

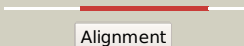

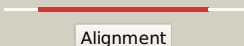

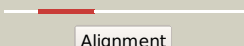
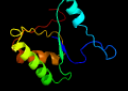
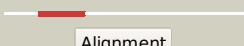

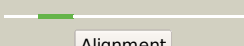

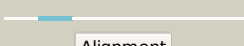


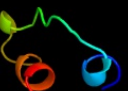








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2818c (-)_3125006_3126154
Date	Wed Aug 7 12:50:48 BST 2019
Unique Job ID	d895f1085aa0925f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4rgpA_	 Alignment		100.0	17	PDB header: unknown function Chain: A: PDB Molecule: csm6_iii-a; PDBTitle: crystal structure of uncharacterized crispr/cas system-associated2 protein csm6 from streptococcus mutans
2	c5yjcB_	 Alignment		100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: csm6; PDBTitle: structural insights into the crispr-cas-associated ribonuclease2 activity of staphylococcus epidermidis csm6
3	c5fshA_	 Alignment		99.6	23	PDB header: hydrolase Chain: A: PDB Molecule: csm6; PDBTitle: crystal structure of thermus thermophilus csm6
4	d1xmx_	 Alignment		97.7	11	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hypothetical protein VC1899
5	c2wteB_	 Alignment		91.9	13	PDB header: antiviral protein Chain: B: PDB Molecule: csa3; PDBTitle: the structure of the crispr-associated protein, csa3, from2 sulfolobus solfataricus at 1.8 angstrom resolution.
6	c2dplA_	 Alignment		51.0	22	PDB header: ligase Chain: A: PDB Molecule: gmp synthase [glutamine-hydrolyzing] subunit b; PDBTitle: crystal structure of the gmp synthase from pyrococcus horikoshii ot3
7	c2c4mA_	 Alignment		35.0	25	PDB header: transferase Chain: A: PDB Molecule: glycogen phosphorylase; PDBTitle: starch phosphorylase: structural studies explain oxanion-dependent2 kinetic stability and regulatory control.
8	d2atia1	 Alignment		34.4	29	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Oligosaccharide phosphorylase
9	c3ddsB_	 Alignment		34.2	29	PDB header: transferase Chain: B: PDB Molecule: glycogen phosphorylase, liver form; PDBTitle: crystal structure of glycogen phosphorylase complexed with an2 anthranilimide based inhibitor gsk261
10	d1l5wa_	 Alignment		33.6	38	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Oligosaccharide phosphorylase
11	c3jq3A_	 Alignment		33.5	13	PDB header: transferase Chain: A: PDB Molecule: lombricine kinase; PDBTitle: crystal structure of lombricine kinase, complexed with substrate adp

12	c4l22A_	Alignment		33.3	38	PDB header: transferase Chain: A: PDB Molecule: phosphorylase; PDBTitle: crystal structure of putative glycogen phosphorylase from2 streptococcus mutans
13	d1ygpa_	Alignment		31.6	25	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Oligosaccharide phosphorylase
14	d2gj4a1	Alignment		31.3	29	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Oligosaccharide phosphorylase
15	c5lrbB_	Alignment		31.3	29	PDB header: transferase Chain: B: PDB Molecule: alpha-1,4 glucan phosphorylase; PDBTitle: plastidial phosphorylase from barley in complex with acarbose
16	c3p52B_	Alignment		29.5	10	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: nh3-dependent nad synthetase from campylobacter jejuni subsp. jejuni2 nctc 11168 in complex with the nitrate ion
17	c3c65A_	Alignment		29.4	12	PDB header: hydrolase Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of bacillus stearotherophilus uvr c' endonuclease2 domain
18	c2dt7A_	Alignment		27.8	14	PDB header: rna binding protein Chain: A: PDB Molecule: splicing factor 3a subunit 3; PDBTitle: solution structure of the second surp domain of human2 splicing factor sf3a120 in complex with a fragment of3 human splicing factor sf3a60
19	c4lw2C_	Alignment		27.1	16	PDB header: lyase Chain: C: PDB Molecule: cysteine sulfinate desulfinate; PDBTitle: structural changes during cysteine desulfurase csda and sulfur-2 acceptor csde interactions provide insight into the trans-3 persulfuration
20	c2yrrA_	Alignment		25.4	16	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class v; PDBTitle: hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8
21	c4q1tD_	Alignment	not modelled	21.6	17	PDB header: transferase Chain: D: PDB Molecule: glutamate 5-kinase; PDBTitle: crystal structure of a glutamate 5-kinase from burkholderia2 thailandensis
22	c5xj0Y_	Alignment	not modelled	21.3	20	PDB header: transferase/transcription Chain: Y: PDB Molecule: gp76; PDBTitle: t. thermophilus rna polymerase holoenzyme bound with gp39 and gp76
23	d3brja1	Alignment	not modelled	20.1	13	Fold: MtIR-like Superfamily: MtIR-like Family: MtIR-like
24	d1ej7l1	Alignment	not modelled	19.9	20	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
25	c4wo8A_	Alignment	not modelled	18.9	13	PDB header: transferase Chain: A: PDB Molecule: taurocyamine kinase; PDBTitle: the substrate-free duplicated taurocyamine kinase from schistosoma2 mansoni
26	c2pc4B_	Alignment	not modelled	18.6	17	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: crystal structure of fructose-bisphosphate aldolase from plasmodium2 falciparum in complex with trap-tail determined at 2.4 angstrom3 resolution
27	c3a2kB_	Alignment	not modelled	18.3	8	PDB header: ligase/rna Chain: B: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils complexed with trna
28	c3qyfA_	Alignment	not modelled	18.3	12	PDB header: antiviral protein Chain: A: PDB Molecule: crispr-associated protein; PDBTitle: crystal structure of the crispr-associated protein sso1393 from2 sulfolobus solfataricus

29	d1pbva_	Alignment	not modelled	18.2	10	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain
30	d1a5ca_	Alignment	not modelled	18.2	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
31	d1h0ca_	Alignment	not modelled	18.1	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
32	c2r09A_	Alignment	not modelled	18.1	12	PDB header: signaling protein Chain: A: PDB Molecule: cytohesin-3; PDBTitle: crystal structure of autoinhibited form of grp1 arf gtpase exchange2 factor
33	c4bqeA_	Alignment	not modelled	17.4	55	PDB header: transferase Chain: A: PDB Molecule: alpha-glucan phosphorylase 2,4-glucan phosphorylase; PDBTitle: arabidopsis thaliana cytosolic alpha-1,4-glucan phosphorylase (phs2)
34	d1bwva1	Alignment	not modelled	17.4	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
35	c5j8qA_	Alignment	not modelled	17.3	9	PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase sufs; PDBTitle: crystal structure of the cysteine desulfurase sufs of bacillus2 subtilis
36	c4q76B_	Alignment	not modelled	17.2	11	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase 2, chloroplastic; PDBTitle: crystal structure of nfs2 c384s mutant, the plastidial cysteine2 desulfurase from arabidopsis thaliana
37	c1ylmA_	Alignment	not modelled	17.1	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein bsu32300; PDBTitle: structure of cytosolic protein of unknown function yute2 from bacillus subtilis
38	c2i53B_	Alignment	not modelled	17.0	24	PDB header: ca-binding protein/proton transport Chain: B: PDB Molecule: voltage-gated sodium channel type v alpha isoform b PDBTitle: solution nmr structure of apo-calmodulin in complex with the iq motif2 of human cardiac sodium channel nav1.5
39	c3tqiB_	Alignment	not modelled	16.6	13	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
40	d1t3ia_	Alignment	not modelled	15.7	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
41	c5uz9B_	Alignment	not modelled	15.4	16	PDB header: immune system/rna Chain: B: PDB Molecule: crispr-associated protein csy2; PDBTitle: cryo em structure of anti-crisprs, acrf1 and acrf2, bound to type i-f2 crrna-guided crispr surveillance complex
42	d1jf9a_	Alignment	not modelled	15.3	5	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
43	d1wdda1	Alignment	not modelled	15.3	23	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
44	c5yepC_	Alignment	not modelled	14.9	12	PDB header: antitoxin/toxin Chain: C: PDB Molecule: toxin-antitoxin system toxin hepn family; PDBTitle: crystal structure of so_3166-so_3165 from shewanella oneidensis
45	c1r19A_	Alignment	not modelled	14.5	14	PDB header: transferase Chain: A: PDB Molecule: arginine kinase; PDBTitle: crystal structure of creatine- adp arginine kinase ternary2 complex
46	c6cetD_	Alignment	not modelled	13.6	20	PDB header: signaling protein Chain: D: PDB Molecule: gator complex protein depdc5; PDBTitle: cryo-em structure of gator1
47	c5kodA_	Alignment	not modelled	13.1	23	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
48	c2j5tF_	Alignment	not modelled	12.9	20	PDB header: transferase Chain: F: PDB Molecule: glutamate 5-kinase; PDBTitle: glutamate 5-kinase from escherichia coli complexed with2 glutamate
49	d1bc9a_	Alignment	not modelled	12.8	10	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain
50	c3iprC_	Alignment	not modelled	12.6	18	PDB header: transferase Chain: C: PDB Molecule: pts system, iia component; PDBTitle: crystal structure of the enterococcus faecalis gluconate2 specific eiaa phosphotransferase system component
51	c2dt8A_	Alignment	not modelled	12.5	18	PDB header: lipid binding protein Chain: A: PDB Molecule: degv family protein; PDBTitle: fatty acid binding of a degv family protein from thermus thermophilus
52	d1bxna1	Alignment	not modelled	12.5	26	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
53	d2r09a1	Alignment	not modelled	12.3	11	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain
54	c4h51B_	Alignment	not modelled	12.2	20	PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of a putative aspartate aminotransferase from2 leishmania major friedlin

