




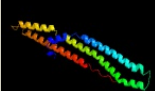

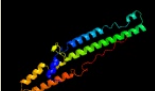

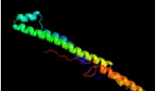

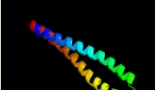












Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0305c_(PPE6)_372820_375711
 Date Tue Jul 23 14:50:37 BST 2019
 Unique Job ID df27703136929600

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	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	16	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		97.8	18	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.1	13	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c4iogD_	 Alignment		96.9	10	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		96.7	8	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		96.6	9	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		95.7	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	d1wa8b1	 Alignment		86.7	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like

12	c4lwsA_	Alignment		86.5	15	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	c4lwsB_	Alignment		84.9	16	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	d1ui5a2	Alignment		80.6	24	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
15	c4i0xA_	Alignment		77.1	24	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
16	c2kg7B_	Alignment		73.9	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
17	c3jywF_	Alignment		72.6	41	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
18	c4i0xJ_	Alignment		72.0	22	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
19	c4yshA_	Alignment		53.2	10	PDB header: oxidoreductase Chain: A: PDB Molecule: glycine oxidase; PDBTitle: crystal structure of glycine oxidase from geobacillus kaustophilus
20	c4kviA_	Alignment		53.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: fatty acid alpha-oxidase; PDBTitle: crystal structure of oryza sativa fatty acid alpha-dioxygenase with2 hydrogen peroxide
21	c2kg7A_	Alignment	not modelled	52.0	38	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
22	c3h6pB_	Alignment	not modelled	45.0	35	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: esat-6 like protein esxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
23	c6ml3A_	Alignment	not modelled	43.8	17	PDB header: transcription/dna Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 24; PDBTitle: zbtb24 zinc fingers 4-8 with 19+1mer dna oligonucleotide (sequence 2)
24	c5jydA_	Alignment	not modelled	41.4	36	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a putative short chain dehydrogenase from2 burkholderia cenocepacia
25	d1p4ea2	Alignment	not modelled	40.6	31	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
26	c4hhsA_	Alignment	not modelled	38.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-dioxygenase; PDBTitle: crystal structure of fatty acid alpha-dioxygenase (arabidopsis2 thaliana)
27	c2mdwA_	Alignment	not modelled	37.8	43	PDB header: de novo protein Chain: A: PDB Molecule: designed protein; PDBTitle: nmr structure of a strand-swapped dimer of the ww domain
						PDB header: lyase Chain: C: PDB Molecule: pcrqlx protein;

