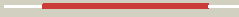













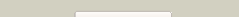


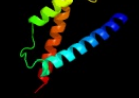


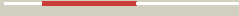

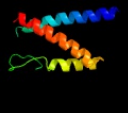

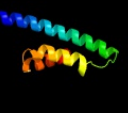




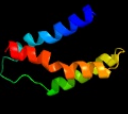



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1885c (-)_2134280_2134879
Date	Fri Aug 2 13:30:50 BST 2019
Unique Job ID	f7a0215a1d6e7cc1

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fp1a1	 Alignment		100.0	100	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Secreted chorismate mutase-like
2	c5ts9H_	 Alignment		100.0	25	PDB header: isomerase Chain: H; PDB Molecule: chorismate mutase; PDBTitle: crystal structure of chorismate mutase from burkholderia phymatum
3	c4oj7E_	 Alignment		100.0	30	PDB header: isomerase Chain: E; PDB Molecule: chorismate mutase; PDBTitle: crystal structure of chorismate mutase from burkholderia thailandensis
4	c2gbbA_	 Alignment		100.0	24	PDB header: isomerase Chain: A; PDB Molecule: putative chorismate mutase; PDBTitle: crystal structure of secreted chorismate mutase from yersinia pestis
5	d1ecma_	 Alignment		99.8	25	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Dimeric chorismate mutase
6	c3rmiA_	 Alignment		99.7	23	PDB header: isomerase Chain: A; PDB Molecule: chorismate mutase protein; PDBTitle: crystal structure of chorismate mutase from bartonella henselae str.2 houston-1 in complex with malate
7	d2gtvx1	 Alignment		99.7	21	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: monomeric chorismate mutase
8	c5go2D_	 Alignment		99.7	14	PDB header: isomerase Chain: D; PDB Molecule: protein aroa(g); PDBTitle: crystal structure of chorismate mutase like domain of bifunctional2 dahp synthase of bacillus subtilis in complex with citrate
9	c6a19A_	 Alignment		99.7	23	PDB header: isomerase Chain: A; PDB Molecule: chorismate mutase; PDBTitle: crystal structure of chorismate mutase from helicobacter pylori in2 complex with prephenate
10	d2d8da1	 Alignment		99.6	19	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Dimeric chorismate mutase
11	d1ybza1	 Alignment		99.5	25	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Dimeric chorismate mutase

12	d2h9da1	Alignment		99.4	21	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Dimeric chorismate mutase
13	c3nvtA	Alignment		99.4	17	PDB header: transferase/isomerase Chain: A: PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; PDBTitle: 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroA) from listeria3 monocytogenes egd-e
14	c2qbvA	Alignment		99.2	13	PDB header: isomerase Chain: A: PDB Molecule: chorismate mutase; PDBTitle: crystal structure of intracellular chorismate mutase from2 mycobacterium tuberculosis
15	c5hubA	Alignment		99.1	12	PDB header: isomerase Chain: A: PDB Molecule: chorismate mutase; PDBTitle: high-resolution structure of chorismate mutase from corynebacterium2 glutamicum
16	c5w6yB	Alignment		97.5	17	PDB header: biosynthetic protein,isomerase Chain: B: PDB Molecule: chorismate mutase; PDBTitle: physcomitrella patens chorismate mutase
17	d5csma	Alignment		97.5	24	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Allosteric chorismate mutase
18	c4ppuA	Alignment		97.3	16	PDB header: isomerase Chain: A: PDB Molecule: chorismate mutase 1, chloroplatic; PDBTitle: crystal structure of atcm1 with tyrosine bound in allosteric site
19	c6h3pB	Alignment		97.2	16	PDB header: plant protein Chain: B: PDB Molecule: chorismate mutase; PDBTitle: crystal structure of the cytoplasmic chorismate mutase from zea mays
20	c6fpgG	Alignment		96.5	25	PDB header: cell invasion Chain: G: PDB Molecule: chromosome 16, whole genome shotgun sequence; PDBTitle: structure of the ustilago maydis chorismate mutase 1 in complex with a2 zea mays kiwellin
21	d1dwka1	Alignment	not modelled	69.9	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Cyanase N-terminal domain
22	c2iv1J	Alignment	not modelled	51.2	25	PDB header: lyase Chain: J: PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase
23	c5kpeA	Alignment	not modelled	49.7	29	PDB header: de novo protein Chain: A: PDB Molecule: de novo beta sheet design protein or664; PDBTitle: solution nmr structure of denovo beta sheet design protein, northeast2 structural genomics consortium (nesg) target or664
24	d1gpja3	Alignment	not modelled	31.9	14	Fold: Ferredoxin-like Superfamily: Glutamyl tRNA-reductase catalytic, N-terminal domain Family: Glutamyl tRNA-reductase catalytic, N-terminal domain
25	d1myla	Alignment	not modelled	28.8	6	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
26	c4l8tA	Alignment	not modelled	28.8	10	PDB header: protein transport Chain: A: PDB Molecule: unconventional myosin-vc; PDBTitle: structure of the cargo binding domain from human myosin vc
27	c3n1bA	Alignment	not modelled	27.7	10	PDB header: transport protein Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 54; PDBTitle: c-terminal domain of vps54 subunit of the garp complex
28	c2ev2B	Alignment	not modelled	27.3	18	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: structure of rv1264n, the regulatory domain of the mycobacterial2 adenyllyl cylcase rv1264, at ph 8.5

