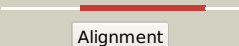

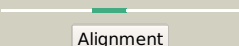

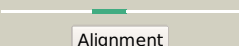
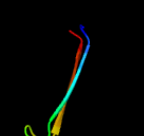
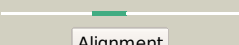
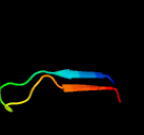

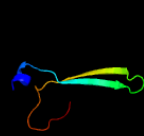
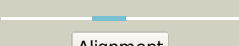
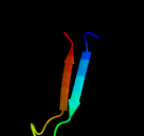

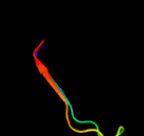

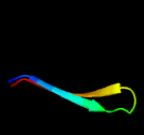



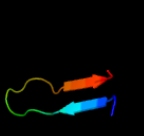

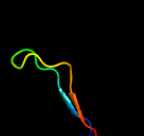


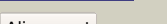

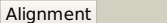
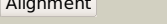
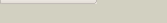



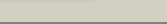



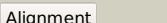
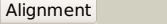
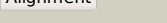



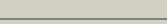


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2762c_(-)_3072647_3073066
Date	Wed Aug 7 12:50:42 BST 2019
Unique Job ID	a4815cf837c10d88

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5uuja_</a>	 Alignment		98.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> alkz; <b>PDBTitle:</b> streptomyces sahachiroi dna glycosylase alkz
2	<a href="#">d2ae8a2</a>	 Alignment		47.4	25	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Imidazole glycerol phosphate dehydratase
3	<a href="#">d1rhya2</a>	 Alignment		45.6	35	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Imidazole glycerol phosphate dehydratase
4	<a href="#">d2f1da2</a>	 Alignment		41.7	25	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Imidazole glycerol phosphate dehydratase
5	<a href="#">c4icxA_</a>	 Alignment		39.5	22	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> centrosomal protein of 120 kda; <b>PDBTitle:</b> n-terminal c2 domain of human cep120
6	<a href="#">c2f1dP_</a>	 Alignment		37.1	25	<b>PDB header:</b> lyase <b>Chain:</b> P; <b>PDB Molecule:</b> imidazoleglycerol-phosphate dehydratase 1; <b>PDBTitle:</b> x-ray structure of imidazoleglycerol-phosphate dehydratase
7	<a href="#">c1rhyB_</a>	 Alignment		37.1	35	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> imidazole glycerol phosphate dehydratase; <b>PDBTitle:</b> crystal structure of imidazole glycerol phosphate dehydratase
8	<a href="#">c2ae8C_</a>	 Alignment		36.1	25	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> imidazoleglycerol-phosphate dehydratase; <b>PDBTitle:</b> crystal structure of imidazoleglycerol-phosphate dehydratase from2 staphylococcus aureus subsp. aureus n315
9	<a href="#">c5dnlA_</a>	 Alignment		31.8	30	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> imidazoleglycerol-phosphate dehydratase; <b>PDBTitle:</b> crystal structure of igpd from pyrococcus furiosus in complex with2 (s)-c348
10	<a href="#">c4lomA_</a>	 Alignment		30.8	35	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> imidazoleglycerol-phosphate dehydratase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis hisb in complex with2 its substrate
11	<a href="#">c6ezmL_</a>	 Alignment		29.1	35	<b>PDB header:</b> lyase <b>Chain:</b> L; <b>PDB Molecule:</b> imidazoleglycerol-phosphate dehydratase; <b>PDBTitle:</b> imidazoleglycerol-phosphate dehydratase from saccharomyces cerevisiae

12	<a href="#">c2aj6A_</a>	Alignment		27.5	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein mw0638; <b>PDBTitle:</b> crystal structure of a putative gnat family acetyltransferase (mw0638)2 from staphylococcus aureus subsp. aureus at 1.63 a resolution
13	<a href="#">c6fwhH_</a>	Alignment		24.0	35	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> imidazoleglycerol-phosphate dehydratase; <b>PDBTitle:</b> acanthamoeba igpd in complex with r-c348 to 1.7a resolution
14	<a href="#">d2hfqa1</a>	Alignment		22.5	17	<b>Fold:</b> NE1680-like <b>Superfamily:</b> NE1680-like <b>Family:</b> NE1680-like
15	<a href="#">c2hfqa_</a>	Alignment		22.5	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> nmr structure of protein ne1680 from nitrosomonas europaea:2 northeast structural genomics consortium target net5
16	<a href="#">d2aj6a1</a>	Alignment		22.2	14	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
17	<a href="#">d1vkoa1</a>	Alignment		20.7	10	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
18	<a href="#">c5i0cA_</a>	Alignment		20.7	6	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yjdj; <b>PDBTitle:</b> crystal structure of predicted acyltransferase yjdj with acyl-coa n-2 acyltransferase domain from escherichia coli str. k-12
19	<a href="#">d2ghvc1</a>	Alignment		19.1	19	<b>Fold:</b> SARS receptor-binding domain-like <b>Superfamily:</b> SARS receptor-binding domain-like <b>Family:</b> SARS receptor-binding domain-like
20	<a href="#">c4rrcA_</a>	Alignment		17.4	20	<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)
21	<a href="#">c1j2oA_</a>	Alignment	not modelled	17.1	38	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fusion of rhombotin-2 and lim domain-binding <b>PDBTitle:</b> structure of flin2, a complex containing the n-terminal lim2 domain of lmo2 and ldb1-lid
22	<a href="#">d1p1ja1</a>	Alignment	not modelled	16.9	11	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
23	<a href="#">c5gyqA_</a>	Alignment	not modelled	16.3	19	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> putative receptor-binding domain of bat-derived coronavirus hku9 spike2 protein
24	<a href="#">c5xqrF_</a>	Alignment	not modelled	15.4	19	<b>PDB header:</b> viral protein <b>Chain:</b> F: <b>PDB Molecule:</b> spike protein s1; <b>PDBTitle:</b> structure of the s1 subunit c-terminal domain from bat-derived2 coronavirus hku5 spike protein
25	<a href="#">c4qzvB_</a>	Alignment	not modelled	13.9	11	<b>PDB header:</b> hydrolase/viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> spike protein s1; <b>PDBTitle:</b> bat-derived coronavirus hku4 uses mers-cov receptor human cd26 for2 cell entry
26	<a href="#">c6hu9u_</a>	Alignment	not modelled	11.2	32	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> U: <b>PDB Molecule:</b> cytochrome b-c1 complex subunit 10; <b>PDBTitle:</b> iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
27	<a href="#">c2r98A_</a>	Alignment	not modelled	10.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetylglutamate synthase; <b>PDBTitle:</b> crystal structure of n-acetylglutamate synthase (selenomet2 substituted) from neisseria gonorrhoeae
28	<a href="#">c3sciE_</a>	Alignment	not modelled	9.6	20	<b>PDB header:</b> hydrolase/viral protein <b>Chain:</b> E: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> crystal structure of spike protein receptor-binding domain from a2 predicted sars coronavirus human strain complexed with human receptor3 ace2

