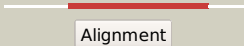

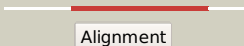

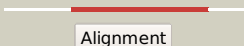


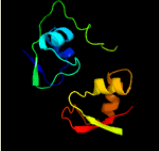




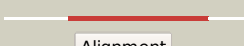
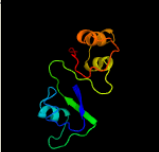

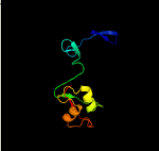





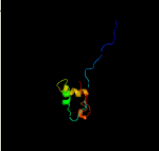




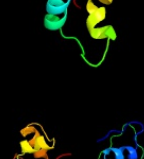


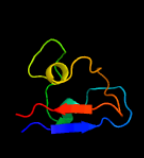
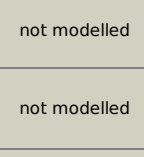


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2719c (-)_3031050_3031547
Date	Wed Aug 7 12:50:37 BST 2019
Unique Job ID	0ee5a811d53f1f9c

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5jceA_	 Alignment		99.9	19	PDB header: sugar binding protein Chain: A: PDB Molecule: chitin elicitor-binding protein; PDBTitle: crystal structure of oscebp complex
2	c5ls2B_	 Alignment		99.8	11	PDB header: plant protein Chain: B: PDB Molecule: lysm type receptor kinase; PDBTitle: receptor mediated chitin perception in legumes is functionally2 seperable from nod factor perception
3	c4uz2D_	 Alignment		99.7	24	PDB header: hydrolase Chain: D: PDB Molecule: cell wall-binding endopeptidase-related protein; PDBTitle: crystal structure of the n-terminal lysm domains from the putative2 nlpc/p60 d,l endopeptidase from t. thermophilus
4	c4b9hA_	 Alignment		99.7	22	PDB header: sugar binding protein Chain: A: PDB Molecule: extracellular protein 6; PDBTitle: cladosporium fulvum lysm effector ecp6 in complex with a2 beta-1,4-linked n-acetyl-d-glucosamine tetramer: i3c heavy3 atom derivative
5	c4ebzA_	 Alignment		99.7	11	PDB header: transferase Chain: A: PDB Molecule: chitin elicitor receptor kinase 1; PDBTitle: crystal structure of the ectodomain of a receptor like kinase
6	c4s3kA_	 Alignment		99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: spore germination protein yaah; PDBTitle: crystal structure of the bacillus megaterium qm b1551 spore cortex-2 lytic enzyme sle1
7	c4s3jC_	 Alignment		99.7	21	PDB header: hydrolase Chain: C: PDB Molecule: cortical-lytic enzyme; PDBTitle: crystal structure of the bacillus cereus spore cortex-lytic enzyme2 sle1
8	c2l9yA_	 Alignment		99.6	21	PDB header: sugar binding protein Chain: A: PDB Molecule: cvnh-lysm lectin; PDBTitle: solution structure of the mocvnh-lysm module from the rice blast2 fungus magnaporthe oryzae protein (mgg_03307)
9	c5fimA_	 Alignment		99.6	26	PDB header: unknown function Chain: A: PDB Molecule: ygau; PDBTitle: the structure of kbp.k from e. coli
10	c2mkxA_	 Alignment		99.5	27	PDB header: hydrolase Chain: A: PDB Molecule: autolysin; PDBTitle: solution structure of lysm the peptidoglycan binding domain of2 autolysin atla from enterococcus faecalis
11	c2djpA_	 Alignment		99.5	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein sb145; PDBTitle: the solution structure of the lysm domain of human2 hypothetical protein sb145

12	c5k2lA_	Alignment		99.5	33	PDB header: hydrolase Chain: A: PDB Molecule: chitinase, lysozyme; PDBTitle: crystal structure of lysm domain from volvox carteri chitinase
13	d1e0ga_	Alignment		99.4	30	Fold: LysM domain Superfamily: LysM domain Family: LysM domain
14	d1y7ma2	Alignment		99.4	23	Fold: LysM domain Superfamily: LysM domain Family: LysM domain
15	c4pxvC_	Alignment		99.2	13	PDB header: sugar binding protein Chain: C: PDB Molecule: chitinase a; PDBTitle: crystal structure of lysm domain from pteris ryukuensis chitinase a
16	c5bumA_	Alignment		99.2	20	PDB header: sugar binding protein Chain: A: PDB Molecule: chitinase a; PDBTitle: crystal structure of lysm domain from equisetum arvense chitinase a
17	c4xcmB_	Alignment		99.1	26	PDB header: hydrolase Chain: B: PDB Molecule: cell wall-binding endopeptidase-related protein; PDBTitle: crystal structure of the putative nlpc/p60 d,l endopeptidase from t.2 thermophilus
18	c6raoG_	Alignment		98.7	26	PDB header: virus like particle Chain: G: PDB Molecule: afp7; PDBTitle: cryo-em structure of the anti-feeding prophage (afp) baseplate, 6-fold2 symmetrised
19	c3sluB_	Alignment		98.4	25	PDB header: hydrolase Chain: B: PDB Molecule: m23 peptidase domain protein; PDBTitle: crystal structure of nmb0315
20	c4lzhA_	Alignment		97.3	16	PDB header: transferase Chain: A: PDB Molecule: l,d-transpeptidase; PDBTitle: l,d-transpeptidase from klebsiella pneumoniae
21	c2ltfA_	Alignment	not modelled	94.3	26	PDB header: viral protein Chain: A: PDB Molecule: tail protein x; PDBTitle: the solution structure of phage p2 gpX
22	c2gu1A_	Alignment	not modelled	88.3	14	PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae
23	c1y7mB_	Alignment	not modelled	82.8	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein bsu14040; PDBTitle: crystal structure of the b. subtilis ykud protein at 2 a2 resolution
24	c2mpwA_	Alignment	not modelled	78.6	31	PDB header: peptidoglycan binding protein Chain: A: PDB Molecule: intimin; PDBTitle: solution structure of the lysm region of the e. coli intimin2 periplasmic domain
25	d1y0pa3	Alignment	not modelled	32.2	14	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
26	c2elhA_	Alignment	not modelled	30.5	23	PDB header: dna binding protein Chain: A: PDB Molecule: cg11849-pa; PDBTitle: solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
27	c2k5eA_	Alignment	not modelled	22.3	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nsg) target gsr195
						PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase, flavoprotein subunit;

