



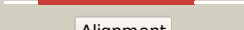

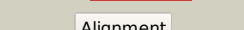







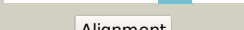


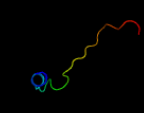

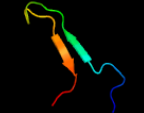

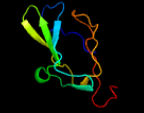


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1864c (-)_2111361_2112116
Date	Fri Aug 2 13:30:47 BST 2019
Unique Job ID	1a8ef8f27e5dba53

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1o65a_	 Alignment		100.0	28	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: MOSC (MOCO sulphurase C-terminal) domain
2	c5yhhA_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized conserved protein yim; PDBTitle: crystal structure of yim from geobacillus stearothermophilus
3	d1oruA_	 Alignment		100.0	21	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: MOSC (MOCO sulphurase C-terminal) domain
4	c6fw2A_	 Alignment		98.4	21	PDB header: oxidoreductase Chain: A: PDB Molecule: mitochondrial amidoxime-reducing component 1, endolysin, PDBTitle: crystal structure of human marc1
5	d2qamn1	 Alignment		51.7	38	Fold: Prokaryotic ribosomal protein L17 Superfamily: Prokaryotic ribosomal protein L17 Family: Prokaryotic ribosomal protein L17
6	c2q8iB_	 Alignment		46.5	16	PDB header: transferase Chain: B: PDB Molecule: dihydropolyllysine-residue acetyltransferase component of PDBTitle: pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
7	c3rj1P_	 Alignment		37.6	33	PDB header: transcription Chain: P: PDB Molecule: mediator of rna polymerase ii transcription subunit 17; PDBTitle: architecture of the mediator head module
8	d1jvwa_	 Alignment		37.1	33	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
9	d1gd8a_	 Alignment		32.6	31	Fold: Prokaryotic ribosomal protein L17 Superfamily: Prokaryotic ribosomal protein L17 Family: Prokaryotic ribosomal protein L17
10	c1vw4L_	 Alignment		32.3	33	PDB header: ribosome Chain: L: PDB Molecule: 54s ribosomal protein l8, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
11	c2dncA_	 Alignment		31.0	15	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase protein x component; PDBTitle: solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase

12	d1q6ha_	Alignment		30.1	29	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
13	d1y8ob1	Alignment		28.8	18	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
14	c2vcdA_	Alignment		28.3	43	PDB header: isomerase Chain: A: PDB Molecule: outer membrane protein mip; PDBTitle: solution structure of the fkbp-domain of legionella pneumophila mip in2 complex with rapamycin
15	d1fd9a_	Alignment		26.6	43	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
16	d1vjea_	Alignment		26.3	26	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: Autoinducer-2 production protein LuxS
17	c2gezE_	Alignment		25.3	33	PDB header: hydrolase Chain: E: PDB Molecule: l-asparaginase alpha subunit; PDBTitle: crystal structure of potassium-independent plant asparaginase
18	c1q6uA_	Alignment		23.8	29	PDB header: isomerase Chain: A: PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase fkpa; PDBTitle: crystal structure of fkpa from escherichia coli
19	d1j98a_	Alignment		23.0	21	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: Autoinducer-2 production protein LuxS
20	c3gwqB_	Alignment		21.9	29	PDB header: lyase Chain: B: PDB Molecule: d-serine deaminase; PDBTitle: crystal structure of a putative d-serine deaminase (bx_e_a4060) from2 burkholderia xenovorans lb400 at 2.00 a resolution
21	c1t3mA_	Alignment	not modelled	21.8	31	PDB header: hydrolase Chain: A: PDB Molecule: putative l-asparaginase; PDBTitle: structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
22	c2ke0A_	Alignment	not modelled	20.0	33	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: solution structure of peptidyl-prolyl cis-trans isomerase from2 burkholderia pseudomallei
23	c5i7pA_	Alignment	not modelled	19.4	40	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp1a,fkbp-type PDBTitle: crystal structure of fkbp12-if(slyd), a chimeric protein of human2 fkbp12 and the insert in flap domain of ecoli slyd
24	d2cqma1	Alignment	not modelled	18.9	19	Fold: Prokaryotic ribosomal protein L17 Superfamily: Prokaryotic ribosomal protein L17 Family: Prokaryotic ribosomal protein L17
25	c3j3vN_	Alignment	not modelled	18.8	28	PDB header: ribosome Chain: N: PDB Molecule: 50s ribosomal protein l17; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
26	c4jysA_	Alignment	not modelled	18.1	24	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of fkbp25 from plasmodium vivax
27	c5w21B_	Alignment	not modelled	16.4	24	PDB header: hydrolase/protein binding Chain: B: PDB Molecule: fibroblast growth factor 23; PDBTitle: crystal structure of a 1:1:1 fgf23-fgfr1c-akltho ternary complex
28	c2vn1A_	Alignment	not modelled	15.9	29	PDB header: isomerase Chain: A: PDB Molecule: 70 kda peptidylprolyl isomerase; PDBTitle: crystal structure of the fk506-binding domain of plasmodium2 falciparum fkbp35 in complex with fk506

