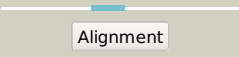

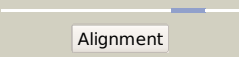

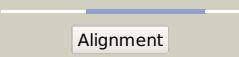
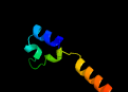
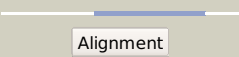

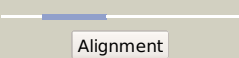

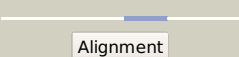
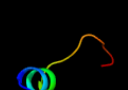
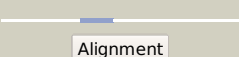

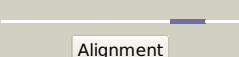





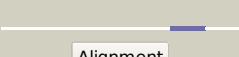



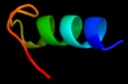
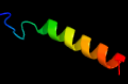







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1638A (-) _1846723_1846980
Date	Fri Aug 2 13:30:23 BST 2019
Unique Job ID	1dd3e966019b021f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1w53a_	 Alignment		38.7	58	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Phosphoserine phosphatase RsbU, N-terminal domain
2	c2qdqA_	 Alignment		28.5	55	PDB header: structural protein Chain: A: PDB Molecule: talin-1; PDBTitle: crystal structure of the talin dimerisation domain
3	c3teqB_	 Alignment		28.2	20	PDB header: signaling protein Chain: B: PDB Molecule: stromal interaction molecule 1; PDBTitle: crystal structure of soar domain
4	c2j6yB_	 Alignment		26.0	27	PDB header: hydrolase Chain: B: PDB Molecule: phosphoserine phosphatase rsbu; PDBTitle: structural and functional characterisation of partner switching2 regulating the environmental stress response in bacillus subtilis
5	c5o7bA_	 Alignment		24.2	30	PDB header: hydrolase Chain: A: PDB Molecule: putative low molecular weight protein-tyrosine-phosphatase PDBTitle: crystal structure of the slr0328 tyrosine phosphatase wz from2 synechocystis sp. pcc 6803
6	c5en7H_	 Alignment		24.1	29	PDB header: splicing Chain: H: PDB Molecule: suppressor of mec and unc defects; PDBTitle: crystal structure of the smu1-red complex (native) of caenorhabditis2 elegans.
7	c6mspA_	 Alignment		21.1	60	PDB header: de novo protein Chain: A: PDB Molecule: de novo designed protein foldit3; PDBTitle: de novo designed protein foldit3
8	c6c52C_	 Alignment		19.7	21	PDB header: de novo protein Chain: C: PDB Molecule: cross-alpha amyloid-like structure alphatet; PDBTitle: cross-alpha amyloid-like structure alphatet
9	c6c52D_	 Alignment		19.7	21	PDB header: de novo protein Chain: D: PDB Molecule: cross-alpha amyloid-like structure alphatet; PDBTitle: cross-alpha amyloid-like structure alphatet
10	c6c52A_	 Alignment		19.7	21	PDB header: de novo protein Chain: A: PDB Molecule: cross-alpha amyloid-like structure alphatet; PDBTitle: cross-alpha amyloid-like structure alphatet
11	c6c52B_	 Alignment		19.7	21	PDB header: de novo protein Chain: B: PDB Molecule: cross-alpha amyloid-like structure alphatet; PDBTitle: cross-alpha amyloid-like structure alphatet

12	c4a9aC_	Alignment		19.2	36	PDB header: translation Chain: C; PDB Molecule: translation machinery-associated protein 46; PDBTitle: structure of rbg1 in complex with tma46 dfrp domain
13	c3ddcB_	Alignment		18.8	15	PDB header: hydrolase/apoptosis Chain: B; PDB Molecule: ras association domain-containing family protein 5; PDBTitle: crystal structure of nore1a in complex with ras
14	c2kjrA_	Alignment		18.3	23	PDB header: chaperone Chain: A; PDB Molecule: cg11242; PDBTitle: solution nmr structure of the n-terminal ubiquitin-like2 domain from tubulin-binding cofactor b, cg11242, from3 drosophila melanogaster. northeast structural genomics4 consortium target fr629a (residues 8-92)
15	c3rgcB_	Alignment		18.3	14	PDB header: chaperone Chain: B; PDB Molecule: possible periplasmic protein; PDBTitle: the virulence factor peb4 and the periplasmic protein cj1289 are two2 structurally related sura-like chaperones in the human pathogen3 campylobacter jejuni
16	c2fekA_	Alignment		18.1	30	PDB header: hydrolase Chain: A; PDB Molecule: low molecular weight protein-tyrosine- PDBTitle: structure of a protein tyrosine phosphatase
17	c3n8kG_	Alignment		17.7	16	PDB header: lyase Chain: G; PDB Molecule: 3-dehydroquinase dehydratase; PDBTitle: type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid
18	d1h05a_	Alignment		17.3	10	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinase dehydratase Family: Type II 3-dehydroquinase dehydratase
19	c5o9zN_	Alignment		16.8	27	PDB header: splicing Chain: N; PDB Molecule: zinc finger matrin-type protein 2; PDBTitle: cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
20	d1u5tb2	Alignment		15.9	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
21	c5tw1E_	Alignment	not modelled	15.4	12	PDB header: transcription activator/transferase/dna Chain: E; PDB Molecule: dna-directed rna polymerase subunit omega; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpA
22	c2qdqB_	Alignment	not modelled	15.0	55	PDB header: structural protein Chain: B; PDB Molecule: tal1n-1; PDBTitle: crystal structure of the talin dimerisation domain
23	c1ql0A_	Alignment	not modelled	14.4	40	PDB header: membrane proteins Chain: A; PDB Molecule: herpes simplex virus protein icp47; PDBTitle: structure of the active domain of the herpes simplex virus2 protein icp47 in water/sodium dodecyl sulfate solution3 determined by nuclear magnetic resonance spectroscopy
24	c4b6wA_	Alignment	not modelled	13.3	32	PDB header: chaperone Chain: A; PDB Molecule: tubulin-specific chaperone; PDBTitle: architecture of trypanosoma brucei tubulin-binding cofactor b
25	d1v6ea_	Alignment	not modelled	13.2	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
26	c1ihqA_	Alignment	not modelled	12.6	54	PDB header: de novo protein Chain: A; PDB Molecule: chimeric peptide glytm1bzip: tropomyosin alpha PDBTitle: glytm1bzip: a chimeric peptide model of the n-terminus of a2 rat short alpha tropomyosin with the n-terminus encoded by3 exon 1b
27	c4nm6A_	Alignment	not modelled	12.5	39	PDB header: oxidoreductase/dna Chain: A; PDB Molecule: methylcytosine dioxygenase tet2; PDBTitle: crystal structure of tet2-dna complex
						Fold: Phosphotyrosine protein phosphatases I-like

