


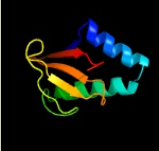




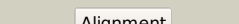



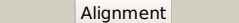


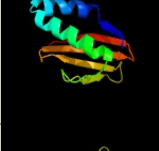
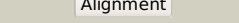

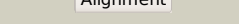
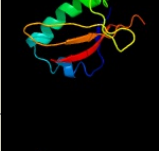
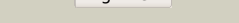




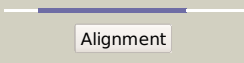
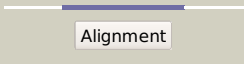
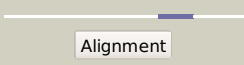
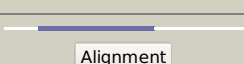
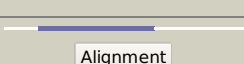
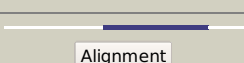
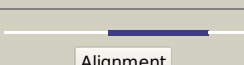

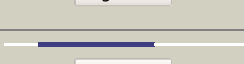
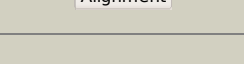
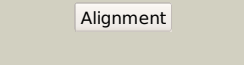
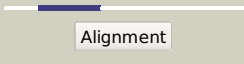
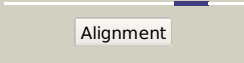
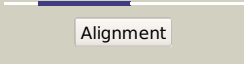
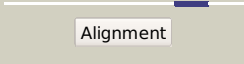
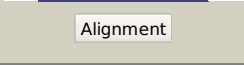
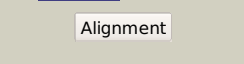
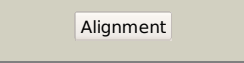
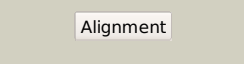
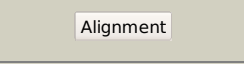
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3358 (-)_3771216_3771473
Date	Fri Aug 9 18:20:02 BST 2019
Unique Job ID	72145dd49612d2fa

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3oeiH_	 Alignment		100.0	100	PDB header: toxin, protein binding Chain: H; PDB Molecule: relk (toxin rv3358); PDBTitle: crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
2	d2a6sa1	 Alignment		100.0	45	Fold: RelE-like Superfamily: RelE-like Family: YoeB/Txe-like
3	c4q2uH_	 Alignment		99.9	18	PDB header: toxin/toxin repressor Chain: H; PDB Molecule: mrna interferase yafq; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
4	d1z8ma1	 Alignment		99.9	20	Fold: RelE-like Superfamily: RelE-like Family: RelE-like
5	c2otrA_	 Alignment		99.9	14	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein hp0892; PDBTitle: solution structure of conserved hypothetical protein hp0892 from2 helicobacter pylori
6	c2kheA_	 Alignment		99.4	33	PDB header: hydrolase Chain: A; PDB Molecule: toxin-like protein; PDBTitle: solution structure of the bacterial toxin rele from thermus2 thermophilus hb8
7	c3bpqD_	 Alignment		99.3	17	PDB header: toxin Chain: D; PDB Molecule: toxin rele3; PDBTitle: crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
8	d1wmia1	 Alignment		99.2	15	Fold: RelE-like Superfamily: RelE-like Family: RelE-like
9	c3g5oC_	 Alignment		99.2	27	PDB header: toxin/antitoxin Chain: C; PDB Molecule: uncharacterized protein rv2866; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
10	c3kixy_	 Alignment		98.6	18	PDB header: ribosome Chain: Y; PDB Molecule: PDBTitle: structure of rele nuclease bound to the 70s ribosome (postcleavage2 state; part 3 of 4)
11	c4mctD_	 Alignment		98.5	23	PDB header: toxin Chain: D; PDB Molecule: killer protein; PDBTitle: p. vulgaris higba structure, crystal form 1

12	c5cw7H_	Alignment		98.0	13	PDB header: toxin Chain: H: PDB Molecule: plasmid stabilization protein pare; PDBTitle: crystal structure of the paaa2-pare2 antitoxin-toxin complex
13	c5cegB_	Alignment		97.9	18	PDB header: toxin Chain: B: PDB Molecule: plasmid stabilization system; PDBTitle: x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum
14	c3kxeB_	Alignment		97.7	21	PDB header: protein binding Chain: B: PDB Molecule: toxin protein pare-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
15	c5ja9D_	Alignment		95.8	18	PDB header: toxin Chain: D: PDB Molecule: toxin higb-2; PDBTitle: crystal structure of the higb2 toxin in complex with nb6
16	c6f8sD_	Alignment		95.7	17	PDB header: toxin Chain: D: PDB Molecule: putative killer protein; PDBTitle: toxin-antitoxin complex grata
17	d3e9va1	Alignment		39.3	17	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
18	c2lo0B_	Alignment		32.6	27	PDB header: protein binding Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of the get5 carboxyl domain from a. fumigatus
19	d2z15a1	Alignment		26.9	17	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
20	d1khba2	Alignment		23.6	26	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain
21	c5j10A_	Alignment	not modelled	20.0	32	PDB header: de novo protein Chain: A: PDB Molecule: peptide design 214hc2_24; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
22	d1s0ua2	Alignment	not modelled	16.0	45	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain Family: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
23	d3bb9a1	Alignment	not modelled	15.7	10	Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like
24	c3sjaG_	Alignment	not modelled	15.5	19	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: golgi to er traffic protein 1; PDBTitle: crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain
25	d2qn6a2	Alignment	not modelled	15.3	36	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain Family: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
26	d1kk1a2	Alignment	not modelled	14.4	45	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain Family: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
27	c3sjbC_	Alignment	not modelled	13.4	18	PDB header: hydrolase/transport protein Chain: C: PDB Molecule: golgi to er traffic protein 1; PDBTitle: crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain
28	c1rb8J_	Alignment	not modelled	13.1	40	PDB header: virus/dna Chain: J: PDB Molecule: small core protein; PDBTitle: the phix174 dna binding protein j in two different capsid2 environments.
						PDB header: oxidoreductase