29	d1icha_	Alignment	not modelled	27.1	10	Fold: DEATH domain Superfamily: DEATH domain Family: DEATH domain, DD
30	c1ichA_	Alignment	not modelled	27.1	10	PDB header: apoptosis Chain: A: PDB Molecule: tumor necrosis factor receptor-1; PDBTitle: solution structure of the tumor necrosis factor receptor-12 death domain
31	c5lewA_	Alignment	not modelled	26.7	14	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii subunit alpha; PDBTitle: dna polymerase
32	d1b28a_	Alignment	not modelled	25.7	6	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
33	c1y66D_	Alignment	not modelled	25.3	17	PDB header: de novo protein Chain: D: PDB Molecule: engrailed homeodomain; PDBTitle: dioxane contributes to the altered conformation and2 oligomerization state of a designed engrailed homeodomain3 variant
34	c6noyB_	Alignment	not modelled	23.7	30	PDB header: structural protein Chain: B: PDB Molecule: maintenance of carboxysome positioning b protein, mcsb; PDBTitle: structure of cyanothecce mcdb
35	c4j5mA_	Alignment	not modelled	23.6	13	PDB header: protein transport Chain: A: PDB Molecule: unconventional myosin-vb; PDBTitle: structure of the cargo binding domain from human myosin vb
36	d1mylb_	Alignment	not modelled	21.5	6	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
37	d2ecca1	Alignment	not modelled	19.7	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
38	c2g8yB_	Alignment	not modelled	19.7	7	PDB header: oxidoreductase Chain: B: PDB Molecule: malate/l-lactate dehydrogenases; PDBTitle: the structure of a putative malate/lactate dehydrogenase from e. coli.
39	d2p7vb1	Alignment	not modelled	17.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
40	c4p9gA_	Alignment	not modelled	17.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4'-dihydroxyacetophenone dioxygenase; PDBTitle: structure of the 2,4'-dihydroxyacetophenone dioxygenase from2 alcaligenes sp.
41	c4jrbA_	Alignment	not modelled	17.3	16	PDB header: lipid binding protein Chain: A: PDB Molecule: green fluorescent protein; PDBTitle: structure of cockroach allergen bla g 1 tandem repeat as a egfp fusion
42	c2wtgA_	Alignment	not modelled	17.0	11	PDB header: oxygen transport Chain: A: PDB Molecule: globin-like protein; PDBTitle: high resolution 3d structure of c.elegans globin-like2 protein glb-1
43	c4clvB_	Alignment	not modelled	16.7	10	PDB header: metal binding protein Chain: B: PDB Molecule: nickel-cobalt-cadmium resistance protein nccx; PDBTitle: crystal structure of dodecylphosphocholine-solubilized nccx2 from cupriavidus metallidurans 31a
44	c2knaA_	Alignment	not modelled	16.3	8	PDB header: apoptosis Chain: A: PDB Molecule: baculoviral iap repeat-containing protein 4; PDBTitle: solution structure of uba domain of xiap
45	d1ku3a_	Alignment	not modelled	16.0	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
46	d2vo9a1	Alignment	not modelled	15.9	3	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: VanY-like
47	c1kcfB_	Alignment	not modelled	15.4	7	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical 30.2 kd protein c25g10.02 in PDBTitle: crystal structure of the yeast mitochondrial holliday2 junction resolvase, ydc2
48	c2k23A_	Alignment	not modelled	15.0	12	PDB header: transport protein Chain: A: PDB Molecule: lipocalin 2; PDBTitle: solution structure analysis of the rlcN2
49	c5wujA_	Alignment	not modelled	14.7	28	PDB header: motor protein Chain: A: PDB Molecule: flagellar m-ring protein; PDBTitle: crystal structure of flif-flig complex from h. pylori
50	c2hnhA_	Alignment	not modelled	13.7	15	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii alpha subunit; PDBTitle: crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii
51	d1kcfa2	Alignment	not modelled	13.0	8	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Mitochondrial resolvase ydc2 catalytic domain
52	c4xp8A_	Alignment	not modelled	13.0	15	PDB header: hydrolase Chain: A: PDB Molecule: etga protein; PDBTitle: structure of etga d60n mutant
53	c2y8pA_	Alignment	not modelled	12.9	17	PDB header: lyase Chain: A: PDB Molecule: endo-type membrane-bound lytic murein transglycosylase a; PDBTitle: crystal structure of an outer membrane-anchored endolytic2 peptidoglycan lytic transglycosylase (mlte) from3 escherichia coli
54	d1cg5b_	Alignment	not modelled	12.8	14	Fold: Globin-like Superfamily: Globin-like Family: Globins

