-like
46	<a href="#">d2d6fa1</a>	Alignment	not modelled	9.5	24	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> GatD N-terminal domain-like <b>Family:</b> GatD N-terminal domain-like
47	<a href="#">d1xyka_</a>	Alignment	not modelled	9.2	25	<b>Fold:</b> Prion-like <b>Superfamily:</b> Prion-like <b>Family:</b> Prion-like
48	<a href="#">d1y0na_</a>	Alignment	not modelled	9.0	10	<b>Fold:</b> YehU-like <b>Superfamily:</b> YehU-like <b>Family:</b> YehU-like
49	<a href="#">c5c5tB_</a>	Alignment	not modelled	8.9	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> prolyl 4-hydroxylase; <b>PDBTitle:</b> the crystal structure of viral collagen prolyl hydroxylase vcph from2 paramecium bursaria chlorella virus-1 - 2og complex
50	<a href="#">d1uw3a_</a>	Alignment	not modelled	8.8	10	<b>Fold:</b> Prion-like <b>Superfamily:</b> Prion-like <b>Family:</b> Prion-like
51	<a href="#">c5lnkh_</a>	Alignment	not modelled	8.8	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> mitochondrial complex i, nd1 subunit; <b>PDBTitle:</b> entire ovine respiratory complex i
52	<a href="#">c3h1yA_</a>	Alignment	not modelled	8.8	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> mannose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of mannose 6-phosphate isomerase from2 salmonella typhimurium bound to substrate (f6p)and metal3 atom (zn)
53	<a href="#">c6cp8D_</a>	Alignment	not modelled	8.8	25	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> D: <b>PDB Molecule:</b> cdii; <b>PDBTitle:</b> contact-dependent growth inhibition toxin-immunity protein complex2 from from e. coli 3006
54	<a href="#">c5x62A_</a>	Alignment	not modelled	8.5	43	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carnosine n-methyltransferase; <b>PDBTitle:</b> crystal structure of a carnosine n-methyltransferase bound by adohcy
55	<a href="#">c5yf1A_</a>	Alignment	not modelled	8.4	86	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carnosine n-methyltransferase; <b>PDBTitle:</b> crystal structure of carnmt1 bound to carnosine and sfg
						<b>Fold:</b> Anticodon-binding domain-like

56	<a href="#">d2amha1</a>	Alignment	not modelled	8.2	6	<b>Superfamily:</b> ITPase-like <b>Family:</b> Maf-like
57	<a href="#">c2pvpB</a>	Alignment	not modelled	7.7	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine-d-alanine ligase; <b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
58	<a href="#">c2c4rL</a>	Alignment	not modelled	7.6	35	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> ribonuclease e; <b>PDBTitle:</b> catalytic domain of e. coli rnase e
59	<a href="#">c2mduA</a>	Alignment	not modelled	6.9	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> pin1 ww domain; <b>PDBTitle:</b> circular permutant of the ww domain with loop 1 excised
60	<a href="#">c3j3aK</a>	Alignment	not modelled	6.9	50	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> 40s ribosomal protein s10; <b>PDBTitle:</b> structure of the human 40s ribosomal proteins
61	<a href="#">c5yk2A</a>	Alignment	not modelled	6.8	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable conserved atp-binding protein abc transporter; <b>PDBTitle:</b> the complex structure of rv3197-erythromycin from mycobacterium2 tuberculosis
62	<a href="#">c3q2oB</a>	Alignment	not modelled	6.5	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit; <b>PDBTitle:</b> crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
63	<a href="#">c5xxuK</a>	Alignment	not modelled	6.4	36	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> ribosomal protein es10; <b>PDBTitle:</b> small subunit of toxoplasma gondii ribosome
64	<a href="#">c3um2E</a>	Alignment	not modelled	6.3	44	<b>PDB header:</b> membrane protein/transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> charged multivesicular body protein 5; <b>PDBTitle:</b> crystal structure of the brox bro1 domain in complex with the c-2 terminal tail of chmp5
65	<a href="#">c3um2B</a>	Alignment	not modelled	6.3	44	<b>PDB header:</b> membrane protein/transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> charged multivesicular body protein 5; <b>PDBTitle:</b> crystal structure of the brox bro1 domain in complex with the c-2 terminal tail of chmp5
66	<a href="#">c3um1E</a>	Alignment	not modelled	6.3	44	<b>PDB header:</b> membrane protein/transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> charged multivesicular body protein 5; <b>PDBTitle:</b> crystal structure of the brox bro1 domain in complex with the c-2 terminal tail of chmp5
67	<a href="#">d1u5la</a>	Alignment	not modelled	6.3	20	<b>Fold:</b> Prion-like <b>Superfamily:</b> Prion-like <b>Family:</b> Prion-like
68	<a href="#">c3um0B</a>	Alignment	not modelled	6.2	44	<b>PDB header:</b> membrane protein/transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> charged multivesicular body protein 5; <b>PDBTitle:</b> crystal structure of the brox bro1 domain in complex with the c-2 terminal tail of chmp5
69	<a href="#">d1i4ya</a>	Alignment	not modelled	6.0	11	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Hemerythrin-like <b>Family:</b> Hemerythrin-like
70	<a href="#">c1jrjA</a>	Alignment	not modelled	5.8	42	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> exendin-4; <b>PDBTitle:</b> solution structure of exendin-4 in 30-vol% trifluoroethanol
71	<a href="#">c5wsxA</a>	Alignment	not modelled	5.7	63	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of sav606
72	<a href="#">c3g5oA</a>	Alignment	not modelled	5.6	28	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein rv2865; <b>PDBTitle:</b> the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
73	<a href="#">c2mdwA</a>	Alignment	not modelled	5.6	15	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> designed protein; <b>PDBTitle:</b> nmr structure of a strand-swapped dimer of the ww domain
74	<a href="#">c4qiwV</a>	Alignment	not modelled	5.6	18	<b>PDB header:</b> transcription <b>Chain:</b> V: <b>PDB Molecule:</b> dna-directed rna polymerase subunit n; <b>PDBTitle:</b> crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
75	<a href="#">d1twfj</a>	Alignment	not modelled	5.6	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> RNA polymerase subunit RPB10 <b>Family:</b> RNA polymerase subunit RPB10
76	<a href="#">c4egjD</a>	Alignment	not modelled	5.5	17	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase from burkholderia2 xenovorans
77	<a href="#">c1e4eB</a>	Alignment	not modelled	5.4	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> vancomycin/teicoplanin a-type resistance protein vana; <b>PDBTitle:</b> d-alanyl-d-lacate ligase
78	<a href="#">c2rukA</a>	Alignment	not modelled	5.2	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> cellular tumor antigen p53; <b>PDBTitle:</b> solution structure of the complex between p53 transactivation domain 22 and tfiih p62 ph domain