29	<a href="#">c3lodA</a>	 Alignment	not modelled	9.4	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acyl-coa n-acyltransferase; <b>PDBTitle:</b> the crystal structure of the putative acyl-coa n-acyltransferase from2 klebsiella pneumoniae subsp.pneumoniae mgh 78578
30	<a href="#">c1p1hD</a>	 Alignment	not modelled	8.8	11	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> inositol-3-phosphate synthase; <b>PDBTitle:</b> crystal structure of the 1l-myo-inositol/nad+ complex
31	<a href="#">c4kqzA</a>	 Alignment	not modelled	8.8	11	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> s protein; <b>PDBTitle:</b> structure of the receptor binding domain (rbd) of mers-cov spike
32	<a href="#">c2atmA</a>	 Alignment	not modelled	7.2	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hyaluronoglucosaminidase; <b>PDBTitle:</b> crystal structure of the recombinant allergen ves v 2
33	<a href="#">c1w18A</a>	 Alignment	not modelled	7.1	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> levansucrase; <b>PDBTitle:</b> crystal structure of levansucrase from gluconacetobacter2 diazotrophicus
34	<a href="#">d1bwva2</a>	 Alignment	not modelled	6.9	28	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RuBisCO, large subunit, small (N-terminal) domain <b>Family:</b> Ribulose 1,5-bisphosphate carboxylase-oxygenase
35	<a href="#">c2hl2A</a>	 Alignment	not modelled	6.8	22	<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="#">c3d8pB</a>	 Alignment	not modelled	6.7	7	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyltransferase of gnat family; <b>PDBTitle:</b> crystal structure of acetyltransferase of gnat family (np_373092.1)2 from staphylococcus aureus mu50 at 2.20 a resolution
37	<a href="#">d1fcga</a>	 Alignment	not modelled	6.2	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Bee venom hyaluronidase
38	<a href="#">c2q0yA</a>	 Alignment	not modelled	6.1	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gcn5-related n-acetyltransferase; <b>PDBTitle:</b> crystal structure of gcn5-related n-acetyltransferase (yp_295895.1)2 from ralstonia eutropha jmp134 at 1.80 a resolution
39	<a href="#">c2eemA</a>	 Alignment	not modelled	6.1	54	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> mytilin-b; <b>PDBTitle:</b> solution structure of the synthetic mytilin
40	<a href="#">c1fcuA</a>	 Alignment	not modelled	5.9	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hyaluronoglucosaminidase; <b>PDBTitle:</b> crystal structure (trigonal) of bee venom hyaluronidase
41	<a href="#">c2vzzA</a>	 Alignment	not modelled	5.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rv0802c; <b>PDBTitle:</b> crystal structure of rv0802c from mycobacterium2 tuberculosis in complex with succinyl-coa
42	<a href="#">c2pe4A</a>	 Alignment	not modelled	5.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hyaluronidase-1; <b>PDBTitle:</b> structure of human hyaluronidase 1, a hyaluronan hydrolyzing enzyme2 involved in tumor growth and angiogenesis
43	<a href="#">c1vkoA</a>	 Alignment	not modelled	5.7	9	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> inositol-3-phosphate synthase; <b>PDBTitle:</b> crystal structure of inositol-3-phosphate synthase (ce21227) from2 caenorhabditis elegans at 2.30 a resolution
44	<a href="#">d1gk8a2</a>	 Alignment	not modelled	5.7	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RuBisCO, large subunit, small (N-terminal) domain <b>Family:</b> Ribulose 1,5-bisphosphate carboxylase-oxygenase
45	<a href="#">c5wvxA</a>	 Alignment	not modelled	5.5	25	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> trypsin/chymotrypsin inhibitor; <b>PDBTitle:</b> crystal structure of bifunctional kunitz type trypsin /amylase2 inhibitor (amtin) from the tubers of alocaasia macrorrhiza
46	<a href="#">c4rasC</a>	 Alignment	not modelled	5.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxidoreductase, nad-binding/iron-sulfur cluster-binding <b>PDBTitle:</b> reductive dehalogenase structure suggests a mechanism for b12-2 dependent dehalogenation
47	<a href="#">c5ys3B</a>	 Alignment	not modelled	5.4	8	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> succinate-acetate permease; <b>PDBTitle:</b> 1.8 angstrom crystal structure of succinate-acetate permease from2 citrobacter koseri
48	<a href="#">c2wpwA</a>	 Alignment	not modelled	5.3	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> orf14; <b>PDBTitle:</b> tandem gnat protein from the clavulanic acid biosynthesis pathway2 (without accoa)
49	<a href="#">c2z5cA</a>	 Alignment	not modelled	5.1	37	<b>PDB header:</b> chaperone/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein ypl144w; <b>PDBTitle:</b> crystal structure of a novel chaperone complex for yeast 20s2 proteasome assembly