29	d2zrk1	Alignment	not modelled	15.3	40	Fold: Prokaryotic ribosomal protein L17 Superfamily: Prokaryotic ribosomal protein L17 Family: Prokaryotic ribosomal protein L17
30	c2f4eB	Alignment	not modelled	14.4	19	PDB header: signaling protein Chain: B: PDB Molecule: atfkbp42; PDBTitle: n-terminal domain of fkbp42 from arabidopsis thaliana
31	c2lgoA	Alignment	not modelled	14.2	38	PDB header: isomerase Chain: A: PDB Molecule: fkbp; PDBTitle: solution nmr structure of a fkbp-type peptidyl-prolyl cis-trans2 isomerase from giardia lamblia, seattle structural genomics center3 for infectious disease target gilaa.00840.a
32	c2qj8B	Alignment	not modelled	14.0	14	PDB header: hydrolase Chain: B: PDB Molecule: mlr6093 protein; PDBTitle: crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
33	c2p39A	Alignment	not modelled	13.5	22	PDB header: signaling protein Chain: A: PDB Molecule: fibroblast growth factor 23; PDBTitle: crystal structure of human fgf23
34	c4pu6A	Alignment	not modelled	13.4	34	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase alpha subunit; PDBTitle: crystal structure of potassium-dependent plant-type l-asparaginase2 from phaseolus vulgaris in complex with k+ cations
35	c4bf8A	Alignment	not modelled	13.2	19	PDB header: isomerase Chain: A: PDB Molecule: fpr4; PDBTitle: fpr4 ppi domain
36	c4g50A	Alignment	not modelled	12.4	33	PDB header: isomerase, protein binding Chain: A: PDB Molecule: ubiquitin-like protein smt3, peptidyl-prolyl cis-trans PDBTitle: crystal structure of a smt fusion peptidyl-prolyl cis-trans isomerase2 with surface mutation d44g from burkholderia pseudomallei complexed3 with cj168
37	c3bboP	Alignment	not modelled	11.3	37	PDB header: ribosome Chain: P: PDB Molecule: ribosomal protein l17; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
38	c2egcA	Alignment	not modelled	11.1	18	PDB header: signaling protein Chain: A: PDB Molecule: sh3 and px domain-containing protein 2a; PDBTitle: solution structure of the fifth sh3 domain from human2 kiaa0418 protein
39	c3b7xA	Alignment	not modelled	11.1	29	PDB header: isomerase Chain: A: PDB Molecule: fk506-binding protein 6; PDBTitle: crystal structure of human fk506-binding protein 6
40	c5hwbA	Alignment	not modelled	11.0	35	PDB header: isomerase Chain: A: PDB Molecule: fk506-binding protein 1a; PDBTitle: aspergillus fumigatus fkbp12 apo protein in p212121 space group
41	c5e68A	Alignment	not modelled	10.4	27	PDB header: lyase Chain: A: PDB Molecule: s-ribosylhomocysteine lyase; PDBTitle: high resolution crystal structure of luxs - quorum sensor molecular2 complex from salmonella typhi at 1.58 angstroms
42	d1wfwA	Alignment	not modelled	10.2	22	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
43	c4v19R	Alignment	not modelled	10.1	19	PDB header: ribosome Chain: R: PDB Molecule: mitoribosomal protein bl17m, mrp17; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
44	c5kodA	Alignment	not modelled	10.0	31	PDB header: ligase Chain: A: PDB Molecule: indole-3-acetic acid-amido synthetase gh3.5; PDBTitle: crystal structure of gh3.5 acyl acid amido synthetase from arabidopsis2 thaliana
45	c3oe2A	Alignment	not modelled	10.0	29	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: 1.6 a crystal structure of peptidyl-prolyl cis-trans isomerase ppiase2 from pseudomonas syringae pv. tomato str. dc3000 (pspto dc3000)
46	c6d2cB	Alignment	not modelled	9.9	47	PDB header: lyase Chain: B: PDB Molecule: ulvan lyase; PDBTitle: structure of ulvan lyase from nonlaben ulvanivorans-nlr48
47	d1q1ca1	Alignment	not modelled	9.9	33	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
48	d2piaa1	Alignment	not modelled	9.8	44	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
49	c1q7lB	Alignment	not modelled	9.6	19	PDB header: hydrolase Chain: B: PDB Molecule: aminoacylase-1; PDBTitle: zn-binding domain of the t347g mutant of human aminoacylase-2 i
50	c1q1cA	Alignment	not modelled	9.6	33	PDB header: isomerase Chain: A: PDB Molecule: fk506-binding protein 4; PDBTitle: crystal structure of n(1-260) of human fkbp52
51	c6h3lB	Alignment	not modelled	9.4	29	PDB header: protein transport Chain: B: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: structural snapshots of the type 9 protein translocon
52	c3cqtA	Alignment	not modelled	9.3	11	PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase fyn; PDBTitle: n53i v55l mutant of fyn sh3 domain
53	c2df6A	Alignment	not modelled	9.2	29	PDB header: signaling protein Chain: A: PDB Molecule: rho guanine nucleotide exchange factor 7; PDBTitle: crystal structure of the sh3 domain of betapix in complex2 with a high affinity peptide from pak2
						Fold: FKBP-like

54	d2ppna1	Alignment	not modelled	9.1	40	Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
55	c2eemA	Alignment	not modelled	9.1	38	PDB header: antibiotic Chain: A; PDB Molecule: mytilin-b; PDBTitle: solution structure of the synthetic mytilin
56	d1a1qa	Alignment	not modelled	9.0	24	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
57	c3o4aC	Alignment	not modelled	9.0	44	PDB header: de novo protein Chain: C; PDB Molecule: de novo designed beta-trefoil architecture with symmetric PDBTitle: crystal structure of symfoil-2: de novo designed beta-trefoil2 architecture with symmetric primary structure
58	c2a8lB	Alignment	not modelled	8.8	32	PDB header: hydrolase Chain: B; PDB Molecule: threonine aspartase 1; PDBTitle: crystal structure of human taspase1 (t234a mutant)
59	c4a0eB	Alignment	not modelled	8.8	27	PDB header: transport protein Chain: B; PDB Molecule: type iii secretion protein; PDBTitle: crystal structure of the cytoplasmic n-terminal domain of yersinia2 pestis yscd
60	d1ng2a2	Alignment	not modelled	8.6	12	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
61	c1t3dB	Alignment	not modelled	8.5	25	PDB header: transferase Chain: B; PDB Molecule: serine acetyltransferase; PDBTitle: crystal structure of serine acetyltransferase from e.coli at 2.2a
62	c3sf4F	Alignment	not modelled	8.3	40	PDB header: signaling protein/protein binding Chain: F; PDB Molecule: protein inscuteable homolog; PDBTitle: crystal structure of the complex between the conserved cell polarity2 proteins inscuteable and lgn
63	c2bz8B	Alignment	not modelled	8.3	18	PDB header: sh3 domain Chain: B; PDB Molecule: sh3-domain kinase binding protein 1; PDBTitle: n-terminal sh3 domain of cin85 bound to cbl-b peptide
64	d1t3da	Alignment	not modelled	8.1	25	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Serine acetyltransferase
65	c3ogfA	Alignment	not modelled	8.0	47	PDB header: de novo protein Chain: A; PDB Molecule: de novo designed dimeric trefoil-fold sub-domain which PDBTitle: crystal structure of difoil-4p homo-trimer: de novo designed dimeric2 trefoil-fold sub-domain which forms homo-trimer assembly
66	c2jmcA	Alignment	not modelled	7.9	18	PDB header: signaling protein Chain: A; PDB Molecule: spectrin alpha chain, brain and p41 peptide PDBTitle: chimera between spc-sh3 and p41
67	d1kt0a3	Alignment	not modelled	7.9	25	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
68	c4rugA	Alignment	not modelled	7.7	11	PDB header: protein binding Chain: A; PDB Molecule: slit-robo rho gtpase-activating protein 2; PDBTitle: crystal structure of slit-robo rho gtpase-activating protein 22 fragment
69	d1jcb1	Alignment	not modelled	7.7	19	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Domains B1 and B5 of PheRS-beta, PheT
70	d1zunb1	Alignment	not modelled	7.7	17	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
71	c2dbmA	Alignment	not modelled	7.7	25	PDB header: transferase, signaling protein Chain: A; PDB Molecule: sh3-containing grb2-like protein 2; PDBTitle: solution structures of the sh3 domain of human sh3-2 containing grb2-like protein 2
72	c4h62Q	Alignment	not modelled	7.6	30	PDB header: transcription Chain: Q; PDB Molecule: mediator of rna polymerase ii transcription subunit 17; PDBTitle: structure of the saccharomyces cerevisiae mediator subcomplex2 med17c/med11c/med22c
73	c4mitE	Alignment	not modelled	7.5	8	PDB header: signaling protein Chain: E; PDB Molecule: serine/threonine protein kinase pak, putative; PDBTitle: crystal structure of e. histolytica racc bound to the ehpk4 pbd
74	d1s0ua1	Alignment	not modelled	7.5	31	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
75	c4mitG	Alignment	not modelled	7.5	8	PDB header: signaling protein Chain: G; PDB Molecule: serine/threonine protein kinase pak, putative; PDBTitle: crystal structure of e. histolytica racc bound to the ehpk4 pbd
76	c4glmD	Alignment	not modelled	7.5	22	PDB header: signaling protein Chain: D; PDB Molecule: dynammin-binding protein; PDBTitle: crystal structure of the sh3 domain of dnmbp protein [homo sapiens]
77	c4u4hA	Alignment	not modelled	7.4	24	PDB header: viral protein Chain: A; PDB Molecule: tegument protein ul21; PDBTitle: crystal structure of hsv-1 ul21 n-terminal domain
78	d1wdka2	Alignment	not modelled	7.4	4	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HCDH C-domain-like
79	c2cucA	Alignment	not modelled	7.3	17	PDB header: signaling protein Chain: A; PDB Molecule: sh3 domain containing ring finger 2;

