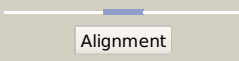

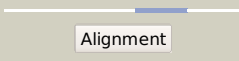

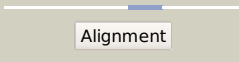

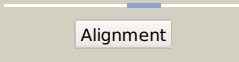
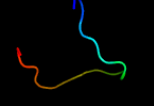
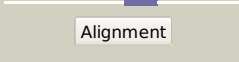
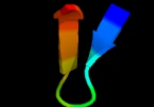
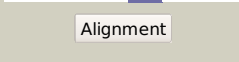

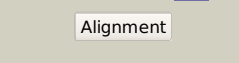
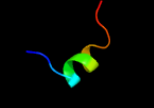
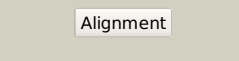

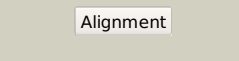
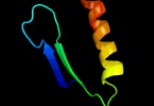
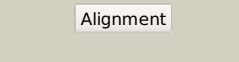

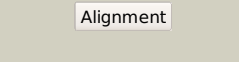

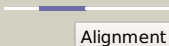
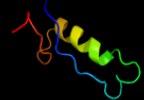
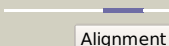
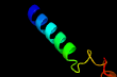
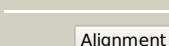
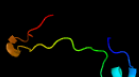
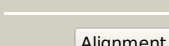
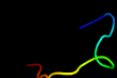
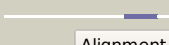
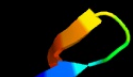
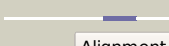
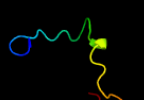
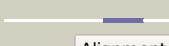
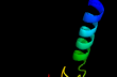

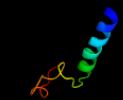

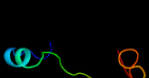
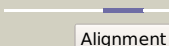


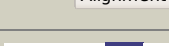
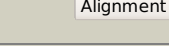
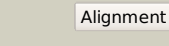

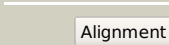
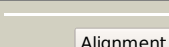


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0398c (-) _476682_477323
Date	Tue Jul 23 14:50:47 BST 2019
Unique Job ID	efb69b694a634ed2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">dlw27a_</a>	 Alignment		29.5	26	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> HAL/PAL-like
2	<a href="#">dls4ea2</a>	 Alignment		26.0	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Galactokinase
3	<a href="#">dlut1a_</a>	 Alignment		24.8	33	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Bacterial adhesins <b>Family:</b> Dr-family adhesin
4	<a href="#">d2vera1</a>	 Alignment		22.4	26	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Bacterial adhesins <b>Family:</b> Dr-family adhesin
5	<a href="#">c3ka5A_</a>	 Alignment		19.8	56	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> ribosome-associated protein y (psrp-1); <b>PDBTitle:</b> crystal structure of ribosome-associated protein y (psrp-1)2 from clostridium acetobutylicum. northeast structural3 genomics consortium target id car123a
6	<a href="#">c2bcmB_</a>	 Alignment		19.5	33	<b>PDB header:</b> cell adhesion <b>Chain:</b> B; <b>PDB Molecule:</b> f1845 fimbrial protein; <b>PDBTitle:</b> daae adhesin
7	<a href="#">d1xrua1</a>	 Alignment		18.7	47	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Kdul-like
8	<a href="#">c3k2tA_</a>	 Alignment		17.9	56	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> lmo2511 protein; <b>PDBTitle:</b> crystal structure of lmo2511 protein from listeria2 monocytogenes, northeast structural genomics consortium3 target lkr84a
9	<a href="#">d1piea2</a>	 Alignment		17.6	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Galactokinase
10	<a href="#">c3nz4A_</a>	 Alignment		16.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> phenylalanine ammonia-lyase; <b>PDBTitle:</b> crystal structure of a taxus phenylalanine aminomutase
11	<a href="#">d1wuuu2</a>	 Alignment		15.4	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Galactokinase