55	c6b2zd	Alignment	not modelled	12.7	24	PDB header: membrane protein Chain: D: PDB Molecule: atp synthase subunit c, mitochondrial; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
56	c2vo9C	Alignment	not modelled	12.2	3	PDB header: hydrolase Chain: C: PDB Molecule: l-alanyl-d-glutamate peptidase; PDBTitle: crystal structure of the enzymatically active domain of the listeria2 monocytogenes bacteriophage 500 endolysin ply500
57	c1dlcA	Alignment	not modelled	12.0	15	PDB header: toxin Chain: A: PDB Molecule: delta-endotoxin cryiiaa; PDBTitle: crystal structure of insecticidal delta-endotoxin from2 bacillus thuringiensis at 2.5 angstroms resolution
58	c5n07A	Alignment	not modelled	11.8	8	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional repressor nsrr; PDBTitle: structure of the [4fe-4s] form of the no response regulator nsrr
59	c5l7sA	Alignment	not modelled	11.3	12	PDB header: signaling protein Chain: A: PDB Molecule: secreted rxlr effector peptide protein; PDBTitle: crystal structure of rxlr effector pexrd54 from phytophthora infestans
60	c6bmcA	Alignment	not modelled	11.2	17	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: the structure of a dimeric type ii dah7ps associated with pyocyanin2 biosynthesis in pseudomonas aeruginosa
61	d1wi3a	Alignment	not modelled	11.2	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
62	c5fwfE	Alignment	not modelled	10.7	16	PDB header: chaperone Chain: E: PDB Molecule: hsp90 co-chaperone cdc37; PDBTitle: atomic cryoem structure of hsp90-cdc37-cdk4 complex
63	d1gbsa	Alignment	not modelled	10.6	6	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: G-type lysozyme
64	d1jhfa1	Alignment	not modelled	10.5	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
65	d1bazb	Alignment	not modelled	10.4	6	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
66	d2ezha	Alignment	not modelled	10.3	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
67	d2d5xa1	Alignment	not modelled	10.2	10	Fold: Globin-like Superfamily: Globin-like Family: Globins
68	d1yifa1	Alignment	not modelled	9.9	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator Rrf2
69	c6hsdB	Alignment	not modelled	9.9	21	PDB header: transcription Chain: B: PDB Molecule: rrf2 family transcriptional regulator; PDBTitle: crystal structure of the oxidized form of the transcription regulator2 rsrr
70	d1ji6a3	Alignment	not modelled	9.9	16	Fold: Toxins' membrane translocation domains Superfamily: delta-Endotoxin (insecticide), N-terminal domain Family: delta-Endotoxin (insecticide), N-terminal domain
71	d1mbaa	Alignment	not modelled	9.7	8	Fold: Globin-like Superfamily: Globin-like Family: Globins
72	c3pt8B	Alignment	not modelled	9.6	13	PDB header: oxygen transport Chain: B: PDB Molecule: hemoglobin iii; PDBTitle: structure of hbii-iii-cn from lucina pectinata at ph 5.0
73	c3gxkB	Alignment	not modelled	9.6	23	PDB header: hydrolase Chain: B: PDB Molecule: goose-type lysozyme 1; PDBTitle: the crystal structure of g-type lysozyme from atlantic cod (gadus2 morhua l.) in complex with nag oligomers sheds new light on substrate3 binding and the catalytic mechanism. native structure to 1.9
74	c3mlgB	Alignment	not modelled	9.5	9	PDB header: de novo protein Chain: B: PDB Molecule: 2x chimera of helicobacter pylori protein hp0242; PDBTitle: 2ouf-2x, a designed knotted protein
75	d1xd7a	Alignment	not modelled	9.4	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator Rrf2
76	c2wy4A	Alignment	not modelled	9.3	12	PDB header: oxygen transport Chain: A: PDB Molecule: single domain haemoglobin; PDBTitle: structure of bacterial globin from campylobacter jejuni at2 1.35 a resolution
77	c2l0gA	Alignment	not modelled	9.2	27	PDB header: protein binding Chain: A: PDB Molecule: dna polymerase iota; PDBTitle: solution nmr structure of ubiquitin-binding motif (ubm2) of human2 polymerase iota
78	d1wh5a	Alignment	not modelled	9.2	0	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
79	c2eq9C	Alignment	not modelled	9.2	25	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
80	c2khuA	Alignment	not modelled	9.0	27	PDB header: transferase/protein binding Chain: A: PDB Molecule: immunoglobulin g-binding protein g, dna PDBTitle: solution structure of the ubiquitin-binding motif of

						human2 polymerase iota
81	c2dkzA_	Alignment	not modelled	8.8	9	PDB header: signaling protein Chain: A: PDB Molecule: hypothetical protein loc64762; PDBTitle: solution structure of the sam_pnt-domain of the2 hypothetical protein loc64762
82	d1fvpa_	Alignment	not modelled	8.8	13	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (LuxF, FP390)
83	c2k29A_	Alignment	not modelled	8.8	14	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
84	d1sr9a1	Alignment	not modelled	8.8	27	Fold: RuvA C-terminal domain-like Superfamily: post-HMGL domain-like Family: DmpG/LeuA communication domain-like
85	d1it2a_	Alignment	not modelled	8.7	8	Fold: Globin-like Superfamily: Globin-like Family: Globins
86	c2gf5A_	Alignment	not modelled	8.7	16	PDB header: apoptosis Chain: A: PDB Molecule: fadd protein; PDBTitle: structure of intact fadd (mort1)
87	c4zvdA_	Alignment	not modelled	8.7	10	PDB header: signaling protein Chain: A: PDB Molecule: diguanylate cyclase dosc; PDBTitle: crystal structure of mid domain of the e. coli dosc - form ii
88	c3d1B_	Alignment	not modelled	8.6	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadp oxidoreductase bf3122; PDBTitle: crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
89	c3s1jC_	Alignment	not modelled	8.6	14	PDB header: oxygen transport, oxygen storage Chain: C: PDB Molecule: hemoglobin-like flavoprotein; PDBTitle: crystal structure of acetate-bound hell's gate globin i
90	d1yt3a2	Alignment	not modelled	8.6	5	Fold: SAM domain-like Superfamily: HRDC-like Family: RNase D C-terminal domains
91	c4u8uW_	Alignment	not modelled	8.5	13	PDB header: oxygen storage/transport Chain: W: PDB Molecule: globin d chain; PDBTitle: the crystallographic structure of the giant hemoglobin from2 glossoscolex paulistus at 3.2 a resolution.
92	c2eq7C_	Alignment	not modelled	8.4	13	PDB header: oxidoreductase Chain: C: PDB Molecule: 2-oxoglutarate dehydrogenase e2 component; PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbd0
93	c3fdqB_	Alignment	not modelled	8.3	17	PDB header: dna binding protein/dna Chain: B: PDB Molecule: motility gene repressor mogr; PDBTitle: recognition of at-rich dna binding sites by the mogr2 repressor
94	d2qfka1	Alignment	not modelled	8.3	8	Fold: Globin-like Superfamily: Globin-like Family: Globins
95	c4q2uM_	Alignment	not modelled	8.2	6	PDB header: toxin/toxin repressor Chain: M: PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
96	c2yqfA_	Alignment	not modelled	8.2	13	PDB header: protein binding Chain: A: PDB Molecule: ankyrin-1; PDBTitle: solution structure of the death domain of ankyrin-1
97	c2zs0A_	Alignment	not modelled	8.2	13	PDB header: oxygen storage, oxygen transport Chain: A: PDB Molecule: extracellular giant hemoglobin major globin subunit a1; PDBTitle: structural basis for the heterotropic and homotropic interactions of2 invertebrate giant hemoglobin
98	d1u9pa1	Alignment	not modelled	8.2	6	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
99	c1x3kA_	Alignment	not modelled	8.1	5	PDB header: oxygen storage/transport Chain: A: PDB Molecule: hemoglobin component v; PDBTitle: crystal structure of a hemoglobin component (ta-v) from2 tokunagayusurika akamusi