



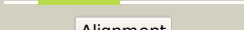
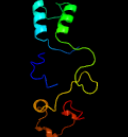



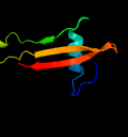

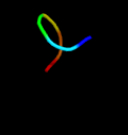

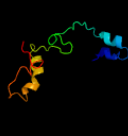

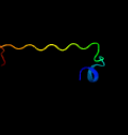
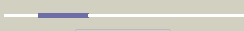
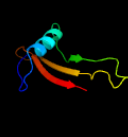

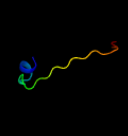



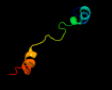
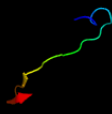
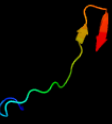

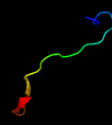
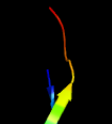

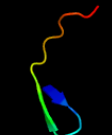


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1775 (-) _2009179_2009997
Date	Fri Aug 2 13:30:38 BST 2019
Unique Job ID	8f4d450c46179f86

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hwpA_	 Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: phlg; PDBTitle: crystal structure and computational analyses provide insights into the2 catalytic mechanism of 2, 4-diacetylphloroglucinol hydrolase phlg3 from pseudomonas fluorescens
2	c5xeyC_	 Alignment		100.0	32	PDB header: hydrolase Chain: C: PDB Molecule: phloretin hydrolase; PDBTitle: discovery and structural analysis of a phloretin hydrolase from the2 opportunistic pathogen mycobacterium abscessus
3	c5zcrB_	 Alignment		62.9	16	PDB header: hydrolase Chain: B: PDB Molecule: maltooligosyl trehalose synthase; PDBTitle: dsm5389 glycosyltrehalose synthase
4	d2ciwa2	 Alignment		44.7	40	Fold: EF Hand-like Superfamily: Cloroperoxidase Family: Cloroperoxidase
5	c2w56B_	 Alignment		27.1	21	PDB header: unknown function Chain: B: PDB Molecule: vc0508; PDBTitle: structure of the hypothetical protein vc0508 from vibrio cholerae2 vsp-ii pathogenicity island
6	c6hu9u_	 Alignment		20.2	67	PDB header: oxidoreductase/electron transport Chain: U: PDB Molecule: cytochrome b-c1 complex subunit 10; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
7	c3hjeA_	 Alignment		15.9	16	PDB header: transferase Chain: A: PDB Molecule: 704aa long hypothetical glycosyltransferase; PDBTitle: crystal structure of sulfolobus tokodaii hypothetical maltooligosyl2 trehalose synthase
8	c3fwtA_	 Alignment		15.2	12	PDB header: cytokine Chain: A: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: crystal structure of leishmania major mif2
9	c2v1IA_	 Alignment		15.1	21	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: structure of the conserved hypothetical protein vc1805 from2 pathogenicity island vpi-2 of vibrio cholerae o1 biovar3 eltor str. n16961 shares structural homology with the4 human p32 protein
10	c3b64A_	 Alignment		14.2	15	PDB header: cytokine Chain: A: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: macrophage migration inhibitory factor (mif) from2 /leishmania major
11	c6gu1B_	 Alignment		11.5	21	PDB header: unknown function Chain: B: PDB Molecule: secreted rxlr effector peptide protein, putative; PDBTitle: sfi3 effector protein from the oomycete plant pathogen phytophthora2 infestans

12	d2bw3a1	Alignment		10.5	11	Fold: Hermes dimerisation domain Superfamily: Hermes dimerisation domain Family: Hermes dimerisation domain
13	c5lnku	Alignment		10.2	21	PDB header: oxidoreductase Chain: U: PDB Molecule: PDBTitle: entire ovine respiratory complex i
14	c5m30A	Alignment		9.9	13	PDB header: secretion system Chain: A: PDB Molecule: type vi secretion protein; PDBTitle: structure of tssk from t6ss eaec in complex with nanobody nb18
15	c5m30B	Alignment		9.9	13	PDB header: secretion system Chain: B: PDB Molecule: type vi secretion protein; PDBTitle: structure of tssk from t6ss eaec in complex with nanobody nb18
16	d1wiga2	Alignment		9.2	40	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
17	c5m30C	Alignment		8.5	13	PDB header: secretion system Chain: C: PDB Molecule: type vi secretion protein; PDBTitle: structure of tssk from t6ss eaec in complex with nanobody nb18
18	c6cp8B	Alignment		8.2	40	PDB header: toxin/antitoxin Chain: B: PDB Molecule: cdia; PDBTitle: contact-dependent growth inhibition toxin-immunity protein complex2 from from e. coli 3006
19	c3wx4A	Alignment		8.1	33	PDB header: viral protein Chain: A: PDB Molecule: anti-restriction endonuclease; PDBTitle: crystal structure of t4 phage arm protein
20	c4bedD	Alignment		7.7	18	PDB header: oxygen transport Chain: D: PDB Molecule: hemocyanin klh1; PDBTitle: keyhole limpet hemocyanin (klh): 9a cryoem structure and molecular2 model of the klh1 didecamer reveal the interfaces and intricate3 topology of the 160 functional units
21	d1ozja	Alignment	not modelled	7.3	24	Fold: SMAD MH1 domain Superfamily: SMAD MH1 domain Family: SMAD MH1 domain
22	c4wlpB	Alignment	not modelled	7.2	33	PDB header: protein binding Chain: B: PDB Molecule: nuclear factor related to kappa-b-binding protein; PDBTitle: crystal structure of uch37-nfrkb inhibited deubiquitylating complex
23	c1bqfA	Alignment	not modelled	6.8	44	PDB header: hormone/growth factor Chain: A: PDB Molecule: protein (growth-blocking peptide); PDBTitle: growth-blocking peptide (gbp) from pseudaletia separata
24	c2nblA	Alignment	not modelled	6.7	71	PDB header: de novo protein Chain: A: PDB Molecule: designed beta-arch; PDBTitle: peptide model of 4-stranded beta-arch
25	c2ckcA	Alignment	not modelled	6.6	16	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
26	d2ckca1	Alignment	not modelled	6.6	16	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
27	c4regA	Alignment	not modelled	6.5	27	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure analysis of pf0642
28	c5tv6A	Alignment	not modelled	6.5	13	PDB header: ligase Chain: A: PDB Molecule: 6-carboxyhexanoate--coa ligase; PDBTitle: a. aeolicus biow with pimelate