79	c2c0vA	Alignment	not modelled	7.3	17	PDBTitle: solution structure of the sh3 domain of the mouse2 hypothetical protein sh3rf2
80	d1ddla	Alignment	not modelled	7.3	26	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Tymoviridae-like VP
81	c2xmfA	Alignment	not modelled	7.3	17	PDB header: motor protein Chain: A: PDB Molecule: myosin 1e sh3; PDBTitle: myosin 1e sh3
82	d1lauya	Alignment	not modelled	7.2	21	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Tymoviridae-like VP
83	c2egaA	Alignment	not modelled	7.2	22	PDB header: signaling protein Chain: A: PDB Molecule: sh3 and px domain-containing protein 2a; PDBTitle: solution structure of the first sh3 domain from human2 kiaa0418 protein
84	c4wfwA	Alignment	not modelled	7.0	13	PDB header: structural protein Chain: A: PDB Molecule: general secretion pathway protein b; PDBTitle: the crystal structure of dickeya dadantii gspb from the type 22 secretion system
85	c5b8iC	Alignment	not modelled	7.0	30	PDB header: hydrolase Chain: C: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of calcineurin a and calcineurin b in complex with2 fkbp12 and fk506 from coccidioides immitis rs
86	c4nnkA	Alignment	not modelled	7.0	29	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: structural basis for targeting the ribosomal protein s1 of2 mycobacterium tuberculosis by pyrazinamide
87	c1apyA	Alignment	not modelled	7.0	25	PDB header: hydrolase Chain: A: PDB Molecule: aspartylglucosaminidase; PDBTitle: human aspartylglucosaminidase
88	c4igzA	Alignment	not modelled	7.0	24	PDB header: protein binding Chain: A: PDB Molecule: sorbin and sh3 domain-containing protein 2; PDBTitle: crystal structure of the sh3 domain of human sorbin and sh3 domain-2 containing protein 2
89	d1ue9a	Alignment	not modelled	6.9	12	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
90	c2l5tA	Alignment	not modelled	6.9	15	PDB header: transferase Chain: A: PDB Molecule: lipamide acyltransferase; PDBTitle: solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
91	d1r9ha	Alignment	not modelled	6.8	24	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
92	d1ujya	Alignment	not modelled	6.8	33	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
93	c2d8jA	Alignment	not modelled	6.7	29	PDB header: transferase Chain: A: PDB Molecule: fyn-related kinase; PDBTitle: solution structure of the sh3 domain of fyn-related kinase
94	c3jxvA	Alignment	not modelled	6.7	21	PDB header: isomerase Chain: A: PDB Molecule: 70 kda peptidyl-prolyl isomerase; PDBTitle: crystal structure of the 3 fkbp domains of wheat fkbp73
95	c2eyxA	Alignment	not modelled	6.7	11	PDB header: signaling protein Chain: A: PDB Molecule: v-crk sarcoma virus ct10 oncogene homolog PDBTitle: c-terminal sh3 domain of ct10-regulated kinase
96	c1x2pA	Alignment	not modelled	6.6	12	PDB header: transferase Chain: A: PDB Molecule: protein arginine n-methyltransferase 2; PDBTitle: solution structure of the sh3 domain of the protein2 arginine n-methyltransferase 2
97	d1hqia	Alignment	not modelled	6.5	17	Fold: Monooxygenase (hydroxylase) regulatory protein Superfamily: Monooxygenase (hydroxylase) regulatory protein Family: Monooxygenase (hydroxylase) regulatory protein
98	c3rrrM	Alignment	not modelled	6.5	40	PDB header: viral protein Chain: M: PDB Molecule: fusion glycoprotein f0; PDBTitle: structure of the rsv f protein in the post-fusion conformation
99	d1k8ma	Alignment	not modelled	6.5	12	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains