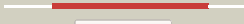



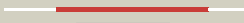

















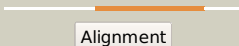

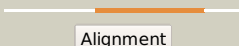

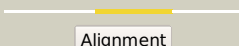

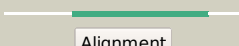

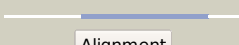

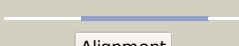

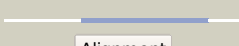


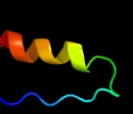
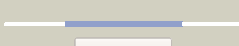


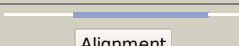

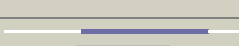
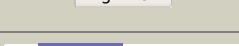
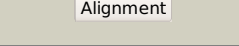
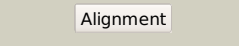




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2816c_(-)_3123635_3123976
Date	Wed Aug 7 12:50:48 BST 2019
Unique Job ID	129926e7ea3f2001

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1zpxw1	 Alignment		100.0	41	Fold: Ferredoxin-like Superfamily: TTP0101/SSO1404-like Family: TTP0101/SSO1404-like
2	c3oq2A	 Alignment		99.9	32	PDB header: immune system Chain: A: PDB Molecule: crispr-associated protein cas2; PDBTitle: structure of a crispr associated protein cas2 from desulfovibrio2 vulgaris
3	c4es2A	 Alignment		99.9	32	PDB header: hydrolase Chain: A: PDB Molecule: bh0342 protein; PDBTitle: double-stranded endonuclease activity in b. halodurans clustered2 regularly interspaced short palindromic repeats (crispr)-associated3 cas2 protein
4	d2i0xa1	 Alignment		99.9	24	Fold: Ferredoxin-like Superfamily: TTP0101/SSO1404-like Family: TTP0101/SSO1404-like
5	c5h1pB	 Alignment		99.9	32	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endoribonuclease cas2; PDBTitle: crispr-associated protein
6	c4qr1B	 Alignment		99.9	32	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endoribonuclease cas2; PDBTitle: crystal structure of streptococcus pyogenes cas2 at ph 6.5
7	d2ivya1	 Alignment		99.9	27	Fold: Ferredoxin-like Superfamily: TTP0101/SSO1404-like Family: TTP0101/SSO1404-like
8	c3excX	 Alignment		99.8	32	PDB header: hydrolase Chain: X: PDB Molecule: uncharacterized protein; PDBTitle: structure of the rna'se sso8090 from sulfolobus solfataricus
9	c5xvnM	 Alignment		98.6	22	PDB header: immune system Chain: M: PDB Molecule: crispr-associated endoribonuclease cas2; PDBTitle: e. far cas1-cas2/prespacer binary complex
10	c4p6iB	 Alignment		91.7	15	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endoribonuclease cas2; PDBTitle: crystal structure of the cas1-cas2 complex from escherichia coli
11	c4makA	 Alignment		90.3	15	PDB header: hydrolase Chain: A: PDB Molecule: crispr-associated endoribonuclease cas2; PDBTitle: crystal structure of a putative ssrna endonuclease cas2, crispr2 adaptation protein from e.coli

12	c3ui3A_	 Alignment		87.6	21	PDB header: rna binding protein Chain: A: PDB Molecule: immunoglobulin g-binding protein g, virulence-associated PDBTitle: structural and biochemical characterization of hp0315 from2 helicobacter pylori as a vapd protein with an endoribonuclease3 activity
13	c3ui3B_	 Alignment		84.8	15	PDB header: rna binding protein Chain: B: PDB Molecule: immunoglobulin g-binding protein g, virulence-associated PDBTitle: structural and biochemical characterization of hp0315 from2 helicobacter pylori as a vapd protein with an endoribonuclease3 activity
14	c5dyrA_	 Alignment		78.9	5	PDB header: dna binding protein Chain: A: PDB Molecule: virulence-associated protein d; PDBTitle: structure of virulence-associated protein d (vapd) from xylella2 fastidiosa
15	c5b7iA_	 Alignment		48.1	20	PDB header: hydrolase/unknown function Chain: A: PDB Molecule: crispr-associated nuclease/helicase cas3 subtype i-f/ypest; PDBTitle: cas3-acrf3 complex
16	c1i3oC_	 Alignment		25.6	13	PDB header: apoptosis Chain: C: PDB Molecule: caspase 3; PDBTitle: crystal structure of the complex of xiap-bir2 and caspase 3
17	c3edqC_	 Alignment		24.3	13	PDB header: hydrolase/hydrolase inhibitor Chain: C: PDB Molecule: caspase-3; PDBTitle: crystal structure of caspase-3 with inhibitor ac-ldesd-cho
18	d1f1ja_	 Alignment		24.1	11	Fold: Caspase-like Superfamily: Caspase-like Family: Caspase catalytic domain
19	c6ia7B_	 Alignment		23.8	9	PDB header: cytosolic protein Chain: B: PDB Molecule: intraflagellar transport protein 22; PDBTitle: t. brucei ift22 gtp-bound crystal structure
20	c3hqtB_	 Alignment		22.5	14	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
21	d2dy1a4	 Alignment	not modelled	22.3	10	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
22	c2ql5A_	 Alignment	not modelled	21.1	10	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: caspase-7; PDBTitle: crystal structure of caspase-7 with inhibitor ac-dmqd-cho
23	c3sipC_	 Alignment	not modelled	20.5	9	PDB header: hydrolase/ligase/hydrolase Chain: C: PDB Molecule: caspase; PDBTitle: crystal structure of drice and diap1-bir1 complex
24	c5v6uA_	 Alignment	not modelled	19.1	11	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: caspase-7; PDBTitle: crystal structure of human caspase-7 soaked with allosteric inhibitor2 2-[(2-acetylphenyl)sulfanyl]benzoic acid
25	c5nnqA_	 Alignment	not modelled	18.1	24	PDB header: transferase Chain: A: PDB Molecule: ctatc; PDBTitle: aspartate transcarbamoylase from chaetomium thermophilum cad-like2 bound to carbamoyl phosphate
26	d1nwba_	 Alignment	not modelled	15.7	20	Fold: HesB-like domain Superfamily: HesB-like domain Family: HesB-like domain
27	c3p45I_	 Alignment	not modelled	14.7	12	PDB header: hydrolase Chain: I: PDB Molecule: caspase-6; PDBTitle: crystal structure of apo-caspase-6 at physiological ph
28	c2kx7A_	 Alignment	not modelled	13.7	25	PDB header: protein binding Chain: A: PDB Molecule: sensor-like histidine kinase yojn; PDBTitle: solution structure of the e.coli rcsd-abl domain (residues 688-795)
29	c1ml4A_	 Alignment	not modelled	13.4	20	PDB header: transferase Chain: A: PDB Molecule: aspartate transcarbamoylase;