28	c5xqgC_	Alignment	not modelled	37.8	22	PDBTitle: crystal structure of a pl 26 exo-rhamnogalacturonan lyase from <i>penicillium chrysogenum</i> complexed with unsaturated galacturonosyl3 rhamnose PDB header: transcription/hydrolase Chain: A: PDB Molecule: maltose-binding periplasmic protein, homeobox protein six1 PDBTitle: crystal structure of mbp-fused human six1 bound to human <i>eya2</i> <i>eya2</i> domain 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 PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein ph0499; PDBTitle: crystal structure of diacetylchitobiose deacetylase from <i>pyrococcus2 horikoshii</i>
29	c4egcA_	Alignment	not modelled	37.5	31	PDB header: transferase Chain: A: PDB Molecule: non-structural protein 5; PDBTitle: structure of the methyltransferase domain from modoc virus,2 a flavivirus with no known vector (nkV)
30	c5nxhB_	Alignment	not modelled	35.4	12	PDB header: transferase Chain: B: PDB Molecule: cytosine-specific methyltransferase; PDBTitle: crystal structure of putative dna cytosine methylase from <i>shigella2 flexneri 2a str. 2457t</i>
31	c3we7A_	Alignment	not modelled	35.2	16	PDB header: transferase Chain: B: PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glcnaC2 transferase homolog: insight into molecular control of3 intracellular glycosylation
32	c2wa1A_	Alignment	not modelled	35.1	24	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
33	c3lx6B_	Alignment	not modelled	34.2	11	PDB header: dna binding protein/recombination/dna Chain: B: PDB Molecule: recombinase flp protein; PDBTitle: flpe w330f mutant-dna holliday junction complex
34	c2vsnB_	Alignment	not modelled	32.6	16	PDB header: antimicrobial protein Chain: A: PDB Molecule: antimicrobial peptide ecamp1; PDBTitle: helical hairpin structure of a novel antimicrobial peptide ecamp1 from2 seeds of barnyard grass (<i>echinocloa crus-galli</i>)
35	d2pgga1	Alignment	not modelled	32.5	23	PDB header: dna binding protein/protein binding Chain: C: PDB Molecule: fanconi anemia group m protein; PDBTitle: the crystal structure of fancm bound mhF complex
36	c1p4eB_	Alignment	not modelled	32.2	31	PDB header: viral protein Chain: A: PDB Molecule: polyhedrin; PDBTitle: crystal structure of operophtera brumata cpv19 polyhedra
37	c2l2rA_	Alignment	not modelled	31.9	41	PDB header: antitumor protein Chain: A: PDB Molecule: p19 arf protein; PDBTitle: solution structure of the n-terminal 37 amino acids of the2 mouse arf tumor suppressor protein
38	c4drbC_	Alignment	not modelled	31.5	17	PDB header: cell cycle/signaling protein Chain: F: PDB Molecule: kinesin-like protein kif23; PDBTitle: the crystal structure of arf6-mklp1 (mitotic kinesin-like protein 1)2 complex
39	c5a99A_	Alignment	not modelled	31.2	23	PDB header: hydrolase Chain: B: PDB Molecule: lmbE-related protein; PDBTitle: crystal structure of the putative deacetylase bc1534 from <i>bacillus2 cereus</i>
40	c1hn3A_	Alignment	not modelled	30.9	46	PDB header: oxidoreductase Chain: C: PDB Molecule: adenylsulfate reductase, subunit a; PDBTitle: adenosine 5'-phosphosulfate reductase in complex with substrate
41	c3vxfF_	Alignment	not modelled	28.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: adenylsulfate reductase; PDBTitle: crystal structure of adenylsulfate reductase from2 <i>desulfovibrio gigas</i>
42	c2ixdB_	Alignment	not modelled	27.1	10	PDB header: transferase Chain: G: PDB Molecule: drfam20c1; PDBTitle: the structure of drfam20c1
43	c2fjaC_	Alignment	not modelled	27.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (prostaglandin h2 synthase-2); PDBTitle: crystal structure of a mixture of arachidonic acid and prostaglandin2 bound to the cyclooxygenase active site of cox-2: prostaglandin3 structure
44	c3gyxA_	Alignment	not modelled	26.9	19	PDB header: oxidoreductase Chain: D: PDB Molecule: cyclooxygenase-2; PDBTitle: cyclooxygenase-2 (prostaglandin synthase-2) complexed with a non-2 selective inhibitor, flurbiprofen
45	c5yh0G_	Alignment	not modelled	26.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: lactoperoxidase; PDBTitle: crystal structure of buffalo lactoperoxidase at 2.75a resolution
46	c1ddxA_	Alignment	not modelled	26.0	26	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
47	c3pghD_	Alignment	not modelled	25.6	23	PDB header: oxidoreductase Chain: D: PDB Molecule: cyclooxygenase-2; PDBTitle: cyclooxygenase-2 (prostaglandin synthase-2) complexed with a non-2 selective inhibitor, flurbiprofen
48	c2gjmA_	Alignment	not modelled	25.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: lactoperoxidase; PDBTitle: crystal structure of buffalo lactoperoxidase at 2.75a resolution
49	d1uila_	Alignment	not modelled	25.4	24	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Myeloperoxidase-like
50	c6qfbB_	Alignment	not modelled	24.6	45	PDB header: lyase Chain: B: PDB Molecule: atp-citrate synthase; PDBTitle: structure of the human atp citrate lyase holoenzyme in complex with2 citrate, coenzyme a and mg.adp
51	d1cvua1	Alignment	not modelled	23.9	23	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
52	d1jnra1	Alignment	not modelled	23.5	22	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain PDB header: dna binding protein/dna

