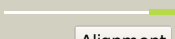
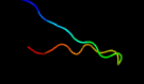

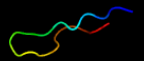
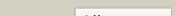







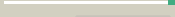




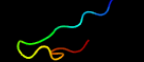




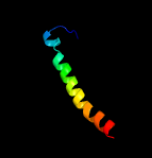

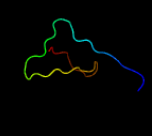
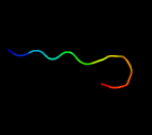

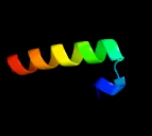
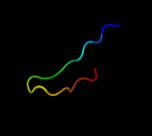
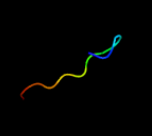
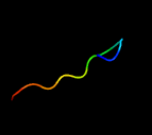


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1733c_(-)_1959862_1960494
Date	Fri Aug 2 13:30:33 BST 2019
Unique Job ID	512a88edd50837f5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1hymB_	 Alignment		61.6	44	PDB header: hydrolase (serine proteinase) Chain: B: PDB Molecule: hydrolyzed cucurbita maxima trypsin inhibitor v; PDBTitle: hydrolyzed trypsin inhibitor (cmti-v, minimized average nmr structure)
2	d1dwma_	 Alignment		47.6	33	Fold: CI-2 family of serine protease inhibitors Superfamily: CI-2 family of serine protease inhibitors Family: CI-2 family of serine protease inhibitors
3	c3rdyA_	 Alignment		45.5	50	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: bwi-1=protease inhibitor/trypsin inhibitor; PDBTitle: crystal structure of buckwheat trypsin inhibitor rbt1 at 1.84 angstrom2 resolution
4	c1vbwA_	 Alignment		45.0	41	PDB header: protein binding Chain: A: PDB Molecule: trypsin inhibitor bgit; PDBTitle: crystal structure of bitter gourd trypsin inhibitor
5	d2snii_	 Alignment		43.8	35	Fold: CI-2 family of serine protease inhibitors Superfamily: CI-2 family of serine protease inhibitors Family: CI-2 family of serine protease inhibitors
6	c2ci2l_	 Alignment		43.0	35	PDB header: proteinase inhibitor (chymotrypsin) Chain: I: PDB Molecule: chymotrypsin inhibitor 2; PDBTitle: crystal and molecular structure of the serine proteinase inhibitor ci- 2 from barley seeds
7	c2kncB_	 Alignment		41.3	22	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
8	d1to2i_	 Alignment		41.3	35	Fold: CI-2 family of serine protease inhibitors Superfamily: CI-2 family of serine protease inhibitors Family: CI-2 family of serine protease inhibitors
9	d1ypci_	 Alignment		40.7	35	Fold: CI-2 family of serine protease inhibitors Superfamily: CI-2 family of serine protease inhibitors Family: CI-2 family of serine protease inhibitors
10	c1tinA_	 Alignment		38.8	44	PDB header: serine protease inhibitor Chain: A: PDB Molecule: trypsin inhibitor v; PDBTitle: three-dimensional structure in solution of cucurbita maxima trypsin2 inhibitor-v determined by nmr spectroscopy
11	c1hjiB_	 Alignment		24.9	44	PDB header: bacteriophage hk022 Chain: B: PDB Molecule: nun-protein; PDBTitle: bacteriophage hk022 nun-protein-nutboxb-rna complex

12	c4tqvj_	Alignment		22.9	20	PDB header: transport protein Chain: J: PDB Molecule: algm2; PDBTitle: crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate
13	d1csei_	Alignment		20.9	18	Fold: Cl-2 family of serine protease inhibitors Superfamily: Cl-2 family of serine protease inhibitors Family: Cl-2 family of serine protease inhibitors
14	c3jt0B_	Alignment		19.8	26	PDB header: structural protein Chain: B: PDB Molecule: lamin-b1; PDBTitle: crystal structure of the c-terminal fragment (426-558) lamin-b1 from2 homo sapiens, northeast structural genomics consortium target hr5546a
15	d2byoa1	Alignment		17.0	17	Fold: LoLA-like prokaryotic lipoproteins and lipoprotein localization factors Superfamily: Prokaryotic lipoproteins and lipoprotein localization factors Family: LppX-like
16	c4qa8A_	Alignment		16.8	17	PDB header: lipid transport Chain: A: PDB Molecule: putative lipoprotein lprf; PDBTitle: crystal structure of lprf from mycobacterium bovis
17	d1em9a_	Alignment		14.5	28	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
18	d1egla_	Alignment		13.9	18	Fold: Cl-2 family of serine protease inhibitors Superfamily: Cl-2 family of serine protease inhibitors Family: Cl-2 family of serine protease inhibitors
19	c1uv7A_	Alignment		13.4	17	PDB header: transport Chain: A: PDB Molecule: general secretion pathway protein m; PDBTitle: periplasmic domain of epsm from vibrio cholerae
20	d1uv7a_	Alignment		13.4	17	Fold: RRF/tRNA synthetase additional domain-like Superfamily: General secretion pathway protein M, EpsM Family: General secretion pathway protein M, EpsM
21	d1p7na_	Alignment	not modelled	13.1	28	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
22	c2lIIA_	Alignment	not modelled	12.9	26	PDB header: structural protein Chain: A: PDB Molecule: lamin-b2; PDBTitle: solution nmr structure of c-terminal globular domain of human lamin-2 b2, northeast structural genomics consortium target hr8546a
23	d1oe1a2	Alignment	not modelled	12.7	21	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
24	c2e63A_	Alignment	not modelled	12.0	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: kiaa1787 protein; PDBTitle: solution structure of the neuz domain in kiaa1787 protein
25	c2hbpA_	Alignment	not modelled	11.9	33	PDB header: endocytosis, protein binding Chain: A: PDB Molecule: cytoskeleton assembly control protein sla1; PDBTitle: solution structure of sla1 homology domain 1
26	c3mhaB_	Alignment	not modelled	11.2	21	PDB header: lipid binding protein Chain: B: PDB Molecule: lipoprotein lprg; PDBTitle: crystal structure of lprg from mycobacterium tuberculosis bound to pim
27	c2bu8A_	Alignment	not modelled	10.7	15	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase kinase isoenzyme 2; PDBTitle: crystal structures of human pyruvate dehydrogenase kinase 2 containing2 physiological and synthetic ligands
28	c2yueA_	Alignment	not modelled	10.4	19	PDB header: rna binding protein Chain: A: PDB Molecule: protein neuralized; PDBTitle: solution structure of the neuz (nhr) domain in neuralized2

						from drosophila melanogaster
29	d1qvpa_	Alignment	not modelled	10.1	30	Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: FeoA-like
30	c6d0gA_	Alignment	not modelled	8.4	11	PDB header: oxidoreductase Chain: A: PDB Molecule: pirin family protein; PDBTitle: 1.78 angstrom resolution crystal structure of quercetin 2,3-2 dioxygenase from acinetobacter baumannii
31	c5lrvA_	Alignment	not modelled	8.2	27	PDB header: hydrolase Chain: A: PDB Molecule: otu domain-containing protein 7b; PDBTitle: structure of cezanne/otud7b otu domain bound to lys11-linked2 diubiquitin
32	d1ivta_	Alignment	not modelled	8.0	26	Fold: Immunoglobulin-like beta-sandwich Superfamily: Lamin A/C globular tail domain Family: Lamin A/C globular tail domain
33	c4kf9A_	Alignment	not modelled	7.9	21	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase protein; PDBTitle: crystal structure of a glutathione transferase family member from2 ralstonia solanacearum, target efi-501780, with bound gsh coordinated3 to a zinc ion, ordered active site
34	c1wq6A_	Alignment	not modelled	7.8	20	PDB header: oncoprotein Chain: A: PDB Molecule: aml1-eto; PDBTitle: the tetramer structure of the nervy homolgy two (nhr2) domain of aml1-2 eto is critical for aml1-eto's activity
35	c2jmbA_	Alignment	not modelled	7.4	55	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein atu4866; PDBTitle: solution structure of the protein atu4866 from agrobacterium2 tumefaciens
36	c3ic8D_	Alignment	not modelled	7.0	38	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized gst-like proteinprotein; PDBTitle: the crystal structure of a gst-like protein from pseudomonas syringae2 to 2.4a
37	c4ardA_	Alignment	not modelled	7.0	20	PDB header: viral protein Chain: A: PDB Molecule: capsid protein p27; PDBTitle: structure of the immature retroviral capsid at 8a resolution by cryo-2 electron microscopy
38	c5nv8A_	Alignment	not modelled	7.0	50	PDB header: transferase Chain: A: PDB Molecule: ef-p arginine 32 rhamnosyl-transferase; PDBTitle: structural basis for earp-mediated arginine glycosylation of2 translation elongation factor ef-p
39	d1qvvia2	Alignment	not modelled	6.9	21	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
40	c3vgxD_	Alignment	not modelled	6.9	25	PDB header: membrane protein Chain: D: PDB Molecule: envelope glycoprotein gp160; PDBTitle: structure of gp41 t21/cp621-652
41	c2vfjA_	Alignment	not modelled	6.9	30	PDB header: hydrolase Chain: A: PDB Molecule: tumor necrosis factor; PDBTitle: structure of the a20 ovarian tumour (otu) domain
42	c6cp8B_	Alignment	not modelled	6.8	25	PDB header: toxin/antitoxin Chain: B: PDB Molecule: cdia; PDBTitle: contact-dependent growth inhibition toxin-immunity protein complex2 from from e. coli 3006
43	c2kgfA_	Alignment	not modelled	6.7	20	PDB header: viral protein Chain: A: PDB Molecule: capsid protein p27; PDBTitle: n-terminal domain of capsid protein from the mason-pfizer2 monkey virus
44	c2v4xA_	Alignment	not modelled	6.5	16	PDB header: viral protein Chain: A: PDB Molecule: capsid protein p27; PDBTitle: crystal structure of jaagsiekte sheep retrovirus capsid n-2 terminal domain
45	d1ufga_	Alignment	not modelled	6.1	26	Fold: Immunoglobulin-like beta-sandwich Superfamily: Lamin A/C globular tail domain Family: Lamin A/C globular tail domain
46	c3dkbA_	Alignment	not modelled	6.0	30	PDB header: hydrolase Chain: A: PDB Molecule: tumor necrosis factor, alpha-induced protein 3; PDBTitle: crystal structure of a20, 2.5 angstrom
47	c5xywD_	Alignment	not modelled	5.5	13	PDB header: protein binding Chain: D: PDB Molecule: gd21652; PDBTitle: crystal structure of drosophila simulans rhino chromoshadow domain in2 complex with n-terminal domain
48	c1ep3B_	Alignment	not modelled	5.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydroorotate dehydrogenase b (pyrk subunit); PDBTitle: crystal structure of lactococcus lactis dihydroorotate dehydrogenase2 b. data collected under cryogenic conditions.
49	c3zv0D_	Alignment	not modelled	5.3	15	PDB header: cell cycle Chain: D: PDB Molecule: h/aca ribonucleoprotein complex subunit 4; PDBTitle: structure of the shq1p-cbf5p complex
50	d1lfra_	Alignment	not modelled	5.3	26	Fold: Immunoglobulin-like beta-sandwich Superfamily: Lamin A/C globular tail domain Family: Lamin A/C globular tail domain