29	c2kruA_		Alignment	not modelled	12.0	6	Chain: A: PDB Molecule: light-independent protochlorophyllide reductase subunit b; PDBTitle: solution nmr structure of the pcg_red domain of light-independent2 protochlorophyllide reductase subunit b from chlorobium tepidum.3 northeast structural genomics consortium target ctr69a
30	d2gykb1		Alignment	not modelled	11.7	10	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
31	c5td6A_		Alignment	not modelled	11.4	17	PDB header: rna binding protein Chain: A: PDB Molecule: fog-3 protein; PDBTitle: c. elegans fog-3 btg/tob domain - h47n, c117a
32	c3e56A_		Alignment	not modelled	10.3	29	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the 2.0 angstrom resolution crystal structure of npr1517, a putative2 heterocyst differentiation inhibitor from nostoc punctiforme
33	c2fh0A_		Alignment	not modelled	10.3	11	PDB header: unknown function Chain: A: PDB Molecule: hypothetical 16.0 kda protein in abf2-chl12 PDBTitle: nmr ensemble of the yeast saccharomyces cerevisiae protein2 ymr074cp core region
34	d1ejja_		Alignment	not modelled	10.0	11	Fold: RuvA C-terminal domain-like Superfamily: Double-stranded DNA-binding domain Family: Double-stranded DNA-binding domain
35	c2qeyA_		Alignment	not modelled	9.9	24	PDB header: lyase Chain: A: PDB Molecule: phosphoenolpyruvate carboxykinase, cytosolic [gtp]; PDBTitle: rat cytosolic pepck in complex with gtp
36	c1wmvA_		Alignment	not modelled	9.6	21	PDB header: oxidoreductase, apoptosis Chain: A: PDB Molecule: ww domain containing oxidoreductase; PDBTitle: solution structure of the second ww domain of wwox
37	d2d5ua1		Alignment	not modelled	9.5	13	Fold: PUG domain-like Superfamily: PUG domain-like Family: PUG domain
38	c2dogA_		Alignment	not modelled	9.0	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable 16s rrna-processing protein rimm; PDBTitle: solution structure of the n-terminal domain of rimm from thermus2 thermophilus hb8
39	d2crua1		Alignment	not modelled	7.7	11	Fold: RuvA C-terminal domain-like Superfamily: Double-stranded DNA-binding domain Family: Double-stranded DNA-binding domain
40	d2ux0a1		Alignment	not modelled	7.4	37	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
41	c6iqcA_		Alignment	not modelled	7.2	11	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein sso0352; PDBTitle: wild-type programmed cell death 5 protein from sulfobolus solfataricus
42	c3d7iB_		Alignment	not modelled	6.9	17	PDB header: lyase Chain: B: PDB Molecule: carboxymuconolactone decarboxylase family protein; PDBTitle: crystal structure of carboxymuconolactone decarboxylase family protein2 possibly involved in oxygen detoxification (1591455) from3 methanococcus jannaschii at 1.75 a resolution
43	c6ms4B_		Alignment	not modelled	6.5	12	PDB header: translation Chain: B: PDB Molecule: density-regulated protein; PDBTitle: crystal structure of the denr-mct-1 complex
44	d1ejxb_		Alignment	not modelled	6.4	29	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
45	c4gicB_		Alignment	not modelled	6.2	28	PDB header: oxidoreductase Chain: B: PDB Molecule: histidinol dehydrogenase; PDBTitle: crystal structure of a putative histidinol dehydrogenase (target psi-2 014034) from methylococcus capsulatus
46	c4z42B_		Alignment	not modelled	5.9	14	PDB header: hydrolase Chain: B: PDB Molecule: urease subunit beta; PDBTitle: crystal structure of urease from yersinia enterocolitica
47	d2jb0b1		Alignment	not modelled	5.8	11	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
48	c2wx4C_		Alignment	not modelled	5.7	9	PDB header: structural protein Chain: C: PDB Molecule: decapping protein 1; PDBTitle: asymmetric trimer of the drosophila melanogaster dcp1 c-2 terminal domain
49	c2l4jA_		Alignment	not modelled	5.6	29	PDB header: transcription Chain: A: PDB Molecule: yes-associated protein 2 (yap2); PDBTitle: yap ww2
50	c2l09A_		Alignment	not modelled	5.5	7	PDB header: oxidoreductase Chain: A: PDB Molecule: asr4154 protein; PDBTitle: solution nmr structure of protein asr4154 from nostoc sp. pcc71202 northeast structural genomics consortium target id nsr143
51	d4ubpb_		Alignment	not modelled	5.5	14	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
52	c2jxnA_		Alignment	not modelled	5.4	11	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein ymr074c; PDBTitle: solution structure of s. cerevisiae pdcd5-like protein ymr074cp
53	c5nb9A_		Alignment	not modelled	5.3	28	PDB header: rna Chain: A: PDB Molecule: rna chaperone proq; PDBTitle: structure of the n-terminal domain of the escherichia coli proq rna2 binding protein