


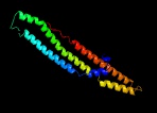

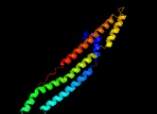

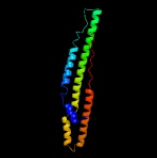

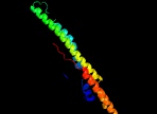
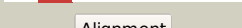
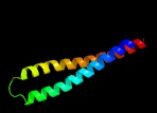
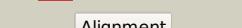

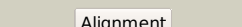

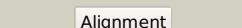
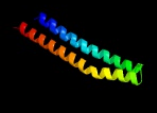
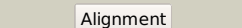





Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3343c_(PPE54)_3729535_3737106
 Date Thu Aug 8 16:20:55 BST 2019
 Unique Job ID 20d8ff8b5133f869

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	d2g38b1	 Alignment		100.0	32	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
3	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
4	c4xy3A_	 Alignment		100.0	22	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		97.1	15	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		96.6	9	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c4iogD_	 Alignment		96.4	16	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		96.0	14	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		95.8	19	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		94.6	16	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c5nxhB_	 Alignment		90.8	12	PDB header: viral protein Chain: B: PDB Molecule: long-tail fiber proximal subunit; PDBTitle: crystal structure of the carboxy-terminal region of the bacteriophage2 t4 proximal long tail fibre protein gp34, residues 744-1289 at 2.93 angstrom resolution

12	c3jywF_	Alignment		76.7	43	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
13	c4i0xA_	Alignment		76.4	17	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
14	d1xkna_	Alignment		68.8	14	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
15	d1wa8b1	Alignment		67.9	14	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
16	c4lwsA_	Alignment		67.9	21	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
17	d1ui5a2	Alignment		67.6	18	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
18	c2vsnB_	Alignment		64.8	14	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
19	d1oy0a_	Alignment		61.4	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
20	c3pe3D_	Alignment		59.4	16	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
21	c3ahrA_	Alignment	not modelled	57.6	28	PDB header: oxidoreductase Chain: A; PDB Molecule: ero1-like protein alpha; PDBTitle: inactive human ero1
22	d2fr1a1	Alignment	not modelled	57.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
23	d3cx5d1	Alignment	not modelled	54.3	28	Fold: Cytochrome c Superfamily: Cytochrome c Family: Cytochrome bc1 domain
24	d1ppjd1	Alignment	not modelled	52.6	22	Fold: Cytochrome c Superfamily: Cytochrome c Family: Cytochrome bc1 domain
25	d1vkpa_	Alignment	not modelled	51.8	24	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
26	d2ewoa1	Alignment	not modelled	51.0	24	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
27	c3ed6B_	Alignment	not modelled	48.4	19	PDB header: oxidoreductase Chain: B; PDB Molecule: betaine aldehyde dehydrogenase; PDBTitle: 1.7 angstrom resolution crystal structure of betaine aldehyde2 dehydrogenase (betb) from staphylococcus aureus
28	c1qcrD_	Alignment	not modelled	47.0	22	PDB header: oxidoreductase Chain: D; PDB Molecule: ubiquinol cytochrome c oxidoreductase; PDBTitle: crystal structure of bovine mitochondrial cytochrome bc12 complex, alpha carbon atoms only
29	c2v7iA_	Alignment	not modelled	46.9	25	PDB header: biosynthetic protein Chain: A; PDB Molecule: prnb; PDBTitle: prnb native

30	c1zrtD	Alignment	not modelled	46.7	41	PDB header: oxidoreductase/metal transport Chain: D: PDB Molecule: cytochrome c1; PDBTitle: rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
31	c4fm9A	Alignment	not modelled	45.9	24	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 2-alpha; PDBTitle: human topoisomerase ii alpha bound to dna
32	c3qx3B	Alignment	not modelled	43.6	31	PDB header: isomerase/dna/isomerase inhibitor Chain: B: PDB Molecule: dna topoisomerase 2-beta; PDBTitle: human topoisomerase iibeta in complex with dna and etoposide
33	c4rqoB	Alignment	not modelled	43.2	29	PDB header: lyase Chain: B: PDB Molecule: l-serine dehydratase; PDBTitle: crystal structure of l-serine dehydratase from legionella pneumophila
34	c3cwbQ	Alignment	not modelled	42.3	25	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
35	c3fpjA	Alignment	not modelled	41.0	17	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
36	c4lwsB	Alignment	not modelled	40.8	12	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
37	c5kf6B	Alignment	not modelled	39.8	21	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein puta; PDBTitle: structure of proline utilization a from sinorhizobium meliloti2 complexed with l-tetrahydrofuroic acid and nad+ in space group p21
38	c4lrVL	Alignment	not modelled	39.6	30	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
39	c5evyX	Alignment	not modelled	39.3	11	PDB header: oxidoreductase Chain: X: PDB Molecule: salicylate hydroxylase; PDBTitle: salicylate hydroxylase substrate complex
40	d2jera1	Alignment	not modelled	39.1	22	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
41	c2yiuE	Alignment	not modelled	38.9	41	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
42	d2cmua1	Alignment	not modelled	38.8	18	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
43	c3u4jB	Alignment	not modelled	38.4	21	PDB header: oxidoreductase Chain: B: PDB Molecule: nad-dependent aldehyde dehydrogenase; PDBTitle: crystal structure of nad-dependent aldehyde dehydrogenase from2 sinorhizobium meliloti
44	c3lhoA	Alignment	not modelled	37.5	42	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
45	c1p84D	Alignment	not modelled	37.4	28	PDB header: oxidoreductase Chain: D: PDB Molecule: cytochrome c1, heme protein; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
46	c5lzkB	Alignment	not modelled	37.1	4	PDB header: structural genomics Chain: B: PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
47	c2fynH	Alignment	not modelled	36.9	35	PDB header: oxidoreductase Chain: H: PDB Molecule: cytochrome c1; PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
48	d1bjta	Alignment	not modelled	35.6	22	Fold: Type II DNA topoisomerase Superfamily: Type II DNA topoisomerase Family: Type II DNA topoisomerase
49	c1bjtA	Alignment	not modelled	35.6	22	PDB header: topoisomerase Chain: A: PDB Molecule: topoisomerase ii; PDBTitle: topoisomerase ii residues 409-1201
50	d2f7fa1	Alignment	not modelled	35.5	17	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
51	c4evxA	Alignment	not modelled	34.3	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative phage endolysin; PDBTitle: crystal structure of putative phage endolysin from s. enterica
52	c2kg7B	Alignment	not modelled	33.9	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
53	c2ve5H	Alignment	not modelled	33.4	18	PDB header: oxidoreductase Chain: H: PDB Molecule: betaine aldehyde dehydrogenase; PDBTitle: crystallographic structure of betaine aldehyde2 dehydrogenase from pseudomonas aeruginosa
54	c5djsA	Alignment	not modelled	32.9	19	PDB header: transferase Chain: A: PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcnaC transferase mutant - k341m
55	c6h2wB	Alignment	not modelled	32.7	17	PDB header: hydrolase Chain: B: PDB Molecule: putative peptidyl-arginine deiminase

55	c002wb_	Alignment	not modelled	32.7	17	family protein; PDBTitle: c. jejuni c315s agmatine deiminase with substrate bound
56	d1byra_	Alignment	not modelled	32.2	28	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Nuclease
57	c5tjrE_	Alignment	not modelled	32.1	20	PDB header: oxidoreductase Chain: E: PDB Molecule: methylmalonate-semialdehyde dehydrogenase; PDBTitle: x-ray crystal structure of a methylmalonate semialdehyde dehydrogenase2 from pseudomonas sp. aac
58	c3r8rj_	Alignment	not modelled	31.9	13	PDB header: transferase Chain: J: PDB Molecule: transaldolase; PDBTitle: transaldolase from bacillus subtilis
59	d2a15a1	Alignment	not modelled	31.3	22	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
60	c2jerG_	Alignment	not modelled	30.8	22	PDB header: hydrolase Chain: G: PDB Molecule: agmatine deiminase; PDBTitle: agmatine deiminase of enterococcus faecalis catalyzing its2 reaction.
61	c4jzaB_	Alignment	not modelled	30.2	35	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
62	c2vakF_	Alignment	not modelled	29.7	25	PDB header: viral protein Chain: F: PDB Molecule: sigma a; PDBTitle: crystal structure of the avian reovirus inner capsid protein sigmaa
63	d2gxfa1	Alignment	not modelled	29.6	12	Fold: Cystatin-like Superfamily: NTF2-like Family: YybH-like
64	d1zbra1	Alignment	not modelled	28.5	16	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
65	d1vpxa_	Alignment	not modelled	28.3	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
66	d1wx0a1	Alignment	not modelled	27.9	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
67	d1c9ka_	Alignment	not modelled	27.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
68	c6ca8A_	Alignment	not modelled	27.7	19	PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase 2; PDBTitle: crystal structure of plasmodium falciparum topoisomerase ii dna-2 binding, cleavage and re-ligation domain
69	c1ga2A_	Alignment	not modelled	27.3	16	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase 9g; PDBTitle: the crystal structure of endoglucanase 9g from clostridium2 cellulolyticum complexed with cellobiose
70	c4gfhA_	Alignment	not modelled	27.1	22	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 2; PDBTitle: topoisomerase ii-dna-amppnp complex
71	d1o66a_	Alignment	not modelled	27.1	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
72	c4nl6C_	Alignment	not modelled	26.2	86	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
73	c4urjA_	Alignment	not modelled	25.9	13	PDB header: unknown function Chain: A: PDB Molecule: protein fam83a; PDBTitle: crystal structure of human bj-tsa-9
74	c3q3hA_	Alignment	not modelled	25.4	15	PDB header: transferase Chain: A: PDB Molecule: hmw1c-like glycosyltransferase; PDBTitle: crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
75	c1ybeA_	Alignment	not modelled	25.3	17	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of a nicotinate phosphoribosyltransferase
76	c5zdhD_	Alignment	not modelled	25.2	13	PDB header: protein transport Chain: D: PDB Molecule: type ii secretion system protein d; PDBTitle: cryoem structure of etec pilotin-secretin asps-gspd complex
77	c2pheC_	Alignment	not modelled	24.9	38	PDB header: transcription Chain: C: PDB Molecule: alpha trans-inducing protein; PDBTitle: model for vp16 binding to pc4
78	c4aoaA_	Alignment	not modelled	24.7	20	PDB header: transferase Chain: A: PDB Molecule: beta-phenylalanine aminotransferase; PDBTitle: biochemical properties and crystal structure of a novel2 beta-phenylalanine aminotransferase from variovorax3 paradoxus
79	d1rp4a_	Alignment	not modelled	24.5	25	Fold: ERO1-like Superfamily: ERO1-like Family: ERO1-like
80	c5fhzF_	Alignment	not modelled	24.2	16	PDB header: oxidoreductase Chain: F: PDB Molecule: aldehyde dehydrogenase family 1 member a3; PDBTitle: human aldehyde dehydrogenase 1a3 complexed with nad(+) and retinoic2 acid
						Fold: Aminoacid dehydrogenase-like, N-terminal domain

81	d1luaa2	Alignment	not modelled	24.0	32	Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Methylene-tetrahydromethanopterin dehydrogenase
82	d1ohwa_	Alignment	not modelled	23.8	7	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
83	d1tpla_	Alignment	not modelled	23.2	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
84	c2k2uB_	Alignment	not modelled	23.2	38	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
85	c6ghrF_	Alignment	not modelled	23.1	65	PDB header: photosynthesis Chain: F; PDB Molecule: cp12 polypeptide; PDBTitle: cyanobacterial gapdh with full-length cp12
86	c3vohA_	Alignment	not modelled	22.8	16	PDB header: hydrolase Chain: A; PDB Molecule: cellobiohydrolase; PDBTitle: ccel6a catalytic domain complexed with cellobiose
87	c3hx8A_	Alignment	not modelled	21.8	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
88	d3cu3a1	Alignment	not modelled	21.5	16	Fold: Cystatin-like Superfamily: NTF2-like Family: BalE/LinA-like
89	d1yymg1	Alignment	not modelled	20.8	23	Fold: gp120 core Superfamily: gp120 core Family: gp120 core
90	c4o5hD_	Alignment	not modelled	20.7	18	PDB header: oxidoreductase Chain: D; PDB Molecule: phenylacetaldehyde dehydrogenase; PDBTitle: x-ray crystal structure of a putative phenylacetaldehyde dehydrogenase2 from burkholderia cenocepacia
91	c5x5uB_	Alignment	not modelled	20.4	19	PDB header: oxidoreductase Chain: B; PDB Molecule: alpha-ketoglutaric semialdehyde dehydrogenase; PDBTitle: crystal structure of alpha-ketoglutarate-semialdehyde dehydrogenase2 (kgsadh) complexed with nad
92	c6cboB_	Alignment	not modelled	20.2	15	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)
93	c2zcaB_	Alignment	not modelled	20.1	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
94	c3rf7A_	Alignment	not modelled	19.9	12	PDB header: oxidoreductase Chain: A; PDB Molecule: iron-containing alcohol dehydrogenase; PDBTitle: crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
95	d2nxya1	Alignment	not modelled	19.6	23	Fold: gp120 core Superfamily: gp120 core Family: gp120 core
96	c2phgB_	Alignment	not modelled	19.6	38	PDB header: transcription Chain: B; PDB Molecule: alpha trans-inducing protein; PDBTitle: model for vp16 binding to tfiib
97	c4aw7A_	Alignment	not modelled	19.3	20	PDB header: hydrolase Chain: A; PDB Molecule: gh86a beta-porphyrinase; PDBTitle: bpg86a: a beta-porphyrinase of glycoside hydrolase family 86 from the2 human gut bacterium bacteroides plebeius
98	c6fhjA_	Alignment	not modelled	19.2	20	PDB header: hydrolase Chain: A; PDB Molecule: protein,protein; PDBTitle: structural dynamics and catalytic properties of a multi-modular2 xanthanase, native.
99	d1bvsa1	Alignment	not modelled	18.6	29	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain