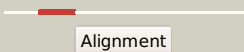
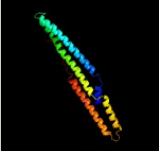
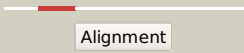

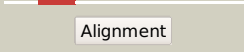


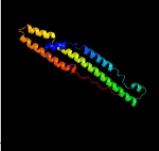

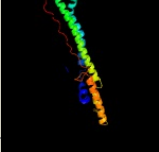
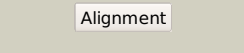

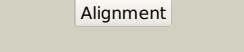
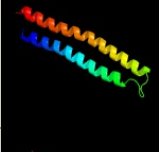

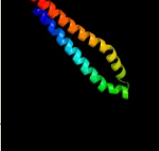
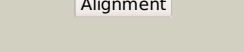
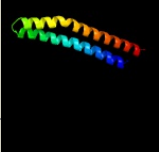
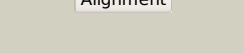
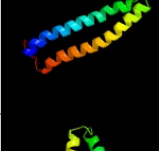
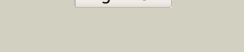
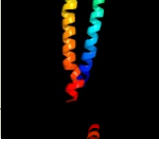


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1753c_(PPE24)_1981621_1984782
 Date Fri Aug 2 13:30:36 BST 2019
 Unique Job ID 34c91258763c1899

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	51	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	c2g38B_	 Alignment		100.0	32	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
3	d2g38b1	 Alignment		100.0	32	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	18	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		97.3	15	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		96.9	11	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c4iogD_	 Alignment		96.6	17	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
8	c3gvmA_	 Alignment		96.5	13	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
9	c3zbhC_	 Alignment		95.9	20	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		95.3	15	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	d1wa8b1	 Alignment		71.5	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like

12	c2vsnB_	Alignment		70.2	10	PDB header: transferase Chain: B: PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glcna2 transferase homolog: insight into molecular control of3 intracellular glycosylation
13	c4lwsA_	Alignment		70.0	20	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c4i0xA_	Alignment		68.2	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
15	c4lwsB_	Alignment		58.2	9	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
16	c3jywF_	Alignment		57.0	48	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
17	c3pe3D_	Alignment		56.0	14	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcna2 transferase and its complex with a peptide2 substrate
18	c2kg7B_	Alignment		46.7	20	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein eshx; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
19	d1ui5a2	Alignment		45.8	16	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
20	c4jzaB_	Alignment		40.3	38	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a legionella phosphoinositide phosphatase:2 insights into lipid metabolism in pathogen host interaction
21	c3ahrA_	Alignment	not modelled	31.8	23	PDB header: oxidoreductase Chain: A: PDB Molecule: ero1-like protein alpha; PDBTitle: inactive human ero1
22	d3cx5d1	Alignment	not modelled	31.5	40	Fold: Cytochrome c Superfamily: Cytochrome c Family: Cytochrome bc1 domain
23	d1ppid1	Alignment	not modelled	31.0	35	Fold: Cytochrome c Superfamily: Cytochrome c Family: Cytochrome bc1 domain
24	c5djsA_	Alignment	not modelled	30.5	17	PDB header: transferase Chain: A: PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcna2 transferase mutant - k341m
25	d1rp4a_	Alignment	not modelled	30.0	23	Fold: ERO1-like Superfamily: ERO1-like Family: ERO1-like
26	c4lrV_	Alignment	not modelled	28.1	40	PDB header: dna binding protein Chain: L: PDB Molecule: dna sulfur modification protein dnde; PDBTitle: crystal structure of dnde from escherichia coli b7a involved in dna2 phosphorothioation modification
27	c3lhoA_	Alignment	not modelled	28.0	44	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of putative hydrolase (yp_751971.1) from shewanella2 frigidimarina ncimb 400 at 1.80 a resolution
28	c1zrtD_	Alignment	not modelled	25.3	50	PDB header: oxidoreductase/metal transport Chain: D: PDB Molecule: cytochrome c1; PDBTitle: rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
29	c3fpjA_	Alignment	not modelled	25.0	11	PDB header: biosynthetic protein, transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of e81q mutant of mtas in complex with

						s-2 adenosylmethionine
30	c5frgA	Alignment	not modelled	24.3	75	PDB header: protein binding Chain: A: PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1
31	c1qcrD	Alignment	not modelled	23.7	35	PDB header: oxidoreductase Chain: D: PDB Molecule: ubiquinol cytochrome c oxidoreductase; PDBTitle: crystal structure of bovine mitochondrial cytochrome bc12 complex, alpha carbon atoms only
32	c3cwbQ	Alignment	not modelled	23.6	33	PDB header: oxidoreductase Chain: Q: PDB Molecule: mitochondrial cytochrome c1, heme protein; PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
33	c4nl6C	Alignment	not modelled	22.8	71	PDB header: splicing Chain: C: PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients
34	d1byra	Alignment	not modelled	22.4	22	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Nuclease
35	c1bkvA	Alignment	not modelled	22.3	50	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
36	c3b5oA	Alignment	not modelled	21.8	38	PDB header: oxidoreductase Chain: A: PDB Molecule: cadd-like protein of unknown function; PDBTitle: crystal structure of a cadd-like protein of unknown function2 (npun_f6505) from nostoc punctiforme pcc 73102 at 1.35 a resolution
37	c4urjA	Alignment	not modelled	21.0	13	PDB header: unknown function Chain: A: PDB Molecule: protein fam83a; PDBTitle: crystal structure of human bj-tsa-9
38	c1bkvB	Alignment	not modelled	21.0	50	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
39	c1bkvC	Alignment	not modelled	21.0	50	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
40	c2yiuE	Alignment	not modelled	21.0	44	PDB header: oxidoreductase Chain: E: PDB Molecule: cytochrome c1, heme protein; PDBTitle: x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
41	c5lzkB	Alignment	not modelled	20.7	6	PDB header: structural genomics Chain: B: PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
42	c3kb4D	Alignment	not modelled	20.3	14	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr8543 protein; PDBTitle: crystal structure of the alr8543 protein in complex with2 geranylgeranyl monophosphate and magnesium ion from nostoc sp. pcc3 7120, northeast structural genomics consortium target nsr141
43	d1luaa2	Alignment	not modelled	20.0	41	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Methylene-tetrahydromethanopterin dehydrogenase
44	c2fynH	Alignment	not modelled	19.9	40	PDB header: oxidoreductase Chain: H: PDB Molecule: cytochrome c1; PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
45	c1p84D	Alignment	not modelled	19.4	40	PDB header: oxidoreductase Chain: D: PDB Molecule: cytochrome c1, heme protein; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
46	c6ghrF	Alignment	not modelled	18.0	53	PDB header: photosynthesis Chain: F: PDB Molecule: cp12 polypeptide; PDBTitle: cyanobacterial gapdh with full-length cp12
47	c2pheC	Alignment	not modelled	17.5	31	PDB header: transcription Chain: C: PDB Molecule: alpha trans-inducing protein; PDBTitle: model for vp16 binding to pc4
48	c3q3hA	Alignment	not modelled	16.4	13	PDB header: transferase Chain: A: PDB Molecule: hmw1c-like glycosyltransferase; PDBTitle: crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
49	c2ke4A	Alignment	not modelled	15.8	75	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
50	d2a15a1	Alignment	not modelled	15.0	22	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
51	c5e8jC	Alignment	not modelled	14.2	43	PDB header: translation Chain: C: PDB Molecule: rrmt-activating mini protein; PDBTitle: crystal structure of mrna cap guanine-n7 methyltransferase in complex2 with ram
52	c3k66A	Alignment	not modelled	13.6	28	PDB header: cell adhesion Chain: A: PDB Molecule: beta-amyloid-like protein; PDBTitle: x-ray crystal structure of the e2 domain of c. elegans apl-1
53	d1xkna	Alignment	not modelled	13.4	21	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
54	c2k2uB	Alignment	not modelled	13.2	33	PDB header: transcription Chain: B: PDB Molecule: alpha trans-inducing protein; PDBTitle: nmr structure of the complex between tfb1 subunit of tfiih2 and the activation domain of vp16 PDB header: lyase Chain: B: PDB Molecule: ...

