
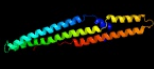
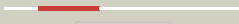
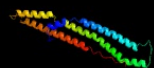

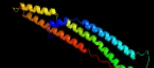



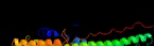









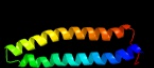


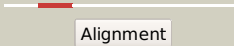
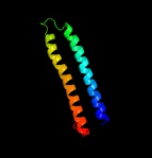
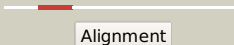

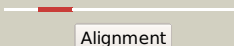
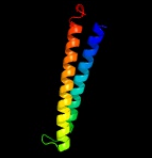
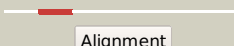
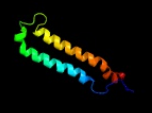
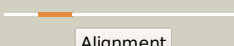
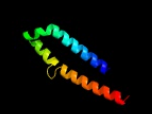
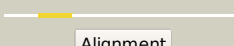

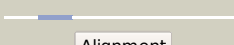


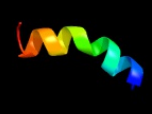

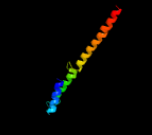
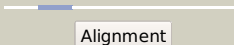
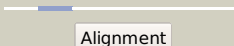
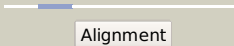
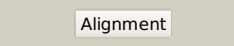
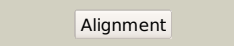

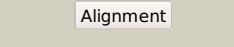
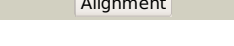


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3159c_(PPE53)_3527388_3529160
 Date Thu Aug 8 16:20:34 BST 2019
 Unique Job ID 15f609231b669385

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	52	PDB header: protein transport Chain: B: PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	d2g38b1	 Alignment		100.0	28	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
3	c2g38B_	 Alignment		100.0	28	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
4	c4xy3A_	 Alignment		100.0	19	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
5	c4wj2A_	 Alignment		99.0	15	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		98.2	14	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c3gvmA_	 Alignment		98.0	10	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
8	c4iogD_	 Alignment		98.0	18	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
9	c3zbhC_	 Alignment		97.9	13	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		97.5	20	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsA_	 Alignment		96.9	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsB_	 Alignment		96.7	10	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	 Alignment		96.5	13	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	c4i0xA_	 Alignment		96.1	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterum abscessus esxef (mab_3112-2 mab_3113) complex
15	c2kg7B_	 Alignment		94.3	18	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein esxh; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	c4i0xJ_	 Alignment		85.0	27	PDB header: structural genomics, unknown function Chain: J: PDB Molecule: esat-6-like protein mab_3113; PDBTitle: crystal structure of the mycobacterum abscessus esxef (mab_3112-2 mab_3113) complex
17	d1ui5a2	 Alignment		79.3	26	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
18	d1xkna_	 Alignment		27.1	17	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
19	c2iu1A_	 Alignment		26.6	33	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
20	c2ahmG_	 Alignment		25.7	18	PDB header: viral protein, replication Chain: G: PDB Molecule: replicase polyprotein 1ab, heavy chain; PDBTitle: crystal structure of sars-cov super complex of non-structural2 proteins: the hexadecamer
21	c3h6pB_	 Alignment	not modelled	24.0	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: esat-6 like protein esxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
22	c2kg7A_	 Alignment	not modelled	22.5	37	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein esxg (pe family protein); PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
23	c5frgA_	 Alignment	not modelled	21.8	63	PDB header: protein binding Chain: A: PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1
24	c2fulE_	 Alignment	not modelled	20.9	33	PDB header: translation Chain: E: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of the c-terminal domain of s. cerevisiae eif5
25	c2l5aA_	 Alignment	not modelled	18.0	22	PDB header: nuclear protein Chain: A: PDB Molecule: histone h3-like centromeric protein cse4, protein scm3, PDBTitle: structural basis for recognition of centromere specific histone h32 variant by nonhistone scm3
26	c3ub0D_	 Alignment	not modelled	15.0	13	PDB header: replication Chain: D: PDB Molecule: non-structural protein 6, nsp6,; PDBTitle: crystal structure of the nonstructural protein 7 and 8 complex of 2 feline coronavirus
27	c1bkvA_	 Alignment	not modelled	15.0	38	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
28	c2kp7A_	 Alignment	not modelled	14.8	20	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endonuclease mus81; PDBTitle: solution nmr structure of the mus81 n-terminal hhh.2

						northeast structural genomics consortium target mmt1a PDB header: oxidoreductase Chain: A: PDB Molecule: f420-reducing hydrogenase, subunit alpha; PDBTitle: cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate
29	c3zfsA_	Alignment	not modelled	14.6	16	
30	c3jywF_	Alignment	not modelled	14.5	61	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
31	c2ke4A_	Alignment	not modelled	14.5	63	PDB header: membrane protein Chain: A: PDB Molecule: cdc42-interacting protein 4; PDBTitle: the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
32	c4n91A_	Alignment	not modelled	14.4	17	PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 anaerococcus prevotii dsm 20548 (apre_1383), target efi-510023, with3 bound alpha/beta d-glucuronate
33	d1paqa_	Alignment	not modelled	14.0	15	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
34	c1paqA_	Alignment	not modelled	14.0	15	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b epsilon PDBTitle: crystal structure of the catalytic fragment of eukaryotic2 initiation factor 2b epsilon
35	c1bkvB_	Alignment	not modelled	13.9	38	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
36	c1bkvC_	Alignment	not modelled	13.9	38	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
37	c2l5bA_	Alignment	not modelled	13.1	53	PDB header: apoptosis Chain: A: PDB Molecule: activator of apoptosis harakiri; PDBTitle: solution structure of the transmembrane domain of bcl-2 member2 harakiri in micelles
38	c3juia_	Alignment	not modelled	11.5	23	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit
39	d2fgga1	Alignment	not modelled	10.5	40	Fold: dsRBD-like Superfamily: Rv2632c-like Family: Rv2632c-like
40	d2ewoa1	Alignment	not modelled	10.1	22	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
41	c3trhl_	Alignment	not modelled	9.7	10	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
42	c4wpyA_	Alignment	not modelled	8.8	15	PDB header: de novo protein Chain: A: PDB Molecule: protein dl-rv1738; PDBTitle: racemic crystal structure of rv1738 from mycobacterium tuberculosis2 (form-ii)
43	c2jwbB_	Alignment	not modelled	8.4	15	PDB header: hydrolase Chain: B: PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine hydrolase.
44	d2jba1	Alignment	not modelled	8.2	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydroxypseudooxynicotine hydrolase-like
45	c3lyrA_	Alignment	not modelled	8.1	5	PDB header: transcription activator Chain: A: PDB Molecule: transcription factor coe1; PDBTitle: human early b-cell factor 1 (ebf1) dna-binding domain
46	c2np3A_	Alignment	not modelled	7.9	9	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family regulator; PDBTitle: crystal structure of tetr-family regulator (sco0857) from streptomyces2 coelicolor a3.
47	c4mnpA_	Alignment	not modelled	7.7	16	PDB header: sugar binding protein Chain: A: PDB Molecule: n-acetylneuraminase-binding protein; PDBTitle: structure of the sialic acid binding protein from fusobacterium2 nucleatum subsp. nucleatum atcc 25586
48	c3mveB_	Alignment	not modelled	7.3	20	PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vv1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
49	c5hl8B_	Alignment	not modelled	7.2	24	PDB header: protein transport Chain: B: PDB Molecule: type ii secretion system protein I; PDBTitle: 1.93 angstrom resolution crystal structure of a pullulanase-specific2 type ii secretion system integral cytoplasmic membrane protein gspI3 (c-terminal fragment; residues 309-397) from klebsiella pneumoniae4 subsp. pneumoniae ntuH-k2044
50	c3b50A_	Alignment	not modelled	7.2	15	PDB header: transport protein Chain: A: PDB Molecule: sialic acid-binding periplasmic protein siap; PDBTitle: structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
51	d1fcda3	Alignment	not modelled	7.2	23	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
52	c2hzkB_	Alignment	not modelled	7.2	15	PDB header: ligand binding, transport protein Chain: B: PDB Molecule: trap-t family sorbitol/mannitol transporter, periplasmic PDBTitle: crystal structures of a sodium-alpha-keto acid binding

