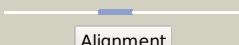
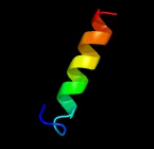

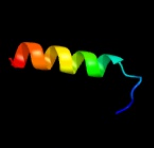
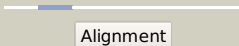
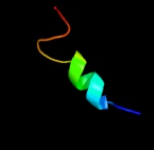



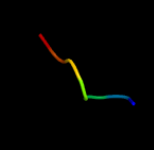
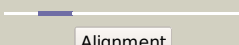
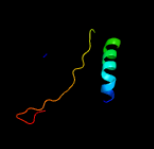
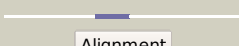
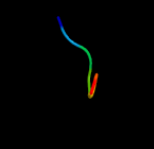
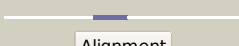


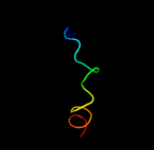

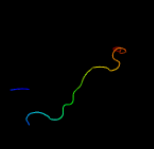




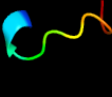

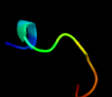

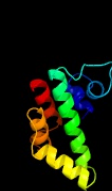
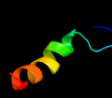
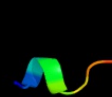


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1678 (-) _1902404_1903306
Date	Fri Aug 2 13:30:27 BST 2019
Unique Job ID	e07df2ea22d1f2e1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3k2kA_	 Alignment		23.0	15	PDB header: hydrolase Chain: A; PDB Molecule: putative carboxypeptidase; PDBTitle: crystal structure of putative carboxypeptidase (yp_103406.1) from2 burkholderia mallei atcc 23344 at 2.49 a resolution
2	c3l2nA_	 Alignment		21.9	20	PDB header: hydrolase Chain: A; PDB Molecule: peptidase m14, carboxypeptidase a; PDBTitle: crystal structure of putative carboxypeptidase a (yp_562911.1) from2 shewanella denitrificans os-217 at 2.39 a resolution
3	c5lnkn_	 Alignment		21.8	25	PDB header: oxidoreductase Chain: N; PDB Molecule: mitochondrial complex i, nd2 subunit; PDBTitle: entire ovine respiratory complex i
4	c5t2xC_	 Alignment		18.7	22	PDB header: unknown function Chain: C; PDB Molecule: uncharacterized protein lpg1670; PDBTitle: crystal structure of uncharacterised protein lpg1670
5	c2hntC_	 Alignment		14.7	43	PDB header: serine protease Chain: C; PDB Molecule: gamma-thrombin; PDBTitle: crystallographic structure of human gamma-thrombin
6	c4ywcA_	 Alignment		14.4	20	PDB header: transcription regulator Chain: A; PDB Molecule: transcription factor myc3; PDBTitle: crystal structure of myc3(5-242) fragment in complex with jaz9(218-2 239) peptide
7	c4xe4A_	 Alignment		14.1	29	PDB header: blood clotting Chain: A; PDB Molecule: coagulation factor xii; PDBTitle: coagulation factor xii protease domain crystal structure
8	c4er8A_	 Alignment		13.5	17	PDB header: dna binding protein/dna Chain: A; PDB Molecule: tnparep for protein; PDBTitle: structure of the rep associates tyrosine transposase bound to a rep2 hairpin
9	c2lcyA_	 Alignment		11.9	10	PDB header: viral protein Chain: A; PDB Molecule: virion spike glycoprotein; PDBTitle: nmr structure of the complete internal fusion loop from ebolavirus gp22 at ph 5.5
10	c5uquyB_	 Alignment		11.8	12	PDB header: viral protein/immune system Chain: B; PDB Molecule: envelope glycoprotein gp2; PDBTitle: crystal structure of marburg virus gp in complex with the human2 survivor antibody mr78
11	c2asuB_	 Alignment		11.0	57	PDB header: hydrolase Chain: B; PDB Molecule: hepatocyte growth factor-like protein; PDBTitle: crystal structure of the beta-chain of hgfl/msp

12	c1q90G_	Alignment		10.6	75	PDB header: photosynthesis Chain: G: PDB Molecule: cytochrome b6f complex subunit petg; PDBTitle: structure of the cytochrome b6f (plastoquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
13	d1q90g_	Alignment		10.6	75	Fold: Single transmembrane helix Superfamily: PetG subunit of the cytochrome b6f complex Family: PetG subunit of the cytochrome b6f complex
14	c5e4vA_	Alignment		9.8	64	PDB header: viral protein Chain: A: PDB Molecule: nucleoprotein,phosphoprotein; PDBTitle: crystal structure of measles n0-p complex
15	d2bs2c1	Alignment		9.5	18	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Fumarate reductase respiratory complex cytochrome b subunit, FrdC
16	c4uftB_	Alignment		9.3	64	PDB header: rna binding protein Chain: B: PDB Molecule: nucleoprotein; PDBTitle: structure of the helical measles virus nucleocapsid
17	c4v11C_	Alignment		9.2	83	PDB header: sugar binding protein Chain: C: PDB Molecule: carbohydrate binding module; PDBTitle: high resolution structure of a novel carbohydrate binding module from2 glycoside hydrolase family 9 (cel9a) from ruminococcus flavefaciens3 fd-1
18	c5dz7A_	Alignment		9.2	18	PDB header: transferase Chain: A: PDB Molecule: polyketide biosynthesis protein pkse; PDBTitle: structural basis of acyl transfer in a trans-at polyketide synthase
19	d1qmha2	Alignment		8.8	17	Fold: IF3-like Superfamily: EPT/RTPC-like Family: RNA 3'-terminal phosphate cyclase, RPTC
20	c4o9pC_	Alignment		8.7	33	PDB header: membrane protein Chain: C: PDB Molecule: nad(p) transhydrogenase subunit alpha 2; PDBTitle: crystal structure of thermus thermophilis transhydrogeanse domain ii2 dimer semet derivative
21	d1r44a_	Alignment	not modelled	8.6	14	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: VanX-like
22	c5lpeB_	Alignment	not modelled	8.5	43	PDB header: hydrolase Chain: B: PDB Molecule: kallikrein-10; PDBTitle: kallikrein-related peptidase 10 complex with zn2+
23	c1eptA_	Alignment	not modelled	8.5	14	PDB header: hydrolase (serine protease) Chain: A: PDB Molecule: porcine e-trypsin; PDBTitle: refined 1.8 angstroms resolution crystal structure of2 porcine epsilon-trypsin
24	c4o8jB_	Alignment	not modelled	8.0	13	PDB header: ligase/rna Chain: B: PDB Molecule: rna 3'-terminal phosphate cyclase; PDBTitle: crystal structure of rtca, the rna 3'-terminal phosphate cyclase from2 pyrococcus horikoshii, in complex with racaaa3'phosphate and adenine.
25	c3csyl_	Alignment	not modelled	8.0	11	PDB header: immune system/viral protein Chain: J: PDB Molecule: envelope glycoprotein gp2; PDBTitle: crystal structure of the trimeric ebola virus glycoprotein2 in complex with a neutralizing antibody from a human survivor
26	c6hwhX_	Alignment	not modelled	7.4	25	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
27	c4a37A_	Alignment	not modelled	7.3	29	PDB header: hydrolase Chain: A: PDB Molecule: metallo-carboxypeptidase; PDBTitle: metallo-carboxypeptidase from pseudomonas aeruginosa
28	c1hiaX_	Alignment	not modelled	7.2	33	PDB header: complex (protease/inhibitor) Chain: X: PDB Molecule: kallikrein; PDBTitle: kallikrein complexed with hirustasin