28	c2lfcA_	Alignment	not modelled	22.1	14	PDBTitle: solution nmr structure of fumarate reductase flavoprotein subunit from 2 lactobacillus plantarum, northeast structural genomics consortium3 target lpr145j
29	c2k53A_	Alignment	not modelled	22.0	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: a3dk08 protein; PDBTitle: nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9
30	d1d4ca3	Alignment	not modelled	20.9	21	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
31	d2gqba1	Alignment	not modelled	20.5	11	Fold: RPA2825-like Superfamily: RPA2825-like Family: RPA2825-like
32	d1lyjb3	Alignment	not modelled	11.6	36	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
33	c4itkA_	Alignment	not modelled	10.6	24	PDB header: electron transport Chain: A: PDB Molecule: apoferreredoxin; PDBTitle: the structure of c.reinhardtii ferreredoxin 2
34	c1rr7A_	Alignment	not modelled	10.6	19	PDB header: transcription Chain: A: PDB Molecule: middle operon regulator; PDBTitle: crystal structure of the middle operon regulator protein of 2 bacteriophage mu
35	d1rr7a_	Alignment	not modelled	10.6	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Middle operon regulator, Mor
36	d2fug33	Alignment	not modelled	10.5	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
37	c6bxwA_	Alignment	not modelled	10.2	16	PDB header: membrane protein Chain: A: PDB Molecule: mitochondrial association factor 1; PDBTitle: crystal structure of toxoplasma gondii mitochondrial association2 factor 1 b (maf1b) in complex with adprribose
38	c5u57B_	Alignment	not modelled	10.2	33	PDB header: oxidoreductase Chain: B: PDB Molecule: (s)-2-hydroxypropylphosphonic acid epoxidase; PDBTitle: psf4 in complex with fe2+ and (s)-2-hpp
39	d2cx1a1	Alignment	not modelled	10.0	33	Fold: PUA domain-like Superfamily: PUA domain-like Family: PUA domain
40	c5vobE_	Alignment	not modelled	9.8	15	PDB header: viral protein/immune system Chain: E: PDB Molecule: envelope glycoprotein ul131a; PDBTitle: crystal structure of hcmv pentamer in complex with neutralizing2 antibody 8i21
41	c2r0qF_	Alignment	not modelled	9.5	37	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
42	d2piaa3	Alignment	not modelled	9.0	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
43	d1wi9a_	Alignment	not modelled	8.8	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PCI domain (PINT motif)
44	c3k3nA_	Alignment	not modelled	8.7	50	PDB header: oxidoreductase Chain: A: PDB Molecule: phd finger protein 8; PDBTitle: crystal structure of the catalytic core domain of human phf8
45	d1bw6a_	Alignment	not modelled	8.3	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
46	c4xalA_	Alignment	not modelled	8.1	31	PDB header: viral protein Chain: A: PDB Molecule: tegument protein vp22; PDBTitle: crystal structure of the conserved core domain of vp22 from hsv-1
47	d1miau3	Alignment	not modelled	7.9	29	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
48	c3pu3A_	Alignment	not modelled	6.7	50	PDB header: protein binding Chain: A: PDB Molecule: phd finger protein 2; PDBTitle: phf2 jumonji domain-nog complex
49	c2y5cB_	Alignment	not modelled	6.6	19	PDB header: electron transport Chain: B: PDB Molecule: adrenodoxin-like protein, mitochondrial; PDBTitle: structure of human ferredoxin 2 (fdx2)in complex with 2fe2s2 cluster
50	c3kvaA_	Alignment	not modelled	6.6	42	PDB header: h3k4me3 binding protein, transferase Chain: A: PDB Molecule: jmjc domain-containing histone demethylation protein 1d; PDBTitle: structure of kiaa1718 jumonji domain in complex with alpha-2 ketoglutarate
51	d2bt6a1	Alignment	not modelled	6.6	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
52	c4iivB_	Alignment	not modelled	6.4	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lmo1499 protein; PDBTitle: 2.6 angstrom crystal structure of putative yceg-like protein lmo14992 from listeria monocytogenes
53	d3c8ya2	Alignment	not modelled	6.4	5	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like

				Family:2Fe-2S ferredoxin domains from multidomain proteins	
54	c2mjdA_	Alignment	not modelled	6.2	22 PDB header: metal binding protein Chain: A: PDB Molecule: adrenodoxin homolog, mitochondrial; PDBTitle: oxidized yeast adrenodoxin homolog 1
55	d1qo8a3	Alignment	not modelled	6.2	14 Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
56	d1qora1	Alignment	not modelled	6.1	14 Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
57	d1i7ha_	Alignment	not modelled	6.0	33 Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
58	c2lvsA_	Alignment	not modelled	6.0	20 PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr solution structure of a crispr repeat binding protein
59	c2auwB_	Alignment	not modelled	5.6	17 PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ne0471; PDBTitle: crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
60	c3p1mG_	Alignment	not modelled	5.4	23 PDB header: electron transport Chain: G: PDB Molecule: adrenodoxin, mitochondrial; PDBTitle: crystal structure of human ferredoxin-1 (fdx1) in complex with iron-2 sulfur cluster
61	c3fmcC_	Alignment	not modelled	5.2	23 PDB header: hydrolase Chain: C: PDB Molecule: putative succinylglutamate desuccinylase / aspartoacylase; PDBTitle: crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
62	c3d79A_	Alignment	not modelled	5.1	13 PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein ph0734; PDBTitle: crystal structure of hypothetical protein ph0734.1 from2 hyperthermophilic archaea pyrococcus horikoshii ot3