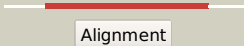

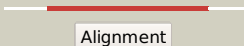

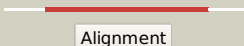







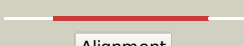













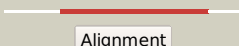

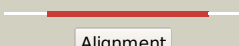

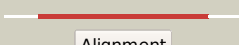

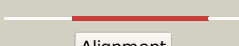
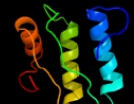






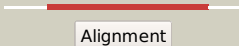
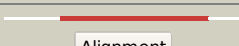
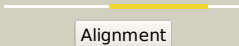
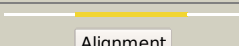
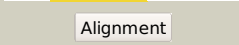
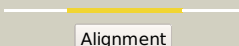
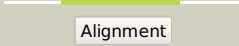



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2638 (-)_2964415_2964861
Date	Wed Aug 7 12:50:28 BST 2019
Unique Job ID	c9abacdfad2467a2

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3t6oA_	 Alignment		99.9	17	PDB header: transport protein Chain: A: PDB Molecule: sulfate transporter/antisigma-factor antagonist stas; PDBTitle: the structure of an anti-sigma-factor antagonist (stas) domain protein2 from planctomyces limnophilus.
2	d1th8b_	 Alignment		99.9	17	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
3	c4hylB_	 Alignment		99.9	18	PDB header: transcription regulator Chain: B: PDB Molecule: stage ii sporulation protein; PDBTitle: the crystal structure of an anti-sigma-factor antagonist from2 haliangium ochraceum dsm 14365
4	d1lauza_	 Alignment		99.9	17	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
5	d1vc1a_	 Alignment		99.9	17	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
6	c3f43A_	 Alignment		99.9	16	PDB header: transcription Chain: A: PDB Molecule: putative anti-sigma factor antagonist tm1081; PDBTitle: crystal structure of a putative anti-sigma factor antagonist (tm1081)2 from thermotoga maritima at 1.59 a resolution
7	c4xs5D_	 Alignment		99.9	13	PDB header: transport protein Chain: D: PDB Molecule: sulfate transporter/antisigma-factor antagonist stas; PDBTitle: crystal structure of sulfate transporter/antisigma-factor antagonist2 stas from dyadobacter fermentans dsm 18053
8	d1h4xa_	 Alignment		99.8	17	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
9	c2vy9A_	 Alignment		99.8	16	PDB header: gene regulation Chain: A: PDB Molecule: anti-sigma-factor antagonist; PDBTitle: molecular architecture of the stressosome, a signal2 integration and transduction hub
10	c2klnA_	 Alignment		99.8	12	PDB header: transport protein Chain: A: PDB Molecule: probable sulphate-transport transmembrane protein, cog0659; PDBTitle: solution structure of stas domain of rv1739c from m. tuberculosis
11	c3lloA_	 Alignment		99.8	16	PDB header: motor protein Chain: A: PDB Molecule: prestin; PDBTitle: crystal structure of the stas domain of motor protein prestin (anion2 transporter slc26a5)