29	c4rwrB_	Alignment	not modelled	6.5	11	PDB header: viral protein Chain: B: PDB Molecule: stage ii sporulation protein d; PDBTitle: 2.1 angstrom crystal structure of stage ii sporulation protein d from2 bacillus anthracis
30	d2v0ea1	Alignment	not modelled	6.2	16	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
31	d1zpya1	Alignment	not modelled	6.1	18	Fold: Ferritin-like Superfamily: Ferritin-like Family: half-ferritin
32	d1ejxa_	Alignment	not modelled	6.1	31	Fold: Urease, gamma-subunit Superfamily: Urease, gamma-subunit Family: Urease, gamma-subunit
33	c5d9gB_	Alignment	not modelled	6.0	15	PDB header: protein binding Chain: B: PDB Molecule: tip41-like protein; PDBTitle: crystal structure of tipl1, tor signaling pathway regulator-like, in2 complex with peptide
34	c4h5bB_	Alignment	not modelled	5.9	37	PDB header: unknown function Chain: B: PDB Molecule: dr_1245 protein; PDBTitle: crystal structure of dr_1245 from deinococcus radiodurans
35	d2ckaa1	Alignment	not modelled	5.8	5	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
36	c2ckaA_	Alignment	not modelled	5.8	5	PDB header: hydrolase Chain: A: PDB Molecule: chromodomain-helicase-dna-binding protein 8; 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
37	c3ps0C_	Alignment	not modelled	5.8	17	PDB header: rna binding protein Chain: C: PDB Molecule: crispr-associated protein, csa2; PDBTitle: the structure of the crispr-associated protein, csa2, from sulfolobus2 solfataricus
38	c2ismA_	Alignment	not modelled	5.6	21	PDB header: sugar binding protein Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of the putative oxidoreductase (glucose2 dehydrogenase) (ttha0570) from thermus thermophilus hb8
39	d1z8ua1	Alignment	not modelled	5.6	24	Fold: Spectrin repeat-like Superfamily: Alpha-hemoglobin stabilizing protein AHSP Family: Alpha-hemoglobin stabilizing protein AHSP
40	c4l6uB_	Alignment	not modelled	5.5	43	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of af1868: cmr1 subunit of the cmr rna silencing2 complex
41	c4wd9B_	Alignment	not modelled	5.4	33	PDB header: biosynthetic protein Chain: B: PDB Molecule: nisin biosynthesis protein nisb; PDBTitle: crystal structure of trna-dependent lantibiotic dehydratase nisb in2 complex with nisa leader peptide
42	c6fbmA_	Alignment	not modelled	5.4	17	PDB header: toxin Chain: A: PDB Molecule: gram-negative insecticidal protein; PDBTitle: crystal structure of gnip1aa from chromobacterium piscinae
43	c5abxB_	Alignment	not modelled	5.3	25	PDB header: translation Chain: B: PDB Molecule: 4e-binding protein mexlti; PDBTitle: complex of c. elegans eif4e-3 with the 4e-binding protein2 mexlti and cap analog
44	c4furD_	Alignment	not modelled	5.3	42	PDB header: hydrolase Chain: D: PDB Molecule: urease subunit gamma 2; PDBTitle: crystal structure of urease subunit gamma 2 from brucella melitensis2 biovar abortus 2308
45	c2jsnA_	Alignment	not modelled	5.3	26	PDB header: protein transport Chain: A: PDB Molecule: trafficking protein particle complex subunit 4; PDBTitle: solution structure of the atypical pdz-like domain of2 synbindin