
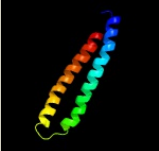

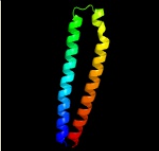



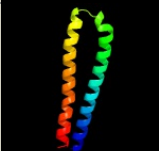

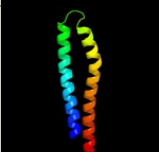

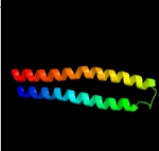

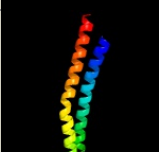

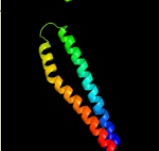

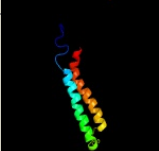

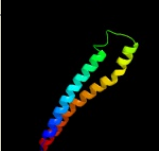

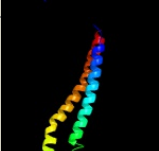
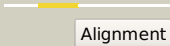

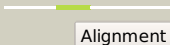

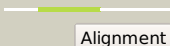
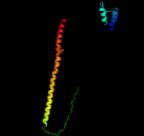




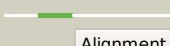
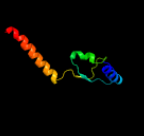
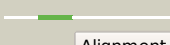
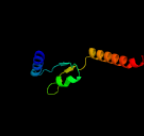



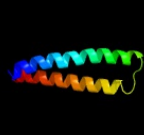
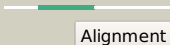
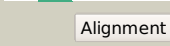
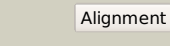
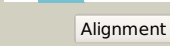
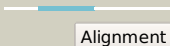
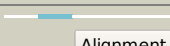




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3439c_(-)_3858439_3859842
Date	Fri Aug 9 18:20:11 BST 2019
Unique Job ID	9fcee1a88586dd88

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wa8a1	 Alignment		94.6	19	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
2	c4lwsA_	 Alignment		94.3	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
3	d1wa8b1	 Alignment		94.3	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
4	c4lwsB_	 Alignment		94.2	14	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
5	c2vs0B_	 Alignment		93.0	14	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
6	c4iogD_	 Alignment		91.9	9	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
7	c3zbhC_	 Alignment		91.3	15	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
8	c3gvmA_	 Alignment		91.2	17	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	c2kg7B_	 Alignment		88.8	15	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
10	d2g38b1	 Alignment		74.1	10	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
11	c2g38B_	 Alignment		74.1	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis

12	c2i56A_	 Alignment		70.3	20	PDB header: isomerase, metal-binding protein Chain: A: PDB Molecule: l-rhamnose isomerase; PDBTitle: crystal structure of l-rhamnose isomerase from pseudomonas2 stutzeri with l-rhamnose
13	c5hypB_	 Alignment		61.3	24	PDB header: immune system Chain: B: PDB Molecule: m28 protein; PDBTitle: structure of human c4b-binding protein alpha cain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m283 protein
14	c6ogdB_	 Alignment		60.9	12	PDB header: toxin Chain: B: PDB Molecule: toxin subunit yena2; PDBTitle: cryo-em structure of yentca in its prepore state
15	c3d3kD_	 Alignment		56.6	13	PDB header: protein binding Chain: D: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
16	c4i0xJ_	 Alignment		54.9	17	PDB header: structural genomics, unknown function Chain: J: PDB Molecule: esat-6-like protein mab_3113; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
17	d1izca_	 Alignment		53.5	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpcH/Hpal aldolase
18	c1izcA_	 Alignment		53.5	16	PDB header: lyase Chain: A: PDB Molecule: macrophomate synthase intermolecular diels-alderase; PDBTitle: crystal structure analysis of macrophomate synthase
19	d1qh8b_	 Alignment		49.6	21	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
20	d1nt2b_	 Alignment		48.2	28	Fold: Nop domain Superfamily: Nop domain Family: Nop domain
21	c4ffcD_	 Alignment	not modelled	41.7	23	PDB header: transferase Chain: D: PDB Molecule: 4-aminobutyrate aminotransferase (gabt); PDBTitle: crystal structure of a 4-aminobutyrate aminotransferase (gabt) from2 mycobacterium abscessus
22	c4i0xA_	 Alignment	not modelled	40.3	20	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
23	c2ykyB_	 Alignment	not modelled	37.0	23	PDB header: transferase Chain: B: PDB Molecule: beta-transaminase; PDBTitle: structural determinants of the beta-selectivity of a bacterial2 aminotransferase
24	c3e04C_	 Alignment	not modelled	36.4	20	PDB header: lyase Chain: C: PDB Molecule: fumarate hydratase; PDBTitle: crystal structure of human fumarate hydratase
25	c5ghfB_	 Alignment	not modelled	35.9	19	PDB header: transferase Chain: B: PDB Molecule: aminotransferase class-iii; PDBTitle: transaminase with l-ala
26	d1dxea_	 Alignment	not modelled	35.8	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpcH/Hpal aldolase
27	c3m1eA_	 Alignment	not modelled	35.0	14	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of benm_dbd
28	c2uval_	 Alignment	not modelled	34.8	21	PDB header: transferase Chain: I: PDB Molecule: fatty acid synthase beta subunits; PDBTitle: crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid

						synthase and is described in remark 400
29	c4gioA_	Alignment	not modelled	33.8	42	PDB header: unknown function Chain: A: PDB Molecule: putative lipoprotein; PDBTitle: crystal structure of campylobacter jejuni cj0090
30	c3w3fB_	Alignment	not modelled	33.6	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: uncharacterized protein blr2150; PDBTitle: crystal structure of ent-kaurene synthase bjks from bradyrhizobium2 japonicum
31	c3id6A_	Alignment	not modelled	33.5	9	PDB header: transferase Chain: A: PDB Molecule: pre mrna splicing protein; PDBTitle: crystal structure of sulfolobus solfataricus nop5 (1-262) and2 fibrillar complex
32	c6akmA_	Alignment	not modelled	33.2	19	PDB header: protein binding Chain: A: PDB Molecule: suppressor of ikbke 1; PDBTitle: crystal structure of slmap-sike1 complex