28	d1p8aa_	Alignment	not modelled	12.4	34	Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
29	c2jmxA_	Alignment	not modelled	12.4	78	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase o subunit, mitochondrial; PDBTitle: oscp-nt (1-120) in complex with n-terminal (1-25) alpha2 subunit from f1-atpase
30	c1t0yA_	Alignment	not modelled	12.2	18	PDB header: chaperone Chain: A: PDB Molecule: tubulin folding cofactor b; PDBTitle: solution structure of a ubiquitin-like domain from tubulin-2 binding cofactor b
31	d1t0ya_	Alignment	not modelled	12.2	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
32	c4zrkE_	Alignment	not modelled	12.1	36	PDB header: signaling protein/transferase Chain: E: PDB Molecule: serine/threonine-protein kinase lats1; PDBTitle: merlin-ferm and lats1 complex
33	c4zrkH_	Alignment	not modelled	12.1	36	PDB header: signaling protein/transferase Chain: H: PDB Molecule: serine/threonine-protein kinase lats1; PDBTitle: merlin-ferm and lats1 complex
34	c4zrkF_	Alignment	not modelled	12.1	36	PDB header: signaling protein/transferase Chain: F: PDB Molecule: serine/threonine-protein kinase lats1; PDBTitle: merlin-ferm and lats1 complex
35	d1uqra_	Alignment	not modelled	11.9	7	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquininate dehydratase Family: Type II 3-dehydroquininate dehydratase
36	c4zrkG_	Alignment	not modelled	11.8	36	PDB header: signaling protein/transferase Chain: G: PDB Molecule: serine/threonine-protein kinase lats1; PDBTitle: merlin-ferm and lats1 complex
37	d2g1da1	Alignment	not modelled	11.2	32	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: Ribosomal protein S24e
38	c3rfwA_	Alignment	not modelled	10.7	16	PDB header: chaperone Chain: A: PDB Molecule: cell-binding factor 2; PDBTitle: the virulence factor peb4 and the periplasmic protein cj1289 are two2 structurally-related sura-like chaperones in the human pathogen3 campylobacter jejuni
39	c5wbuQ_	Alignment	not modelled	10.7	40	PDB header: transferase Chain: Q: PDB Molecule: proline-rich akt1 substrate 1; PDBTitle: crystal structure of mtor(delta)-mlst8-pras40(alpha-helix & beta-2 strand) complex
40	c5wbuR_	Alignment	not modelled	10.7	40	PDB header: transferase Chain: R: PDB Molecule: proline-rich akt1 substrate 1; PDBTitle: crystal structure of mtor(delta)-mlst8-pras40(alpha-helix & beta-2 strand) complex
41	d1gtza_	Alignment	not modelled	10.6	14	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquininate dehydratase Family: Type II 3-dehydroquininate dehydratase
42	c3fd0B_	Alignment	not modelled	10.5	30	PDB header: lyase Chain: B: PDB Molecule: putative cystathionine beta-lyase involved in aluminum PDBTitle: crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_470671.1) from listeria innocua at 2.12 a3 resolution
43	c3ht4B_	Alignment	not modelled	10.4	40	PDB header: lyase Chain: B: PDB Molecule: aluminum resistance protein; PDBTitle: crystal structure of the q81a77_baccr protein from bacillus cereus.2 northeast structural genomics consortium target bcr213
44	c5ietA_	Alignment	not modelled	10.3	30	PDB header: gene regulation Chain: A: PDB Molecule: bacterial proteasome activator; PDBTitle: crystal structure of mycobacterium tuberculosis atp-independent2 proteasome activator
45	c6b4eD_	Alignment	not modelled	10.1	46	PDB header: transport protein Chain: D: PDB Molecule: nucleoporin nup42; PDBTitle: crystal structure of saccharomyces cerevisiae gle1 ctd-nup42 gbm2 complex
46	c5ez1B_	Alignment	not modelled	9.1	19	PDB header: isomerase Chain: B: PDB Molecule: putative peptidyl-prolyl cis-trans isomerase hp_0175; PDBTitle: crystal structure of cell binding factor 2 from helicobacter pylori in2 complex with i2ca
47	c4h9kA_	Alignment	not modelled	8.5	35	PDB header: hydrolase Chain: A: PDB Molecule: hog cholera virus; PDBTitle: crystal structure of cleavage site mutant of npro of classical swine2 fever virus.
48	c5en6C_	Alignment	not modelled	8.5	29	PDB header: splicing Chain: C: PDB Molecule: suppressor of mec and unc defects; PDBTitle: crystal structure of the smu1-red complex (semet) of caenorhabditis2 elegans
49	c3rh0A_	Alignment	not modelled	8.1	35	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase; PDBTitle: corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
50	c2wmyH_	Alignment	not modelled	7.9	22	PDB header: hydrolase Chain: H: PDB Molecule: putative acid phosphatase wzb; PDBTitle: crystal structure of the tyrosine phosphatase wzb from2 escherichia coli k30 in complex with sulphate.
51	c3plwA_	Alignment	not modelled	7.7	60	PDB header: hydrolase Chain: A: PDB Molecule: recombination enhancement function protein; PDBTitle: ref protein from p1 bacteriophage
52	c2ktrA_	Alignment	not modelled	7.6	17	PDB header: signaling protein, transport protein Chain: A: PDB Molecule: sequestosome-1; PDBTitle: nmr structure of p62 pb1 dimer determined based on pcs
						PDB header: isomerase

53	c4wo7A_	Alignment	not modelled	7.5	0	Chain: A: PDB Molecule: foldase protein prsa; PDBTitle: crystal structure of prsa from bacillus subtilis
54	c4rhcH_	Alignment	not modelled	7.4	9	PDB header: lyase Chain: H: PDB Molecule: 3-dehydroquinatase; PDBTitle: crystal structure of 3-dehydroquinatase from acetobacter2 baumannii at 2.68 a resolution
55	c5xyiY_	Alignment	not modelled	7.3	15	PDB header: ribosome Chain: Y: PDB Molecule: ribosomal protein s24e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
56	c5lqzU_	Alignment	not modelled	7.1	44	PDB header: hydrolase Chain: U: PDB Molecule: atp synthase oscp subunit; PDBTitle: structure of f-atpase from pichia angusta, state1
57	d1abva_	Alignment	not modelled	7.1	22	Fold: ATPD N-terminal domain-like Superfamily: N-terminal domain of the delta subunit of the F1F0-ATP synthase Family: N-terminal domain of the delta subunit of the F1F0-ATP synthase
58	c2qhvA_	Alignment	not modelled	7.0	9	PDB header: transferase Chain: A: PDB Molecule: lipoyltransferase; PDBTitle: structural basis of octanoic acid recognition by lipoate-protein2 ligase b
59	c2qhsA_	Alignment	not modelled	7.0	9	PDB header: transferase Chain: A: PDB Molecule: lipoyltransferase; PDBTitle: structural basis of octanoic acid recognition by lipoate-protein2 ligase b
60	c5mpyB_	Alignment	not modelled	7.0	15	PDB header: plant protein Chain: B: PDB Molecule: multiple organellar rna editing factor 9, chloroplastic; PDBTitle: crystal structure of arabidopsis thaliana rna editing factor morf9
61	c3j21Y_	Alignment	not modelled	7.0	27	PDB header: ribosome Chain: Y: PDB Molecule: 50s ribosomal protein l30p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
62	d1s2xa_	Alignment	not modelled	6.8	40	Fold: STAT-like Superfamily: Cag-Z Family: Cag-Z
63	c1s2xA_	Alignment	not modelled	6.8	40	PDB header: unknown function Chain: A: PDB Molecule: cag-z; PDBTitle: crystal structure of cag-z from helicobacter pylori
64	c2a7uB_	Alignment	not modelled	6.5	22	PDB header: hydrolase Chain: B: PDB Molecule: atp synthase delta chain; PDBTitle: nmr solution structure of the e.coli f-atpase delta subunit n-terminal2 domain in complex with alpha subunit n-terminal 22 residues
65	c2zkro_	Alignment	not modelled	6.5	33	PDB header: ribosomal protein/rna Chain: O: PDB Molecule: rna expansion segment es30; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
66	c3bhpA_	Alignment	not modelled	6.3	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0291 protein yncz; PDBTitle: crystal structure of upf0291 protein yncz from bacillus2 subtilis at resolution 2.0 a. northeast structural3 genomics consortium target sr384
67	c2kj6A_	Alignment	not modelled	6.3	32	PDB header: chaperone Chain: A: PDB Molecule: tubulin folding cofactor b; PDBTitle: nmr solution structure of a tubulin folding cofactor b2 obtained from arabidopsis thaliana: northeast structural3 genomics consortium target ar3436a
68	c3hvyC_	Alignment	not modelled	6.2	20	PDB header: lyase Chain: C: PDB Molecule: cystathionine beta-lyase family protein, ynbb b.subtilis PDBTitle: crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_348457.1) from clostridium acetobutylicum at3 2.00 a resolution
69	c3u80A_	Alignment	not modelled	5.9	5	PDB header: unknown function Chain: A: PDB Molecule: 3-dehydroquinatase, type ii; PDBTitle: 1.60 angstrom resolution crystal structure of a 3-dehydroquinatase2 dehydratase-like protein from bifidobacterium longum
70	c3gwpA_	Alignment	not modelled	5.9	20	PDB header: lyase Chain: A: PDB Molecule: carbon-sulfur lyase involved in aluminum resistance; PDBTitle: crystal structure of carbon-sulfur lyase involved in aluminum2 resistance (yp_878183.1) from clostridium novyi nt at 2.90 a3 resolution
71	d1wjna_	Alignment	not modelled	5.9	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
72	c4axqC_	Alignment	not modelled	5.8	40	PDB header: translation Chain: C: PDB Molecule: protein cup; PDBTitle: structure of eif4e-cup complex
73	c3lwzC_	Alignment	not modelled	5.7	12	PDB header: lyase Chain: C: PDB Molecule: 3-dehydroquinatase; PDBTitle: 1.65 angstrom resolution crystal structure of type ii 3-dehydroquinatase2 dehydratase (aroq) from yersinia pestis
74	d1ywx1	Alignment	not modelled	5.6	20	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: Ribosomal protein S24e
75	c6cv6L_	Alignment	not modelled	5.5	12	PDB header: lyase Chain: L: PDB Molecule: 3-dehydroquinatase; PDBTitle: crystal structure of 3-dehydroquinatase dehydratase, type ii, from2 burkholderia phymatum stm815
76	c5xauC_	Alignment	not modelled	5.5	13	PDB header: cell adhesion Chain: C: PDB Molecule: laminin subunit gamma-1; PDBTitle: crystal structure of integrin binding fragment of laminin-

				511	
77	c2c49A_	Alignment	not modelled	5.5	33 PDB header: transferase Chain: A: PDB Molecule: sugar kinase mj0406; PDBTitle: crystal structure of methanocaldococcus jannaschii nucleoside kinase -2 an archaeal member of the ribokinase family
78	d1gqoa_	Alignment	not modelled	5.2	7 Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquininate dehydratase Family: Type II 3-dehydroquininate dehydratase
79	c3cvjB_	Alignment	not modelled	5.2	23 PDB header: isomerase Chain: B: PDB Molecule: putative phosphoheptose isomerase; PDBTitle: crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
80	d1q1va_	Alignment	not modelled	5.1	21 Fold: Another 3-helical bundle Superfamily: DEK C-terminal domain Family: DEK C-terminal domain