						subunit from a2 trap transporter in its open form
53	c4grdA	Alignment	not modelled	7.0	19	PDB header: lyase, isomerase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
54	c6hu9u	Alignment	not modelled	6.9	18	PDB header: oxidoreductase/electron transport Chain: U: PDB Molecule: cytochrome b-c1 complex subunit 10; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
55	c5lzkB	Alignment	not modelled	6.9	4	PDB header: structural genomics Chain: B: PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
56	c5ec0A	Alignment	not modelled	6.8	33	PDB header: structural protein Chain: A: PDB Molecule: alp7a; PDBTitle: crystal structure of actin-like protein alp7a
57	c3qthA	Alignment	not modelled	6.8	8	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a dinb-like protein (cps_3021) from colwellia2 psychrerythraea 34h at 2.20 a resolution
58	c4k0dB	Alignment	not modelled	6.7	26	PDB header: signaling protein Chain: B: PDB Molecule: periplasmic sensor hybrid histidine kinase; PDBTitle: periplasmic sensor domain of sensor histidine kinase, adeh_2942
59	c5vmoB	Alignment	not modelled	6.4	50	PDB header: viral protein/apoptosis Chain: B: PDB Molecule: bcl-2 interacting mediator of cell death; PDBTitle: crystal structure of grouper iridovirus giv66:bim complex
60	c3j21Y	Alignment	not modelled	6.4	25	PDB header: ribosome Chain: Y: PDB Molecule: 50s ribosomal protein l30p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
61	d1luaa2	Alignment	not modelled	6.4	29	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Methylene-tetrahydromethanopterin dehydrogenase
62	c2dbfA	Alignment	not modelled	6.4	20	PDB header: signaling protein Chain: A: PDB Molecule: nuclear factor nf-kappa-b p105 subunit; PDBTitle: solution structure of the death domain in human nuclear2 factor nf-kappa-b p105 subunit
63	c2nvjA	Alignment	not modelled	6.3	40	PDB header: hydrolase Chain: A: PDB Molecule: 25mer peptide from vacuolar atp synthase subunit PDBTitle: nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
64	c3r5zB	Alignment	not modelled	6.3	10	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420
65	c3j3bF	Alignment	not modelled	6.3	31	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7; PDBTitle: structure of the human 60s ribosomal proteins
66	c3rggD	Alignment	not modelled	6.2	13	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase, pure protein; PDBTitle: crystal structure of treponema denticola pure bound to air
67	d1kx5a	Alignment	not modelled	6.2	20	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
68	c2kwuA	Alignment	not modelled	6.1	31	PDB header: protein binding/signaling protein Chain: A: PDB Molecule: dna polymerase iota; PDBTitle: solution structure of ubm2 of murine polymerase iota in complex with2 ubiquitin
69	c4i6jB	Alignment	not modelled	6.0	22	PDB header: transcription Chain: B: PDB Molecule: tf-box/lrr-repeat protein 3; PDBTitle: a ubiquitin ligase-substrate complex
70	c1nauA	Alignment	not modelled	5.9	23	PDB header: hormone/growth factor Chain: A: PDB Molecule: glucagon; PDBTitle: nmr solution structure of the glucagon antagonist [deshis1,2 desphe6, glu9]glucagon amide in the presence of3 perdeuterated dodecylphosphocholine micelles
71	c1d1dA	Alignment	not modelled	5.9	14	PDB header: viral protein Chain: A: PDB Molecule: protein (capsid protein); PDBTitle: nmr solution structure of the capsid protein from rous2 sarcoma virus
72	c6ansD	Alignment	not modelled	5.7	14	PDB header: unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 burkholderia cenocepacia
73	c3j39F	Alignment	not modelled	5.7	38	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
74	c2hueB	Alignment	not modelled	5.7	20	PDB header: dna binding protein Chain: B: PDB Molecule: histone h3; PDBTitle: structure of the h3-h4 chaperone asf1 bound to histones h3 and h4
75	c4c5eG	Alignment	not modelled	5.7	33	PDB header: transcription Chain: G: PDB Molecule: polycomb protein pho; PDBTitle: crystal structure of the minimal pho-sfmbt complex (p21 spacegroup)
76	c4c5eH	Alignment	not modelled	5.7	33	PDB header: transcription Chain: H: PDB Molecule: polycomb protein pho; PDBTitle: crystal structure of the minimal pho-sfmbt complex (p21 spacegroup)
77	c5ietA	Alignment	not modelled	5.6	32	PDB header: gene regulation Chain: A: PDB Molecule: bacterial proteasome activator; PDBTitle: crystal structure of mycobacterium tuberculosis atp-