55	c4eplA_	Alignment	not modelled	12.0	15	PDB header: ligase Chain: A: PDB Molecule: jasmonic acid-amido synthetase jar1; PDBTitle: crystal structure of arabidopsis thaliana gh3.11 (jar1) in complex2 with ja-ile
56	d1rbla1	Alignment	not modelled	12.0	20	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
57	d1zara1	Alignment	not modelled	11.9	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Rio2 serine protein kinase N-terminal domain
58	d1un8a4	Alignment	not modelled	11.7	16	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DAK1
59	c1mgpA_	Alignment	not modelled	11.5	15	PDB header: lipid binding protein Chain: A: PDB Molecule: hypothetical protein tm841; PDBTitle: hypothetical protein tm841 from thermotoga maritima reveals2 fatty acid binding function
60	d1mgpa_	Alignment	not modelled	11.5	15	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DegV-like
61	c3j21e_	Alignment	not modelled	11.4	38	PDB header: ribosome Chain: E: PDB Molecule: 50s ribosomal protein l5p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
62	c6bbqA_	Alignment	not modelled	11.2	12	PDB header: lipid binding protein Chain: A: PDB Molecule: cytohesin-3, adp-ribosylation factor 6; PDBTitle: model for extended volume of truncated monomeric cytohesin-3 (grp1;2 amino acids 63-399) e161a arf6 q67l fusion protein
63	c1bwvA_	Alignment	not modelled	11.2	14	PDB header: lyase Chain: A: PDB Molecule: protein (ribulose biphosphate carboxylase); PDBTitle: activated ribulose 1,5-biphosphate carboxylase/oxygenase (rubisco)2 complexed with the reaction intermediate analogue 2-carboxyarabinitol3 1,5-biphosphate
64	d1r8se_	Alignment	not modelled	10.9	9	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain
65	c4x9xA_	Alignment	not modelled	10.8	16	PDB header: transferase Chain: A: PDB Molecule: degv domain-containing protein mw1315; PDBTitle: biochemical roles for conserved residues in the bacterial fatty acid2 binding protein family
66	d1m15a1	Alignment	not modelled	10.7	15	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
67	c3lfhF_	Alignment	not modelled	10.6	13	PDB header: transferase Chain: F: PDB Molecule: phosphotransferase system, mannose/fructose-specific PDBTitle: crystal structure of manxa from thermoanaerobacter tengcongensis
68	c6ov0D_	Alignment	not modelled	10.5	18	PDB header: immune system/rna Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of csm6 in complex with a4>p by soaking a4>p into2 csm6
69	c3uowB_	Alignment	not modelled	10.4	13	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
70	c5w70B_	Alignment	not modelled	10.3	19	PDB header: transferase Chain: B: PDB Molecule: l-glutamine:2-deoxy-scylo-inosose aminotransferase; PDBTitle: x-ray structure of rbmb from streptomyces ribosidificus
71	c5ijgB_	Alignment	not modelled	10.1	21	PDB header: hydrolase Chain: B: PDB Molecule: cys/met metabolism pyridoxal-phosphate-dependent enzyme; PDBTitle: crystal structure of o-acetylhomoserine sulfhydrylase from brucella2 melitensis at 2.0 a resolution
72	c3ffrA_	Alignment	not modelled	10.1	14	PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase serc; PDBTitle: crystal structure of a phosphoserine aminotransferase serc (chu_0995)2 from cytophaga hutchinsonii atcc 33406 at 1.75 a resolution
73	c3zrrB_	Alignment	not modelled	10.1	16	PDB header: transferase Chain: B: PDB Molecule: serine-pyruvate aminotransferase (agxt); PDBTitle: crystal structure and substrate specificity of a thermophilic2 archaeal serine : pyruvate aminotransferase from sulfobolus3 solfataricus
74	d1g0wa1	Alignment	not modelled	9.9	16	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
75	c3ct4B_	Alignment	not modelled	9.8	18	PDB header: transferase Chain: B: PDB Molecule: pts-dependent dihydroxyacetone kinase, dihydroxyacetone- PDBTitle: structure of dha-kinase subunit dhak from l. lactis
76	c2vx0B_	Alignment	not modelled	9.5	10	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
77	d8ruca1	Alignment	not modelled	9.5	20	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
78	d1xnga1	Alignment	not modelled	9.4	10	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
79	c3ub7A_	Alignment	not modelled	9.3	56	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronidase-phage associated;