29	c6dexB	Alignment	not modelled	7.1	35	PDB header: recombination Chain: B; PDB Molecule: suppressor of hydroxyurea sensitivity protein 2; PDBTitle: structure of eremothecium gossypii shu1:shu2 complex
30	c1mntnB	Alignment	not modelled	7.0	71	PDB header: complex (hydrolase/inhibitor) Chain: B; PDB Molecule: alpha-chymotrypsin; PDBTitle: bovine alpha-chymotrypsin:bpti crystallization
31	c6cumA	Alignment	not modelled	6.9	52	PDB header: transferase Chain: A; PDB Molecule: lao/ao transport system atpase; PDBTitle: crystal structure of a c-terminal proteolytic fragment of a protein2 annotated as an lao/ao transport system atpase but likely meab and3 mmaa-like gtpase from mycobacterium smegmatis
32	c4bxaA	Alignment	not modelled	6.7	57	PDB header: blood clotting Chain: A; PDB Molecule: factor x-like protease; PDBTitle: crystal structure of the prothrombinase complex from the2 venom of pseudonaja textilis
33	c2laqA	Alignment	not modelled	6.6	100	PDB header: signaling protein Chain: A; PDB Molecule: accessory gland-specific peptide 70a; PDBTitle: solution structure of the sex peptide from drosophila melanogaster
34	d1q3xa1	Alignment	not modelled	6.6	57	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
35	c2k9pA	Alignment	not modelled	6.6	30	PDB header: membrane protein Chain: A; PDB Molecule: pheromone alpha factor receptor; PDBTitle: structure of tm1_tm2 in lppg micelles
36	d1luaa2	Alignment	not modelled	6.5	36	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Methylene-tetrahydromethanopterin dehydrogenase
37	c3s88J	Alignment	not modelled	6.5	13	PDB header: immune system/viral protein Chain: J; PDB Molecule: envelope glycoprotein; PDBTitle: crystal structure of sudan ebolavirus glycoprotein (strain gulu) bound2 to 16f6
38	d2d8xa2	Alignment	not modelled	6.5	86	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
39	d1kigh	Alignment	not modelled	6.4	57	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
40	c3f1sB	Alignment	not modelled	6.4	33	PDB header: hydrolase inhibitor/hydrolase Chain: B; PDB Molecule: vitamin k-dependent protein z; PDBTitle: crystal structure of protein z complexed with protein z-dependent2 inhibitor
41	c5f34A	Alignment	not modelled	6.3	25	PDB header: transferase Chain: A; PDB Molecule: phosphatidylinositol mannoside acyltransferase; PDBTitle: crystal structure of membrane associated pata from mycobacterium2 smegmatis in complex with s-hexadecyl coenzyme a - p21 space group
42	d1os8a	Alignment	not modelled	6.1	43	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
43	c5ldwf	Alignment	not modelled	5.8	18	PDB header: oxidoreductase Chain: F; PDB Molecule: nadh dehydrogenase [ubiquinone] flavoprotein 1, PDBTitle: structure of mammalian respiratory complex i, class1
44	c5lc5f	Alignment	not modelled	5.8	18	PDB header: oxidoreductase Chain: F; PDB Molecule: nadh dehydrogenase [ubiquinone] flavoprotein 1, PDBTitle: structure of mammalian respiratory complex i, class2
45	c5yimC	Alignment	not modelled	5.7	41	PDB header: transferase Chain: C; PDB Molecule: sdea; PDBTitle: structure of a legionella effector
46	c6ijo9	Alignment	not modelled	5.6	19	PDB header: photosynthesis Chain: 9; PDB Molecule: lhca9; PDBTitle: photosystem i of chlamydomonas reinhardtii
47	c3w94B	Alignment	not modelled	5.5	57	PDB header: hydrolase Chain: B; PDB Molecule: enteropeptidase-1; PDBTitle: structure of oryzias latipes enteropeptidase light chain
48	c2iu6B	Alignment	not modelled	5.5	20	PDB header: transferase Chain: B; PDB Molecule: dihydroxyacetone kinase; PDBTitle: regulation of the dha operon of lactococcus lactis
49	c2x4yB	Alignment	not modelled	5.4	75	PDB header: transcription Chain: B; PDB Molecule: histone h3.2; PDBTitle: molecular basis of histone h3k36me3 recognition by the pwwp domain of2 brpf1.
50	c1w0zU	Alignment	not modelled	5.4	29	PDB header: hydrolase Chain: U; PDB Molecule: urokinase-type plasminogen activator; PDBTitle: urokinase type plasminogen activator
51	d2hlca	Alignment	not modelled	5.4	29	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
52	d2p81a1	Alignment	not modelled	5.3	60	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
53	c2k9iB	Alignment	not modelled	5.2	60	PDB header: dna binding protein Chain: B; PDB Molecule: uncharacterized protein orf56; PDBTitle: nmr structure of plasmid copy control protein orf56 from sulfobolus2 islandicus
54	c2b9IA	Alignment	not modelled	5.2	67	PDB header: immune system/protein binding Chain: A; PDB Molecule: prophenoloxidase activating factor; PDBTitle: crystal structure of prophenoloxidase activating factor-ii from the2 beetle holotrichia diomphalia

55	c1fiwA_	Alignment	not modelled	5.2	57	PDB header: hydrolase Chain: A: PDB Molecule: beta-acrosin heavy chain; PDBTitle: three-dimensional structure of beta-acrosin from ram spermatozoa
56	d1h4wa_	Alignment	not modelled	5.1	14	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
57	c1bhxB_	Alignment	not modelled	5.1	43	PDB header: serine protease Chain: B: PDB Molecule: alpha thrombin; PDBTitle: x-ray structure of the complex of human alpha thrombin with the2 inhibitor sdz 229-357
58	c4u4cB_	Alignment	not modelled	5.0	43	PDB header: hydrolase Chain: B: PDB Molecule: protein air2,poly(a) rna polymerase protein 2; PDBTitle: the molecular architecture of the tramp complex reveals the2 organization and interplay of its two catalytic activities
59	c5fcrA_	Alignment	not modelled	5.0	14	PDB header: hydrolase Chain: A: PDB Molecule: complement factor d; PDBTitle: mouse complement factor d