29	c1m9A	Alignment	not modelled	13.4	20	PDBTitle: the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: mucosa-associated lymphoid tissue lymphoma translocation PDBTitle: human malt1 (caspase domain) in complex with an irreversible peptidic2 inhibitor
30	c3v4oA	Alignment	not modelled	12.5	13	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
31	d2bm0a4	Alignment	not modelled	12.3	23	PDB header: hydrolase Chain: D: PDB Molecule: caspase-1; PDBTitle: structure of pro-sf-caspase-1
32	c2nn3D	Alignment	not modelled	12.2	19	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: caspase-7 subunit p20; PDBTitle: crystal structure of caspase-7 complexed with xiap
33	c1i51A	Alignment	not modelled	11.9	11	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
34	d1kona	Alignment	not modelled	11.4	16	PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of glda from e.coli
35	c5zxID	Alignment	not modelled	11.3	10	PDB header: transferase Chain: A: PDB Molecule: putative trna (cytidine(34)-2'-o)-methyltransferase; PDBTitle: structural insights into the 2-oh methylation of c/u34 on trna
36	c5co4A	Alignment	not modelled	11.1	25	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: apopain; PDBTitle: crystal structure of the complex of apopain with the tetrapeptide2 inhibitor ace-dvad-fmc
37	c1cp3B	Alignment	not modelled	10.1	12	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
38	d1rlga	Alignment	not modelled	9.5	14	PDB header: motor protein Chain: J: PDB Molecule: dynein light intermediate chain region of the dynein2 tail/dynactin/bicdr1 complex
39	c6f1yi	Alignment	not modelled	9.4	16	PDB header: transport protein Chain: D: PDB Molecule: small rab-related gtpase; PDBTitle: intraflagellar transport complex 25-27 from chlamydomonas
40	c2yc2D	Alignment	not modelled	8.5	14	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
41	d1yu8x1	Alignment	not modelled	8.5	44	PDB header: hydrolase Chain: B: PDB Molecule: cell death protein 3; PDBTitle: crystal structure of ced-3
42	c4m9rB	Alignment	not modelled	8.4	14	PDB header: hydrolase Chain: A: PDB Molecule: metacaspase mca2; PDBTitle: the structure of metacaspase 2 from t. brucei determined in the2 presence of samarium
43	c4afpA	Alignment	not modelled	8.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: methylenetetrahydrofolate reductase; PDBTitle: structure of human 5,10-methylenetetrahydrofolate reductase (mthfr)
44	c6fcxA	Alignment	not modelled	8.1	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sh3 domain-binding glutamic acid-rich-like PDBTitle: solution structure of the sh3 domain-binding glutamic acid-2 rich-like protein 2
45	c2ct6A	Alignment	not modelled	8.1	16	PDB header: dna binding protein Chain: A: PDB Molecule: protein lsr2; PDBTitle: crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 1 21 1 space group
46	c4e1pA	Alignment	not modelled	7.9	14	PDB header: dna binding protein Chain: A: PDB Molecule: protein lsr2; PDBTitle: crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 31 2 1 space group
47	c4e1rA	Alignment	not modelled	7.9	14	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: mucosa-associated lymphoid tissue lymphoma translocation PDBTitle: crystal structure of the malt1 paracaspase (p21 form)
48	c3uoab	Alignment	not modelled	7.8	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein cbu_1566; PDBTitle: structure of a yebc family protein (cbu_1566) from coxiella burnetii
49	c4f3qA	Alignment	not modelled	7.7	9	PDB header: hydrolase Chain: A: PDB Molecule: mitochondrial rho gtpase 1; PDBTitle: hmiro ef hand and cgtpase domains in the gmppcp-bound state
50	c5kszA	Alignment	not modelled	7.6	18	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
51	d1gyxa	Alignment	not modelled	7.4	29	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
52	d1unca	Alignment	not modelled	7.3	22	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
53	d1gz0a1	Alignment	not modelled	7.2	10	PDB header: transferase Chain: G: PDB Molecule: hypothetical trna/rrna methyltransferase yjfh; PDBTitle: 23s ribosomal rna g2251 2'-o-methyltransferase r1mb
54	c1gz0G	Alignment	not modelled	7.2	10	Fold: Kix domain of CBP (creb binding protein)

55	d1sb0a_	Alignment	not modelled	7.1	56	Superfamily: Kix domain of CBP (creb binding protein) Family: Kix domain of CBP (creb binding protein)
56	c5iftB_	Alignment	not modelled	7.0	14	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: caspase 3, apoptosis-related cysteine protease a; PDBTitle: zebra fish caspase-3
57	d1n0ua4	Alignment	not modelled	6.9	18	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
58	c3bacA_	Alignment	not modelled	6.8	18	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: structural basis for the inhibition of bacterial nad+2 dependent dna ligase
59	d1y0ya2	Alignment	not modelled	6.8	12	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
60	c6ambB_	Alignment	not modelled	6.5	13	PDB header: signaling protein Chain: B: PDB Molecule: afadin; PDBTitle: crystal structure of the afadin ra1 domain in complex with hras
61	c2xvzA_	Alignment	not modelled	6.5	19	PDB header: metal binding protein Chain: A: PDB Molecule: chelataase, putative; PDBTitle: cobalt chelataase cbik (periplasmatic) from desulvobrio2 vulgaris hildenborough (co-crystallized with cobalt)
62	c2lu1A_	Alignment	not modelled	6.4	50	PDB header: hydrolase Chain: A: PDB Molecule: subtilase; PDBTitle: pfsb2 solution nmr structure
63	c1pyoA_	Alignment	not modelled	6.3	16	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: caspase-2; PDBTitle: crystal structure of human caspase-2 in complex with acetyl-leu-asp-2 glu-ser-asp-cho
64	d2alea1	Alignment	not modelled	6.1	11	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
65	d2c9wc1	Alignment	not modelled	6.1	19	Fold: POZ domain Superfamily: POZ domain Family: BTB/POZ domain
66	d1unda_	Alignment	not modelled	6.0	33	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
67	c4w8hA_	Alignment	not modelled	5.8	26	PDB header: signaling protein Chain: A: PDB Molecule: toll-receptor-related 2; PDBTitle: crystal structure of the tir domain of the toll-related receptor trr-22 from the lower metazoan hydra magnipapillata (crystal form ii)
68	d2czwa1	Alignment	not modelled	5.8	14	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
69	c4m3lC_	Alignment	not modelled	5.8	5	PDB header: ligase Chain: C: PDB Molecule: e3 ubiquitin-protein ligase trim63; PDBTitle: crystal structure of the coiled coil domain of murf1
70	c1kmcB_	Alignment	not modelled	5.7	12	PDB header: apoptosis/hydrolase Chain: B: PDB Molecule: caspase-7; PDBTitle: crystal structure of the caspase-7 / xiap-bir2 complex
71	c5gwmB_	Alignment	not modelled	5.7	13	PDB header: signaling protein Chain: B: PDB Molecule: metabotropic gaba-b receptor subtype 3, isoform a; PDBTitle: solution structure of heterodimeric coiled-coil domain of drosophila2 gabab receptor 1 and 3
72	c5widB_	Alignment	not modelled	5.6	22	PDB header: flavoprotein Chain: B: PDB Molecule: flavodoxin; PDBTitle: structure of a flavodoxin from the domain archaea
73	c2lbwA_	Alignment	not modelled	5.6	11	PDB header: rna binding protein Chain: A: PDB Molecule: h/aca ribonucleoprotein complex subunit 2; PDBTitle: solution structure of the s. cerevisiae h/aca rnp protein nhp2p-s82w2 mutant
74	c2op8A_	Alignment	not modelled	5.5	19	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase ywhb; PDBTitle: crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
75	c2funB_	Alignment	not modelled	5.5	9	PDB header: apoptosis/hydrolase Chain: B: PDB Molecule: caspase-8; PDBTitle: alternative p35-caspase-8 complex
76	c4c0lA_	Alignment	not modelled	5.5	26	PDB header: hydrolase Chain: A: PDB Molecule: mitochondrial rho gtpase; PDBTitle: crystal structure of drosophila miro ef hand and cgtpase domains2 bound to one magnesium ion and mg:gdp (mggdp-miros)
77	d1jq5a_	Alignment	not modelled	5.4	11	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
78	c3l6vA_	Alignment	not modelled	5.4	22	PDB header: isomerase Chain: A: PDB Molecule: dna gyrase subunit a; PDBTitle: crystal structure of the xanthomonas campestris gyrase a c-2 terminal domain
79	c5xyiM_	Alignment	not modelled	5.3	17	PDB header: ribosome Chain: M: PDB Molecule: ribosomal protein l7ae, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
80	d1ludxa3	Alignment	not modelled	5.3	22	Fold: Obg GTP-binding protein C-terminal domain Superfamily: Obg GTP-binding protein C-terminal domain Family: Obg GTP-binding protein C-terminal domain
						Fold: Bacillus chorismate mutase-like

81	dlvqof1	Alignment	not modelled	5.3	14	Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
82	d2fc3a1	Alignment	not modelled	5.3	11	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
83	c3kewA_	Alignment	not modelled	5.1	11	PDB header: transferase Chain: A: PDB Molecule: dhha1 domain protein; PDBTitle: crystal structure of probable alanyl-trna-synthase from clostridium2 perfringens
84	c3a1qF_	Alignment	not modelled	5.1	43	PDB header: gene regulation/signaling protein Chain: F: PDB Molecule: ubiquitin interaction motif-containing protein 1; PDBTitle: crystal structure of the mouse rap80 uims in complex with2 lys63-linked di-ubiquitin