12	c3mg1A_	 Alignment		99.8	15	PDB header: transport protein Chain: A: PDB Molecule: sulfate permease family protein; PDBTitle: crystal structure of permease family protein from vibrio cholerae
13	c5ezbB_	 Alignment		99.8	12	PDB header: transport protein Chain: B: PDB Molecule: chicken prestin stas domain,chicken prestin stas domain; PDBTitle: chicken prestin stas domain
14	c3oirA_	 Alignment		99.8	15	PDB header: transport protein Chain: A: PDB Molecule: sulfate transporter sulfate transporter family protein; PDBTitle: crystal structure of sulfate transporter family protein from wolinnella2 succinogenes
15	c3ny7A_	 Alignment		99.8	12	PDB header: membrane protein Chain: A: PDB Molecule: sulfate transporter; PDBTitle: stas domain of ychm bound to acp
16	c6rtfA_	 Alignment		99.7	16	PDB header: membrane protein Chain: A: PDB Molecule: solute carrier family 26 member 9,solute carrier family 26 PDBTitle: structure of murine solute carrier 26 family member a9 (slc26a9) anion2 transporter in an intermediate state
17	c6ic4K_	 Alignment		99.6	22	PDB header: protein transport Chain: K: PDB Molecule: ttg2e; PDBTitle: cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
18	c3lk1B_	 Alignment		99.5	13	PDB header: transport protein Chain: B: PDB Molecule: antisigma-factor antagonist stas; PDBTitle: crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides
19	c5da0A_	 Alignment		99.3	14	PDB header: transport protein Chain: A: PDB Molecule: sulphate transporter; PDBTitle: structure of the the slc26 transporter slc26dg in complex with a2 nanobody
20	c3ih9A_	 Alignment		96.0	12	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure analysis of mglu in its tris form
21	d2q31a1	 Alignment	not modelled	94.9	14	Fold: Spollaa-like Superfamily: Spollaa-like Family: Sfri0576-like
22	c3bl4B_	 Alignment	not modelled	91.1	15	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein with unknown function (arth_0117) from2 arthrobacter sp. fb24 at 2.20 a resolution
23	c2pr7A_	 Alignment	not modelled	79.4	12	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase/epoxide hydrolase family; PDBTitle: crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
24	c4eogA_	 Alignment	not modelled	75.2	18	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of csx1 of pyrococcus furiosus
25	d2ooka1	 Alignment	not modelled	73.9	20	Fold: Spollaa-like Superfamily: Spollaa-like Family: Sfri0576-like
26	c3bezC_	 Alignment	not modelled	71.5	15	PDB header: hydrolase Chain: C: PDB Molecule: protease 4; PDBTitle: crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
27	c3rstH_	 Alignment	not modelled	63.5	10	PDB header: hydrolase Chain: H: PDB Molecule: signal peptide peptidase sppa; PDBTitle: crystal structure of bacillus subtilis signal peptide peptidase a
28	c2deoA_	 Alignment	not modelled	55.5	13	PDB header: hydrolase Chain: A: PDB Molecule: 441aa long hypothetical nfd protein; PDBTitle: 1510-n membrane protease specific for a stomatin

						homolog from2 pyrococcus horikoshii PDB header: cell cycle Chain: A: PDB Molecule: septum site-determining protein minc; PDBTitle: crystal structure of the septum site-determining protein minc from2 salmonella typhimurium
29	c3ghfA	Alignment	not modelled	47.1	14	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
30	c3kc2A	Alignment	not modelled	41.6	15	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen-iii synthetase; PDBTitle: crystal structure of uroporphyrinogen iii synthase from pseudomonas2 syringae pv. tomato dc3000
31	c3re1B	Alignment	not modelled	36.7	26	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure of a major fragment of the salt-tolerant2 glutaminase from micrococcus luteus k-3
32	c2dfwA	Alignment	not modelled	31.4	13	Fold: SSO1389-like Superfamily: SSO1389-like Family: Cas DxTHG
33	d2i71a1	Alignment	not modelled	30.6	15	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein ph0822; PDBTitle: crystal structure of ph0822
34	c2yx6C	Alignment	not modelled	30.0	15	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
35	d1o13a	Alignment	not modelled	29.9	18	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
36	d1t3va	Alignment	not modelled	27.5	18	PDB header: hydrolase Chain: G: PDB Molecule: putative atp-dependent clp protease proteolytic subunit; PDBTitle: crystallography and mutagenesis point to an essential role for the n-2 terminus of human mitochondrial clpp
37	c1tg6G	Alignment	not modelled	27.2	11	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: crystal structure of hemd (pa5259) from pseudomonas aeruginosa (pao1)2 at 2.22 a resolution
38	c4es6A	Alignment	not modelled	27.1	24	PDB header: biosynthetic protein Chain: U: PDB Molecule: duf1987 domain-containing protein; PDBTitle: siac of pseudomonas aeruginosa
39	c6k4fU	Alignment	not modelled	25.1	16	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
40	d1yg6a1	Alignment	not modelled	24.9	7	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
41	d2cbya1	Alignment	not modelled	24.4	16	PDB header: hydrolase Chain: D: PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: structure of clpp from bacillus subtilis in orthorhombic crystal form
42	c3kthD	Alignment	not modelled	23.1	9	PDB header: hydrolase Chain: B: PDB Molecule: 2-keto-3-deoxy-d-manno-octulosonate 8-phosphate PDBTitle: crystal structure of 2-keto-3-deoxyoctulosonate 8-phosphate2 phosphohydrolase from bacteroides thetaiotaomicron
43	c4hgnB	Alignment	not modelled	21.9	13	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
44	d1tg6a1	Alignment	not modelled	21.8	11	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
45	d1ccwa	Alignment	not modelled	19.9	21	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: crystal structure of an uroporphyrinogen-iii synthase (sama_3255) from2 shewanella amazonensis sb2b at 1.65 a resolution
46	c3mw8A	Alignment	not modelled	19.4	15	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
47	c6ov0D	Alignment	not modelled	18.6	16	PDB header: hydrolase Chain: C: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase kdsc; PDBTitle: crystal structure of 3-deoxy-d-manno-octulosonate 8-2 phosphate phosphatase from moraxella catarrhalis in3 complex with magnesium ion, phosphate ion and kdo molecule
48	c4umfC	Alignment	not modelled	18.4	23	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
49	d1rdua	Alignment	not modelled	18.1	18	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
50	d2csua3	Alignment	not modelled	17.5	9	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ada polyprotein; PDBTitle: nmr structure of e. coli ada protein in complex with dna
51	c1zgwA	Alignment	not modelled	17.4	29	PDB header: protein binding Chain: B: PDB Molecule: blue-light photoreceptor; PDBTitle: full-length solution structure of ytvA, a lov-photoreceptor protein2 and regulator of bacterial stress response
52	c2mwgB	Alignment	not modelled	17.3	16	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
53	d1eo1a	Alignment	not modelled	16.2	22	

54	c3n07B	Alignment	not modelled	16.0	19	PDB header: hydrolase Chain: B: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; PDBTitle: structure of putative 3-deoxy-d-manno-octulosonate 8-phosphate2 phosphatase from vibrio cholerae
55	d1qyia	Alignment	not modelled	15.7	15	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
56	d1eyfa	Alignment	not modelled	15.6	29	Fold: Ada DNA repair protein, N-terminal domain (N-Ada 10) Superfamily: Ada DNA repair protein, N-terminal domain (N-Ada 10) Family: Ada DNA repair protein, N-terminal domain (N-Ada 10)
57	c2wfbA	Alignment	not modelled	15.4	24	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative uncharacterized protein orp; PDBTitle: high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
58	c2re2A	Alignment	not modelled	13.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein ta1041; PDBTitle: crystal structure of a putative iron-molybdenum cofactor (femo-co)2 dinitrogenase (ta1041m) from thermoplasma acidophilum dsm 1728 at3 1.30 a resolution
59	c1wloA	Alignment	not modelled	13.7	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sufoe protein; PDBTitle: solution structure of the hypothetical protein from thermus2 thermophilus hb8
60	d1wzca1	Alignment	not modelled	13.4	5	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
61	c2qtdA	Alignment	not modelled	13.0	6	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein mj0327; PDBTitle: crystal structure of a putative dinitrogenase (mj0327) from2 methanocaldococcus jannaschii dsm at 1.70 a resolution
62	d1fmfa	Alignment	not modelled	12.7	18	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
63	c2bg5C	Alignment	not modelled	12.2	13	PDB header: transferase Chain: C: PDB Molecule: phosphoenolpyruvate-protein kinase; PDBTitle: crystal structure of the phosphoenolpyruvate-binding enzyme i-domain2 from the thermoanaerobacter tengcongensis pep: sugar3 phosphotransferase system (pts)
64	c2p9iH	Alignment	not modelled	12.0	17	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: hypothetical protein aq2171; PDBTitle: crystal structure of aq2171 from aquifex aeolicus
65	c3ufxG	Alignment	not modelled	12.0	11	PDB header: ligase Chain: G: PDB Molecule: succinyl-coa synthetase beta subunit; PDBTitle: thermus aquaticus succinyl-coa synthetase in complex with gdp-mn2+
66	c3n1uA	Alignment	not modelled	11.9	19	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, had superfamily, subfamily iii a; PDBTitle: structure of putative had superfamily (subfamily iii a) hydrolase from2 legionella pneumophila
67	d3c9ua2	Alignment	not modelled	11.8	17	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
68	d2nu7b1	Alignment	not modelled	11.2	7	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
69	c2hroA	Alignment	not modelled	10.6	7	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of the full-lenght enzyme i of the pts system from2 staphylococcus carnosus
70	c2cbyG	Alignment	not modelled	10.5	11	PDB header: hydrolase Chain: G: PDB Molecule: atp-dependent clp protease proteolytic subunit 1; PDBTitle: crystal structure of the atp-dependent clp protease proteolytic2 subunit 1 (clpp1) from mycobacterium tuberculosis
71	c4yaja	Alignment	not modelled	10.3	17	PDB header: ligase Chain: A: PDB Molecule: alpha subunit of acetyl-coenzyme a synthetase PDBTitle: ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form)
72	c2hx1D	Alignment	not modelled	9.4	9	PDB header: hydrolase Chain: D: PDB Molecule: predicted sugar phosphatases of the had superfamily; PDBTitle: crystal structure of possible sugar phosphatase, had superfamily2 (zp_00311070.1) from cytophaga hutchinsonii atcc 33406 at 2.10 a3 resolution
73	d1ys9a1	Alignment	not modelled	9.3	23	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
74	c3mn1B	Alignment	not modelled	9.3	19	PDB header: hydrolase Chain: B: PDB Molecule: probable yrbi family phosphatase; PDBTitle: crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
75	d2csua2	Alignment	not modelled	8.9	17	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
76	d7reqa2	Alignment	not modelled	8.9	8	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
77	c3efaA	Alignment	not modelled	8.6	16	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase; PDBTitle: crystal structure of putative n-acetyltransferase from lactobacillus2 plantarum
78	d1ro5a	Alignment	not modelled	8.3	16	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat)