53	c6e93A_	Alignment	not modelled	23.2	14	Chain: A; PDB Molecule: zinc finger and btb domain-containing protein 38; PDBTitle: crystal structure of zbttb38 c-terminal zinc fingers 6-9 in complex2 with methylated dna
54	c1bkvA_	Alignment	not modelled	22.5	38	PDB header: structural protein Chain: A; PDB Molecule: t3-785; PDBTitle: collagen
55	c2oyuP_	Alignment	not modelled	22.4	18	PDB header: oxidoreductase Chain: P; PDB Molecule: prostaglandin g/h synthase 1; PDBTitle: indomethacin-(s)-alpha-ethyl-ethanolamide bound to cyclooxygenase-1
56	d1c25a_	Alignment	not modelled	22.1	24	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
57	c5lc5F_	Alignment	not modelled	21.9	21	PDB header: oxidoreductase Chain: F; PDB Molecule: nahd dehydrogenase [ubiquinone] flavoprotein 1, PDBTitle: structure of mammalian respiratory complex i, class2
58	c5wvmA_	Alignment	not modelled	21.9	26	PDB header: sugar binding protein Chain: A; PDB Molecule: maltose-binding periplasmic protein,two-component system PDBTitle: crystal structure of baes cocrystallized with 2 mm indole
59	c1bkvB_	Alignment	not modelled	21.3	38	PDB header: structural protein Chain: B; PDB Molecule: t3-785; PDBTitle: collagen
60	c1bkvC_	Alignment	not modelled	21.3	38	PDB header: structural protein Chain: C; PDB Molecule: t3-785; PDBTitle: collagen
61	c3lhlA_	Alignment	not modelled	21.1	19	PDB header: hydrolase Chain: A; PDB Molecule: putative agmatinase; PDBTitle: crystal structure of a putative agmatinase from clostridium difficile
62	d1uana_	Alignment	not modelled	20.5	15	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
63	d1pq3a_	Alignment	not modelled	20.3	10	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
64	c2vfiA_	Alignment	not modelled	20.2	17	PDB header: hydrolase Chain: A; PDB Molecule: tumor necrosis factor; PDBTitle: structure of the a20 ovarian tumour (otu) domain
65	c5cgzA_	Alignment	not modelled	20.1	16	PDB header: lyase Chain: A; PDB Molecule: 4-oxalmesaconate hydratase; PDBTitle: crystal structure of galb, the 4-carboxy-2-hydroxymuconate hydratase,2 from pseudomonas putida kt2440
66	c3ahrA_	Alignment	not modelled	20.0	25	PDB header: oxidoreductase Chain: A; PDB Molecule: ero1-like protein alpha; PDBTitle: inactive human ero1
67	c5oejB_	Alignment	not modelled	19.6	19	PDB header: transcription Chain: B; PDB Molecule: tra1 subunit within the chromatin modifying complex saga; PDBTitle: structure of tra1 subunit within the chromatin modifying complex saga
68	c3bkhA_	Alignment	not modelled	19.5	29	PDB header: hydrolase Chain: A; PDB Molecule: lytic transglycosylase; PDBTitle: crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
69	c5gxyA_	Alignment	not modelled	19.2	23	PDB header: hydrolase Chain: A; PDB Molecule: glucanase; PDBTitle: crystal structure of endoglucanase celq from clostridium thermocellum2 complexed with cellobiose and tris
70	c1ryiB_	Alignment	not modelled	18.6	7	PDB header: oxidoreductase Chain: B; PDB Molecule: glycine oxidase; PDBTitle: structure of glycine oxidase with bound inhibitor glycolate
71	c5eduB_	Alignment	not modelled	18.6	20	PDB header: hydrolase/hydrolase inhibitor Chain: B; PDB Molecule: maltose-binding periplasmic protein, histone deacetylase 6 PDBTitle: crystal structure of human histone deacetylase 6 catalytic domain 2 in2 complex with trichostatin a
72	d3fapb_	Alignment	not modelled	18.0	19	Fold: Four-helical up-and-down bundle Superfamily: FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP) Family: FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP)
73	c5frgA_	Alignment	not modelled	17.9	50	PDB header: protein binding Chain: A; PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1
74	c5xomB_	Alignment	not modelled	17.3	26	PDB header: transferase Chain: B; PDB Molecule: glycosaminoglycan xylosylkinase; PDBTitle: hydra fam20
75	c2xn1B_	Alignment	not modelled	17.2	20	PDB header: hydrolase Chain: B; PDB Molecule: alpha-galactosidase; PDBTitle: structure of alpha-galactosidase from lactobacillus acidophilus ncfm2 with tris
76	c5t1dC_	Alignment	not modelled	17.1	10	PDB header: viral protein Chain: C; PDB Molecule: glycoprotein 42; PDBTitle: crystal structure of ebv ghgl/gp42/e1d1 complex
77	c2dmiA_	Alignment	not modelled	16.8	13	PDB header: transcription Chain: A; PDB Molecule: teashirt homolog 3; PDBTitle: solution structure of the first and the second zf-c2h2 like2 domains of human teashirt homolog 3
78	c2eqfA_	Alignment	not modelled	16.7	44	PDB header: hydrolase Chain: A; PDB Molecule: tumor necrosis factor, alpha-induced protein 3; PDBTitle: solution structure of the 7th a20-type zinc finger domain2