33	d1xm5a_	Alignment	not modelled	32.7	39	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Predicted metal-dependent hydrolase
34	c2yy0D_	Alignment	not modelled	30.1	16	PDB header: transcription Chain: D: PDB Molecule: c-myc-binding protein; PDBTitle: crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
35	d1qm4a2	Alignment	not modelled	29.6	19	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
36	c3n8uB_	Alignment	not modelled	29.0	16	PDB header: hydrolase Chain: B: PDB Molecule: imelysin peptidase; PDBTitle: crystal structure of an imelysin peptidase (bacova_03801) from2 bacteroides ovatus at 1.44 a resolution
37	c3oksB_	Alignment	not modelled	28.1	15	PDB header: transferase Chain: B: PDB Molecule: 4-aminobutyrate transaminase; PDBTitle: crystal structure of 4-aminobutyrate transaminase from mycobacterium2 smegmatis
38	d1sffa_	Alignment	not modelled	27.6	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
39	d2d0ta1	Alignment	not modelled	27.1	13	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
40	c3n5mD_	Alignment	not modelled	26.7	16	PDB header: transferase Chain: D: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystals structure of a bacillus anthracis aminotransferase
41	c2n39A_	Alignment	not modelled	26.0	17	PDB header: dna binding protein Chain: A: PDB Molecule: chromodomain-helicase-dna-binding protein 1; PDBTitle: nmr solution structure of a c-terminal domain of the chromodomain2 helicase dna-binding protein 1
42	d2fr2a1	Alignment	not modelled	25.4	33	Fold: Lipocalins Superfamily: Lipocalins Family: Rv2717c-like
43	d1zoda1	Alignment	not modelled	25.3	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
44	c1wqsA_	Alignment	not modelled	25.0	55	PDB header: hydrolase Chain: A: PDB Molecule: 3c-like protease; PDBTitle: crystal structure of norovirus 3c-like protease
45	d1c3ca_	Alignment	not modelled	24.7	12	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
46	c3hhgF_	Alignment	not modelled	24.6	16	PDB header: transcription regulator Chain: F: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: structure of crga, a lysr-type transcriptional regulator from2 neisseria meningitidis.
47	c5fo5A_	Alignment	not modelled	24.1	11	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator metr; PDBTitle: structure of the dna-binding domain of escherichia coli methionine2 biosynthesis regulator metr
48	d1ob0a2	Alignment	not modelled	24.0	36	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
49	d1tvia_	Alignment	not modelled	22.5	29	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Predicted metal-dependent hydrolase
50	d1u94a2	Alignment	not modelled	22.4	25	Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain
51	c3o0lB_	Alignment	not modelled	21.8	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pfam duf1425 family member (shew_1734) from2 shewanella sp. pv-4 at 1.81 a resolution
52	c4arpB_	Alignment	not modelled	21.5	16	PDB header: hydrolase Chain: B: PDB Molecule: pesticin; PDBTitle: structure of the inactive pesticin e178a mutant
53	d1xp8a2	Alignment	not modelled	21.1	21	Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain
54	c2v5jB_	Alignment	not modelled	21.0	18	PDB header: lyase Chain: B: PDB Molecule: 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; PDBTitle: apo class ii aldolase hpch
						Fold: beta-Grasp (ubiquitin-like)

55	d2al6a3	Alignment	not modelled	20.5	15	Superfamily: Ubiquitin-like Family: First domain of FERM
56	d1e43a2	Alignment	not modelled	20.5	28	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
57	c3id5E	Alignment	not modelled	20.4	10	PDB header: transferase/ribosomal protein/rna Chain: E: PDB Molecule: pre mrna splicing protein; PDBTitle: crystal structure of sulfolobus solfataricus c/d rnp assembled with2 nop5, fibrillarlin, l7ae and a split half c/d rna
58	c1bplA	Alignment	not modelled	20.3	32	PDB header: glycosyltransferase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: glycosyltransferase
59	c4gq6A	Alignment	not modelled	20.2	33	PDB header: transcription/transcription inhibitor Chain: A: PDB Molecule: menin; PDBTitle: human menin in complex with mll peptide
60	c2fwvA	Alignment	not modelled	20.1	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein mtbuf_01000852; PDBTitle: crystal structure of rv0813
61	c2jq3A	Alignment	not modelled	19.9	27	PDB header: lipid binding protein Chain: A: PDB Molecule: apolipoprotein c-iii; PDBTitle: structure and dynamics of human apolipoprotein c-iii
62	c2nnwC	Alignment	not modelled	19.7	14	PDB header: transferase Chain: C: PDB Molecule: nop5/nop56 related protein; PDBTitle: alternative conformations of nop56/58-fibrillarlin complex and2 implication for induced-fit assenly of box c/d rnps
63	d1jm6a1	Alignment	not modelled	19.5	23	Fold: Bromodomain-like Superfamily: alpha-ketoacid dehydrogenase kinase, N-terminal domain Family: alpha-ketoacid dehydrogenase kinase, N-terminal domain
64	c3re2A	Alignment	not modelled	19.5	33	PDB header: unknown function Chain: A: PDB Molecule: predicted protein; PDBTitle: crystal structure of menin reveals the binding site for mixed lineage2 leukemia (mll) protein
65	d2c0sa1	Alignment	not modelled	19.4	23	Fold: ROP-like Superfamily: BAS1536-like Family: BAS1536-like
66	c4mf4F	Alignment	not modelled	19.2	20	PDB header: lyase Chain: F: PDB Molecule: hpch/hpai aldolase/citrate lyase family protein; PDBTitle: crystal structure of a hpch/hpal aldolase/citrate lyase family protein2 from burkholderia cenocepacia j2315
67	c1odpA	Alignment	not modelled	19.1	44	PDB header: lipid transport Chain: A: PDB Molecule: apoa-i peptide; PDBTitle: peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.6, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
68	c1odrA	Alignment	not modelled	19.1	44	PDB header: lipid transport Chain: A: PDB Molecule: apoa-i peptide; PDBTitle: peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.0, 37 degrees celsius and peptide:dpc mole ratio3 of 1:40
69	c1odqA	Alignment	not modelled	19.1	44	PDB header: lipid transport Chain: A: PDB Molecule: apoa-i peptide; PDBTitle: peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 3.7, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
70	c5i92E	Alignment	not modelled	19.0	21	PDB header: isomerase Chain: E: PDB Molecule: glutamate-1-semialdehyde 2,1-aminomutase; PDBTitle: crystal structure of glutamate-1-semialdehyde 2,1-aminomutase (gsa)2 from pseudomonas aeruginosa
71	d2a13a1	Alignment	not modelled	19.0	33	Fold: Lipocalins Superfamily: Lipocalins Family: Rv2717c-like
72	c3u88B	Alignment	not modelled	18.9	33	PDB header: transcription Chain: B: PDB Molecule: menin; PDBTitle: crystal structure of human menin in complex with mll1 and ledgf
73	c4wvxB	Alignment	not modelled	18.7	22	PDB header: hydrolase, ligase Chain: B: PDB Molecule: v(d)j recombination-activating protein 1; PDBTitle: crystal structure of the core rag1/2 recombinase
74	d1gkza1	Alignment	not modelled	18.5	23	Fold: Bromodomain-like Superfamily: alpha-ketoacid dehydrogenase kinase, N-terminal domain Family: alpha-ketoacid dehydrogenase kinase, N-terminal domain
75	c6nd4a	Alignment	not modelled	18.5	23	PDB header: ribosome Chain: A: PDB Molecule: mpp10; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
76	d2gipa2	Alignment	not modelled	18.4	29	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
77	d1ubea2	Alignment	not modelled	17.9	19	Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain
78	d1mo6a2	Alignment	not modelled	17.8	14	Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain
79	c2obvA	Alignment	not modelled	17.4	17	PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine synthetase isoform type-1; PDBTitle: crystal structure of the human s-adenosylmethionine synthetase 1 in2 complex with the product
80	c2uv1B	Alignment	not modelled	17.3	17	PDB header: inhibitor Chain: B: PDB Molecule: host-nuclease inhibitor protein gam;

80	c2uv1B	Alignment	not modelled	17.3	17	PDBTitle: hexagonal crystal form of gams from bacteriophage lambda. PDB header: recombination activator
81	c3viqC	Alignment	not modelled	17.2	20	Chain: C; PDB Molecule: swi5-dependent recombination dna repair protein 1; PDBTitle: crystal structure of swi5-sfr1 complex from fission yeast
82	c3fzvC	Alignment	not modelled	17.2	10	PDB header: transcription regulator Chain: C; PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of pa01 protein, putative lysr family2 transcriptional regulator from pseudomonas aeruginosa
83	c3ia8A	Alignment	not modelled	16.8	8	PDB header: metal binding protein Chain: A; PDB Molecule: thap domain-containing protein 4; PDBTitle: the structure of the c-terminal heme nitrobindin domain of thap2 domain-containing protein 4 from homo sapiens
84	c3ispA	Alignment	not modelled	16.7	11	PDB header: transcription Chain: A; PDB Molecule: hth-type transcriptional regulator PDBTitle: crystal structure of argp from mycobacterium tuberculosis
85	c5vtmX	Alignment	not modelled	16.7	13	PDB header: transport protein Chain: X; PDB Molecule: type ii secretion system protein k; PDBTitle: the crystal structure of minor pseudopilin ternary complex of xcpvwx2 from the type 2 secretion system of pseudomonas aeruginosa
86	c4akkA	Alignment	not modelled	16.4	22	PDB header: transcription Chain: A; PDB Molecule: nitrate regulatory protein; PDBTitle: structure of the nasr transcription antiterminator
87	c3qd7X	Alignment	not modelled	16.3	9	PDB header: hydrolase Chain: X; PDB Molecule: uncharacterized protein ydal; PDBTitle: crystal structure of ydal, a stand-alone small muts-related protein2 from escherichia coli
88	c2ideE	Alignment	not modelled	16.1	18	PDB header: biosynthetic protein Chain: E; PDB Molecule: molybdenum cofactor biosynthesis protein c; PDBTitle: crystal structure of the molybdenum cofactor biosynthesis protein c2 (ttha1789) from thermus thermophilus hb8
89	c6dk9I	Alignment	not modelled	16.1	15	PDB header: lyase Chain: I; PDB Molecule: dna damage-inducible protein; PDBTitle: yeast ddi2 cyanamide hydratase
90	c5tf0B	Alignment	not modelled	16.1	15	PDB header: hydrolase Chain: B; PDB Molecule: glycosyl hydrolase family 3 n-terminal domain protein; PDBTitle: crystal structure of glycosyl hydrolase family 3 n-terminal domain2 protein from bacteroides intestinalis
91	c5z4yB	Alignment	not modelled	16.0	10	PDB header: dna binding protein Chain: B; PDB Molecule: cys regulon transcriptional activator; PDBTitle: crystal structure of pacysb ntd domain with space group p4
92	c5xfsB	Alignment	not modelled	16.0	15	PDB header: protein transport Chain: B; PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with espq5 from m.2 tuberculosis
93	c5y9sD	Alignment	not modelled	15.9	7	PDB header: transcription Chain: D; PDB Molecule: vv2_1132; PDBTitle: crystal structure of vv2_1132, a lysr family transcriptional regulator
94	c3cq0B	Alignment	not modelled	15.7	13	PDB header: transferase Chain: B; PDB Molecule: putative transaldolase ygr043c; PDBTitle: crystal structure of tal2_yeast
95	c5ed9A	Alignment	not modelled	15.7	26	PDB header: transport protein Chain: A; PDB Molecule: sun domain-containing protein 2; PDBTitle: crystal structure of cc1 of mouse sun2
96	c3so4C	Alignment	not modelled	15.4	16	PDB header: transferase Chain: C; PDB Molecule: methionine-adenosyltransferase; PDBTitle: methionine-adenosyltransferase from entamoeba histolytica
97	c5ydcA	Alignment	not modelled	15.3	13	PDB header: transcription regulator Chain: A; PDB Molecule: uncharacterized hth-type transcriptional regulator rv1828; PDBTitle: crystal structure of mercury soaked c-terminal domain of rv1828 from2 mycobacterium tuberculosis
98	c4e0uB	Alignment	not modelled	15.1	23	PDB header: transferase Chain: B; PDB Molecule: cyclic dipeptide n-prenyltransferase; PDBTitle: crystal structure of cdpnpt in complex with thiolodiphosphate and (s)-2 benzodiazependione
99	c3ghpA	Alignment	not modelled	15.0	50	PDB header: structural protein Chain: A; PDB Molecule: cellulosomal scaffoldin adaptor protein b; PDBTitle: structure of the second type ii cohesin module from the adaptor scaa2 scaffoldin of acetivibrio cellulolyticus (including long c-terminal3 linker)