						Family: Autoinducer synthetase
79	c3ezuA_	Alignment	not modelled	8.1	13	PDB header: signaling protein Chain: A: PDB Molecule: ggdef domain protein; PDBTitle: crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution
80	c2dgdD_	Alignment	not modelled	8.0	12	PDB header: lyase Chain: D: PDB Molecule: 223aa long hypothetical arylmalonate decarboxylase; PDBTitle: crystal structure of st0656, a function unknown protein from2 sulfolobus tokodaii
81	c2hwgA_	Alignment	not modelled	8.0	7	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
82	c3d8tB_	Alignment	not modelled	8.0	15	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: thermus thermophilus uroporphyrinogen iii synthase
83	c2obnA_	Alignment	not modelled	8.0	36	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf1611 family protein (ava_3511) from anaebaena2 variabilis atcc 29413 at 2.30 a resolution
84	c2r8zC_	Alignment	not modelled	7.4	18	PDB header: hydrolase Chain: C: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; PDBTitle: crystal structure of yrbi phosphatase from escherichia coli in complex2 with a phosphate and a calcium ion
85	c3uosH_	Alignment	not modelled	7.4	19	PDB header: ribosome Chain: H: PDB Molecule: 50s ribosomal protein l10; PDBTitle: crystal structure of release factor rf3 trapped in the gtp state on a2 rotated conformation of the ribosome (without viomycin)
86	c3dcmX_	Alignment	not modelled	7.2	15	PDB header: transferase Chain: X: PDB Molecule: uncharacterized protein tm_1570; PDBTitle: crystal structure of the thermotoga maritima spout family ma-2 methyltransferase protein tm1570 in complex with s-adenosyl- l-3 methionine
87	d1tqyb1	Alignment	not modelled	7.1	12	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
88	d2qale1	Alignment	not modelled	7.0	22	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
89	c4hluC_	Alignment	not modelled	6.9	11	PDB header: hydrolase Chain: C: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: structure of the ecfA-a' heterodimer bound to adp
90	c3jywF_	Alignment	not modelled	6.8	14	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
91	c3c3mA_	Alignment	not modelled	6.6	17	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of the n-terminal domain of response regulator2 receiver protein from methanoculleus marisnigri jr1
92	c6meIB_	Alignment	not modelled	6.6	10	PDB header: ligase Chain: B: PDB Molecule: succinate--coa ligase [adp-forming] subunit beta; PDBTitle: succinyl-coa synthase from campylobacter jejuni
93	d1ay7b_	Alignment	not modelled	6.6	9	Fold: Barstar-like Superfamily: Barstar-related Family: Barstar-related
94	d1pkpa1	Alignment	not modelled	6.5	22	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
95	c3mmzA_	Alignment	not modelled	6.5	17	PDB header: hydrolase Chain: A: PDB Molecule: putative had family hydrolase; PDBTitle: crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
96	c5wb4H_	Alignment	not modelled	6.4	18	PDB header: transferase Chain: H: PDB Molecule: n-acetylglucosaminyldiphosphoundecaprenol n-acetyl-beta-d- PDBTitle: crystal structure of the tara wall teichoic acid glycosyltransferase
97	c1jr2A_	Alignment	not modelled	6.3	16	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: structure of uroporphyrinogen iii synthase
98	d1jr2a_	Alignment	not modelled	6.3	16	Fold: HemD-like Superfamily: HemD-like Family: HemD-like
99	d2g0ta1	Alignment	not modelled	5.8	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like