55	c4rqoB_	Alignment	not modelled	12.8	32	Chain: B: PDB Molecule: l-serine dehydratase; PDBTitle: crystal structure of l-serine dehydratase from legionella pneumophila
56	c5jn6A_	Alignment	not modelled	12.7	56	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the nmr solution structure of rpa3313
57	d1yymg1	Alignment	not modelled	12.7	31	Fold: gp120 core Superfamily: gp120 core Family: gp120 core
58	d2qxfa1	Alignment	not modelled	12.6	12	Fold: Cystatin-like Superfamily: NTF2-like Family: YybH-like
59	c5muul_	Alignment	not modelled	12.5	37	PDB header: virus Chain: I: PDB Molecule: major outer capsid protein; PDBTitle: dsrna bacteriophage phi6 nucleocapsid
60	c2yikA_	Alignment	not modelled	12.4	10	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: catalytic domain of clostridium thermocellum celt
61	c4grdA_	Alignment	not modelled	12.4	18	PDB header: lyase, isomerase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
62	d2nxya1	Alignment	not modelled	12.0	31	Fold: gp120 core Superfamily: gp120 core Family: gp120 core
63	c3rjqA_	Alignment	not modelled	11.9	31	PDB header: viral protein/immune system Chain: A: PDB Molecule: c186 gp120; PDBTitle: crystal structure of anti-hiv llama vhh antibody a12 in complex with2 c186 gp120
64	c5tszA_	Alignment	not modelled	11.9	22	PDB header: cell invasion Chain: A: PDB Molecule: pv cell-traversal protein; PDBTitle: crystal structure of plasmodium vivax celtos
65	c2zcaB_	Alignment	not modelled	11.1	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative uncharacterized protein tthb189; PDBTitle: crystal structure of tthb189, a crispr-associated protein,2 cse2 family from thermus thermophilus hb8
66	d1g03a_	Alignment	not modelled	10.8	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
67	d2fr1a1	Alignment	not modelled	10.7	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
68	c2kwuA_	Alignment	not modelled	10.7	38	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	d3cu3a1	Alignment	not modelled	10.4	20	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
70	c5cgaC_	Alignment	not modelled	10.3	31	PDB header: transferase Chain: C: PDB Molecule: hydroxyethylthiazole kinase; PDBTitle: structure of hydroxyethylthiazole kinase thim from staphylococcus2 aureus in complex with substrate analog 2-(1,3,5-trimethyl-1h-3 pyrazole-4-yl)ethanol
71	c3jwdA_	Alignment	not modelled	10.2	31	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 gp120 envelope glycoprotein; PDBTitle: structure of hiv-1 gp120 with gp41-interactive region: layered2 architecture and basis of conformational mobility
72	c6cboB_	Alignment	not modelled	10.1	16	PDB header: transferase Chain: B: PDB Molecule: c-6' aminotransferase; PDBTitle: x-ray structure of genb1 from micromonospora echinospora in complex2 with neamine and plp (as the external aldimine)
73	d2b4cg1	Alignment	not modelled	10.0	31	Fold: gp120 core Superfamily: gp120 core Family: gp120 core
74	c1fqvK_	Alignment	not modelled	10.0	30	PDB header: ligase Chain: K: PDB Molecule: skp2; PDBTitle: insights into scf ubiquitin ligases from the structure of2 the skp1-skp2 complex
75	c3pf6C_	Alignment	not modelled	9.9	50	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein pp-luz7_gp033; PDBTitle: the structure of uncharacterized protein pp-luz7_gp033 from2 pseudomonas phage luz7.
76	c5aizA_	Alignment	not modelled	9.8	15	PDB header: zinc-binding protein Chain: A: PDB Molecule: zinc finger miz domain-containing protein 1; PDBTitle: the pias-like coactivator zmiz1 is a direct and selective cofactor2 of notch1 in t-cell development and leukemia
77	c6o9l6_	Alignment	not modelled	9.7	40	PDB header: transcription/dna Chain: 6: PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the closed state
78	c3bkhA_	Alignment	not modelled	9.6	18	PDB header: hydrolase Chain: A: PDB Molecule: lytic transglycosylase; PDBTitle: crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
79	c3j5ml_	Alignment	not modelled	9.5	31	PDB header: viral protein/immune system Chain: I: PDB Molecule: bg505 sosp gp120; PDBTitle: cryo-em structure of the bg505 sosp.664 hiv-1 env trimer with 3 pgv042 fabs
80	c5i4rA_	Alignment	not modelled	9.5	43	PDB header: toxin/antitoxin Chain: A: PDB Molecule: contact-dependent inhibitor a; PDBTitle: contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdi/ef-tu complex (trypsin-modified)

81	c3r8rj_	Alignment	not modelled	9.4	11	PDB header: transferase Chain: J; PDB Molecule: transaldolase; PDBTitle: transaldolase from bacillus subtilis
82	d1b93a_	Alignment	not modelled	9.4	29	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
83	c2phgB_	Alignment	not modelled	9.4	31	PDB header: transcription Chain: B; PDB Molecule: alpha trans-inducing protein; PDBTitle: model for vp16 binding to tfiib
84	c3ngbl_	Alignment	not modelled	9.3	38	PDB header: viral protein/immune system Chain: I; PDB Molecule: envelope glycoprotein gp160; PDBTitle: crystal structure of broadly and potently neutralizing antibody vrc012 in complex with hiv-1 gp120
85	c4ph2A_	Alignment	not modelled	9.3	39	PDB header: viral protein Chain: A; PDB Molecule: blv capsid - n-terminal domain; PDBTitle: mature n-terminal domain of capsid protein from bovine leukemia virus
86	d1jpdx2	Alignment	not modelled	9.3	21	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
87	c5te4G_	Alignment	not modelled	9.1	31	PDB header: immune system Chain: G; PDB Molecule: hiv-1 clade g strain x2088 gp120; PDBTitle: crystal structure of broadly neutralizing vrc01-class antibody n6 in2 complex with hiv-1 clade g strain x2088 gp120 core
88	c2bn5B_	Alignment	not modelled	9.1	75	PDB header: nuclear protein Chain: B; PDB Molecule: u1 small nuclear ribonucleoprotein 70 kda; PDBTitle: p-element somatic inhibitor protein complex with u1-70k2 proline-rich peptide
89	c4xb6D_	Alignment	not modelled	8.9	18	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
90	c4l7zC_	Alignment	not modelled	8.8	11	PDB header: lyase Chain: C; PDB Molecule: hpch/hpai aldolase; PDBTitle: crystal structure of chloroflexus aurantiacus malyl-coa lyase
91	c3hx8A_	Alignment	not modelled	8.8	21	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
92	d1vpxa_	Alignment	not modelled	8.8	8	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
93	c1ga2A_	Alignment	not modelled	8.8	16	PDB header: hydrolase Chain: A; PDB Molecule: endoglucanase 9g; PDBTitle: the crystal structure of endoglucanase 9g from clostridium2 cellulolyticum complexed with cellobiose
94	d1vefa1	Alignment	not modelled	8.7	24	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
95	c3wa8B_	Alignment	not modelled	8.7	15	PDB header: rna binding protein Chain: B; PDB Molecule: crispr-associated protein, cse2 family; PDBTitle: crystal structure of m. ruber casb
96	c3rhtB_	Alignment	not modelled	8.7	30	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: (gatase1)-like protein; PDBTitle: crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus
97	c3r5zB_	Alignment	not modelled	8.7	17	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
98	c5evyX_	Alignment	not modelled	8.6	16	PDB header: oxidoreductase Chain: X; PDB Molecule: salicylate hydroxylase; PDBTitle: salicylate hydroxylase substrate complex
99	c2kg7A_	Alignment	not modelled	8.6	35	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