79	c4wlrA	Alignment	not modelled	9.3	30	PDBTitle: the partial structure of a group a streptococcal phage-2 encoded tail fibre hyaluronate lyase hylp2
80	c4nncA	Alignment	not modelled	9.3	16	PDB header: lyase Chain: A: PDB Molecule: obca, oxalate biosynthetic component a; PDBTitle: ternary complex of obca with c4-coa adduct and oxalate
81	c2dr1A	Alignment	not modelled	9.1	21	PDB header: transferase Chain: A: PDB Molecule: 386aa long hypothetical serine aminotransferase; PDBTitle: crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
82	c1rldB	Alignment	not modelled	9.1	20	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribulose 1,5 bisphosphate carboxylase/oxygenase (large) PDBTitle: solid-state phase transition in the crystal structure of ribulose 1,5-2 biphosphate carboxylase(/slash)oxygenase
83	d1gpmA	Alignment	not modelled	9.1	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
84	c6dkeA	Alignment	not modelled	9.0	13	PDB header: transferase Chain: A: PDB Molecule: fatty acid kinase (fak) b1 protein; PDBTitle: the x-ray crystal structure of streptococcus pneumoniae fatty acid2 kinase (fak) b1 protein loaded with palmitic acid (c16:0) to 1.763 angstrom resolution
85	c2g7zB	Alignment	not modelled	9.0	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein spy1493; PDBTitle: conserved degv-like protein of unknown function from streptococcus2 pyogenes m1 gas binds long-chain fatty acids
86	d1r0ka2	Alignment	not modelled	9.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
87	c4c2mQ	Alignment	not modelled	8.7	13	PDB header: transcription Chain: Q: PDB Molecule: dna-directed rna polymerase i subunit rpa135; PDBTitle: structure of rna polymerase i at 2.8 a resolution
88	c3mtqA	Alignment	not modelled	8.6	19	PDB header: transferase Chain: A: PDB Molecule: putative phosphoenolpyruvate-dependent sugar PDBTitle: crystal structure of a putative phosphoenolpyruvate-dependent sugar2 phosphotransferase system (pts) permease (kpn_04802) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a resolution
89	d1svda1	Alignment	not modelled	8.6	23	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
90	c6hxiC	Alignment	not modelled	8.5	4	PDB header: lyase Chain: C: PDB Molecule: citrate lyase, subunit 1; PDBTitle: structure of atp citrate lyase from methanotrix soehngenii in complex2 with citrate and coenzyme a
91	d1ttha	Alignment	not modelled	8.4	13	Fold: Anti-sigma factor AsiA Superfamily: Anti-sigma factor AsiA Family: Anti-sigma factor AsiA
92	c3mmtC	Alignment	not modelled	8.2	19	PDB header: hydrolase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: crystal structure of fructose bisphosphate aldolase from bartonella2 henselae, bound to fructose bisphosphate
93	c5svaU	Alignment	not modelled	8.2	11	PDB header: transcription, transferase/dna Chain: U: PDB Molecule: mediator of rna polymerase ii transcription subunit 7; PDBTitle: mediator-rna polymerase ii pre-initiation complex
94	d1zd0a1	Alignment	not modelled	8.2	10	Fold: PF0523-like Superfamily: PF0523-like Family: PF0523-like
95	d1vrpa1	Alignment	not modelled	8.2	11	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
96	c1gpmD	Alignment	not modelled	8.1	17	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
97	d2ckca1	Alignment	not modelled	8.1	30	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
98	c2ckcA	Alignment	not modelled	8.1	30	PDB header: hydrolase Chain: A: PDB Molecule: chromodomain-helicase-dna-binding protein 7; PDBTitle: solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
99	d1wtya	Alignment	not modelled	7.9	15	Fold: Four-helical up-and-down bundle Superfamily: Nucleotidyltransferase substrate binding subunit/domain Family: Family 1 bi-partite nucleotidyltransferase subunit