12	<a href="#">c4babC_</a>	 Alignment		14.8	21	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> phenylalanine aminomutase; <b>PDBTitle:</b> redesign of a phenylalanine aminomutase into a beta-phenylalanine2 ammonia lyase
13	<a href="#">c2o6yF_</a>	 Alignment		14.4	24	<b>PDB header:</b> lyase <b>Chain:</b> F; <b>PDB Molecule:</b> putative histidine ammonia-lyase; <b>PDBTitle:</b> tyrosine ammonia-lyase from rhodobacter sphaeroides
14	<a href="#">c4k6lC_</a>	 Alignment		13.7	31	<b>PDB header:</b> toxin <b>Chain:</b> C; <b>PDB Molecule:</b> putative pertussis-like toxin subunit; <b>PDBTitle:</b> structure of typhoid toxin
15	<a href="#">c2qjvB_</a>	 Alignment		13.6	44	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized iolb-like protein; <b>PDBTitle:</b> crystal structure of an iolb-like protein (stm4420) from salmonella2 typhimurium lt2 at 1.90 a resolution
16	<a href="#">c3lyvF_</a>	 Alignment		12.4	75	<b>PDB header:</b> chaperone <b>Chain:</b> F; <b>PDB Molecule:</b> ribosome-associated factor y; <b>PDBTitle:</b> crystal structure of a domain of ribosome-associated factor y from2 streptococcus pyogenes serotype m6. northeast structural genomics3 consortium target id dr64a
17	<a href="#">c1yxeA_</a>	 Alignment		12.0	25	<b>PDB header:</b> immune system <b>Chain:</b> A; <b>PDB Molecule:</b> apical membrane antigen 1; <b>PDBTitle:</b> structure and inter-domain interactions of domain ii from the blood2 stage malarial protein, apical membrane antigen 1
18	<a href="#">c3unvB_</a>	 Alignment		11.7	11	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> admh; <b>PDBTitle:</b> pantoea agglomerans phenylalanine aminomutase
19	<a href="#">c6s7qG_</a>	 Alignment		11.0	18	<b>PDB header:</b> lyase <b>Chain:</b> G; <b>PDB Molecule:</b> ergothionase; <b>PDBTitle:</b> crystal structure of ergothioneine degrading enzyme ergothionase from2 treponema denticola in complex with desmethyl-ergothioneine sulfonic3 acid
20	<a href="#">c3dwqD_</a>	 Alignment		10.8	30	<b>PDB header:</b> toxin <b>Chain:</b> D; <b>PDB Molecule:</b> subtilase cytotoxin, subunit b; <b>PDBTitle:</b> crystal structure of the a-subunit of the ab5 toxin from e.2 coli with neu5gc-2,3gal-1,3glcnac
21	<a href="#">c2qveA_</a>	 Alignment	not modelled	10.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> tyrosine aminomutase; <b>PDBTitle:</b> crystal structure of sgtam bound to mechanism based inhibitor
22	<a href="#">c4rqoB_</a>	 Alignment	not modelled	10.0	22	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> l-serine dehydratase; <b>PDBTitle:</b> crystal structure of l-serine dehydratase from legionella pneumophila
23	<a href="#">d1gkma_</a>	 Alignment	not modelled	9.9	18	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> HAL/PAL-like
24	<a href="#">c3czoD_</a>	 Alignment	not modelled	9.4	14	<b>PDB header:</b> lyase <b>Chain:</b> D; <b>PDB Molecule:</b> histidine ammonia-lyase; <b>PDBTitle:</b> crystal structure of double mutant phenylalanine ammonia-lyase from2 anabaena variabilis
25	<a href="#">c5zktA_</a>	 Alignment	not modelled	9.3	41	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> putative transcription factor pcf6; <b>PDBTitle:</b> crystal structure of tcp domain of pcf6 in oryza sativa
26	<a href="#">d1wkta_</a>	 Alignment	not modelled	8.6	43	<b>Fold:</b> gamma-Crystallin-like <b>Superfamily:</b> gamma-Crystallin-like <b>Family:</b> Yeast killer toxin
27	<a href="#">c5whvF_</a>	 Alignment	not modelled	8.5	31	<b>PDB header:</b> toxin <b>Chain:</b> F; <b>PDB Molecule:</b> artb protein; <b>PDBTitle:</b> crystal structure of artb
28	<a href="#">c3d0jA_</a>	 Alignment	not modelled	8.2	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein ca_c3497; <b>PDBTitle:</b> crystal structure of conserved protein of unknown function ca_c34972 from clostridium acetobutylicum atcc 824
		 Alignment				<b>PDB header:</b> hydrolase

29	<a href="#">c3rnvA_</a>	Alignment	not modelled	8.0	32	<b>Chain:</b> A: <b>PDB Molecule:</b> helper component proteinase; <b>PDBTitle:</b> structure of the autocatalytic cysteine protease domain of potyvirus2 helper-component proteinase
30	<a href="#">c5zktB_</a>	Alignment	not modelled	7.9	41	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcription factor pcf6; <b>PDBTitle:</b> crystal structure of tcp domain of pcf6 in oryza sativa
31	<a href="#">c2n2uA_</a>	Alignment	not modelled	7.6	23	<b>PDB header:</b> unknown function, structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> or358; <b>PDBTitle:</b> solution nmr structure of de novo designed ferredoxin fold protein2 sfr3, northeast structural genomics consortium (nesg) target or358
32	<a href="#">c3zldB_</a>	Alignment	not modelled	7.5	56	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> rhoptry neck protein 2; <b>PDBTitle:</b> crystal structure of toxoplasma gondii sporozoite ama1 in2 complex with a 36 aa region of sporozoite ron2
33	<a href="#">d3cnxa1</a>	Alignment	not modelled	7.4	50	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SAV4671-like
34	<a href="#">d2fgga1</a>	Alignment	not modelled	7.3	26	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> Rv2632c-like <b>Family:</b> Rv2632c-like
35	<a href="#">c3a9lB_</a>	Alignment	not modelled	7.2	33	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> poly-gamma-glutamate hydrolase; <b>PDBTitle:</b> structure of bacteriophage poly-gamma-glutamate hydrolase
36	<a href="#">c1rfoC_</a>	Alignment	not modelled	7.0	60	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> whisker antigen control protein; <b>PDBTitle:</b> trimeric foldon of the t4 phagehead fibrin
37	<a href="#">c6dk9l_</a>	Alignment	not modelled	7.0	15	<b>PDB header:</b> lyase <b>Chain:</b> I: <b>PDB Molecule:</b> dna damage-inducible protein; <b>PDBTitle:</b> yeast ddi2 cyanamide hydratase
38	<a href="#">d1cz5a2</a>	Alignment	not modelled	6.9	12	<b>Fold:</b> Cdc48 domain 2-like <b>Superfamily:</b> Cdc48 domain 2-like <b>Family:</b> Cdc48 domain 2-like
39	<a href="#">d1ldpa_</a>	Alignment	not modelled	6.7	50	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
40	<a href="#">c5onkA_</a>	Alignment	not modelled	6.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> yndl; <b>PDBTitle:</b> native yndl
41	<a href="#">d2rgqa1</a>	Alignment	not modelled	6.4	38	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
42	<a href="#">d2dsta1</a>	Alignment	not modelled	6.2	28	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> TTHA1544-like
43	<a href="#">c5vfbB_</a>	Alignment	not modelled	6.0	31	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> malate synthase g; <b>PDBTitle:</b> 1.36 angstrom resolution crystal structure of malate synthase g from2 pseudomonas aeruginosa in complex with glycolic acid.
44	<a href="#">c4wpyA_</a>	Alignment	not modelled	5.6	19	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein dl-rv1738; <b>PDBTitle:</b> racemic crystal structure of rv1738 from mycobacterium tuberculosis2 (form-ii)
45	<a href="#">c5x3lA_</a>	Alignment	not modelled	5.6	54	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> pilosulin-1; <b>PDBTitle:</b> solution structure of a novel antimicrobial peptide, p1, from jumper2 ant myrmecia pilosula
46	<a href="#">c1sseA_</a>	Alignment	not modelled	5.3	56	<b>PDB header:</b> transcription activator <b>Chain:</b> A: <b>PDB Molecule:</b> ap-1 like transcription factor yap1; <b>PDBTitle:</b> solution structure of the oxidized form of the yap1 redox2 domain
47	<a href="#">c2lnbA_</a>	Alignment	not modelled	5.3	40	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> z-dna-binding protein 1; <b>PDBTitle:</b> solution nmr structure of n-terminal domain (6-74) of human zbp12 protein, northeast structural genomics consortium target hr8174a.
48	<a href="#">c1htlC_</a>	Alignment	not modelled	5.2	30	<b>PDB header:</b> enterotoxin <b>Chain:</b> C: <b>PDB Molecule:</b> heat-labile enterotoxin, subunit a; <b>PDBTitle:</b> mutation of a buried residue causes lack of activity but no2 conformational change: crystal structure of e. coli heat-3 labile enterotoxin mutant val 97--> lys
49	<a href="#">c5yysC_</a>	Alignment	not modelled	5.2	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> l-fucokinase, l-fucose-1-p guanylyltransferase; <b>PDBTitle:</b> cryo-em structure of l-fucokinase, gdp-fucose pyrophosphorylase (fkp)2 in bacteroides fragilis