						independent2 proteasome activator PDB header: unknown function Chain: D: PDB Molecule: putative orphan protein; PDBTitle: crystal structure of a putative ketosteroid isomerase (sfri_1973) from2 shewanella frigidimarina ncimb 400 at 1.80 a resolution
78	c3bb9D_	Alignment	not modelled	5.6	9	
79	d1eqzg_	Alignment	not modelled	5.5	20	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
80	c1jrjA_	Alignment	not modelled	5.5	27	PDB header: hormone/growth factor Chain: A: PDB Molecule: exendin-4; PDBTitle: solution structure of exendin-4 in 30-vol% trifluoroethanol
81	c2jtwA_	Alignment	not modelled	5.5	50	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane helix 7 of yeast vatpase; PDBTitle: solution structure of tm7 bound to dpc micelles
82	c4oanB_	Alignment	not modelled	5.4	19	PDB header: membrane protein/protein transport Chain: B: PDB Molecule: trap dicarboxylate transporter dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 rhodospseudomonas palustris haa2 (rpb_2686), target efi-510221, with3 density modeled as (s)-2-hydroxy-2-methyl-3-oxobutanoate ((s)-2-4 acetolactate)
83	c4deyB_	Alignment	not modelled	5.3	18	PDB header: transport protein Chain: B: PDB Molecule: voltage-dependent l-type calcium channel subunit alpha-1c; PDBTitle: crystal structure of the voltage dependent calcium channel beta-22 subunit in complex with the cav1.2 i-ii linker.
84	c1d0rA_	Alignment	not modelled	5.3	40	PDB header: hormone/growth factor Chain: A: PDB Molecule: glucagon-like peptide-1-(7-36)-amide; PDBTitle: solution structure of glucagon-like peptide-1-(7-36)-amide in2 trifluoroethanol/water
85	c2yfwC_	Alignment	not modelled	5.3	20	PDB header: cell cycle Chain: C: PDB Molecule: histone h3-like centromeric protein cse4; PDBTitle: heterotetramer structure of kluyveromyces lactis cse4,h4
86	d1zbra1	Alignment	not modelled	5.2	14	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
87	c4xb6D_	Alignment	not modelled	5.2	15	PDB header: transferase Chain: D: PDB Molecule: alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; PDBTitle: structure of the e. coli c-p lyase core complex
88	c4k8nF_	Alignment	not modelled	5.1	17	PDB header: lipid transport Chain: F: PDB Molecule: glycolipid transfer protein domain-containing protein 1; PDBTitle: crystal structure of human ceramide-1-phosphate transfer protein2 (cptp) in complex with 18:1 ceramide-1-phosphate (18:1-c1p)
89	c3hx8A_	Alignment	not modelled	5.1	27	PDB header: isomerase Chain: A: PDB Molecule: putative ketosteroid isomerase; PDBTitle: crystal structure of putative ketosteroid isomerase (np_103587.1) from2 mesorhizobium loti at 1.45 a resolution
90	c4ja0A_	Alignment	not modelled	5.1	10	PDB header: protein binding Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase; PDBTitle: crystal structure of the invertebrate bi-functional purine2 biosynthesis enzyme paics at 2.8 a resolution