						from human tumor necrosis factor, alpha-induced protein3
79	c4rqoB_	Alignment	not modelled	16.6	32	PDB header: lyase Chain: B: PDB Molecule: l-serine dehydratase; PDBTitle: crystal structure of l-serine dehydratase from legionella pneumophila
80	c5meeB_	Alignment	not modelled	16.5	33	PDB header: oxidoreductase Chain: B: PDB Molecule: arachidonate 15-lipoxygenase; PDBTitle: cyanothece lipoxygenase 2 (csplox2) variant - I304v
81	c5ojsT_	Alignment	not modelled	16.4	20	PDB header: transcription Chain: T: PDB Molecule: transcription-associated protein 1; PDBTitle: cryo-em structure of the saga and nua4 coactivator subunit tra1
82	c2k42B_	Alignment	not modelled	16.4	47	PDB header: signaling protein Chain: B: PDB Molecule: espfu; PDBTitle: solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehec effector
83	c3elyA_	Alignment	not modelled	16.4	67	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: wesselsbron virus methyltransferase in complex with adohcy
84	c1pggB_	Alignment	not modelled	16.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: prostaglandin h2 synthase-1; PDBTitle: prostaglandin h2 synthase-1 complexed with 1-(4-iodobenzoyl)-5-2 methoxy-2-methylindole-3-acetic acid (iodoindomethacin), trans model
85	c1ht8B_	Alignment	not modelled	16.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: prostaglandin h2 synthase-1; PDBTitle: the 2.7 angstrom resolution model of ovine cox-1 complexed with2 alclofenac
86	c3kfvA_	Alignment	not modelled	16.0	19	PDB header: cell adhesion Chain: A: PDB Molecule: tight junction protein zo-3; PDBTitle: crystal structure of the sh3-kinase fragment of tight junction protein2 3 (tjp3) in apo-form
87	c3mmrA_	Alignment	not modelled	15.9	12	PDB header: hydrolase Chain: A: PDB Molecule: arginase; PDBTitle: structure of plasmodium falciparum arginase in complex with abh
88	d2nn6g2	Alignment	not modelled	15.8	67	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
89	d1t2a_	Alignment	not modelled	15.8	29	Fold: 5-bladed beta-propeller Superfamily: Tachylectin-2 Family: Tachylectin-2
90	c3c7tB_	Alignment	not modelled	15.8	25	PDB header: hydrolase Chain: B: PDB Molecule: ecdysteroid-phosphate phosphatase; PDBTitle: crystal structure of the ecdysone phosphate phosphatase, eppase, from2 bombix mori in complex with tungstate
91	c2oxtC_	Alignment	not modelled	15.8	67	PDB header: viral protein Chain: C: PDB Molecule: nucleoside-2'-o-methyltransferase; PDBTitle: crystal structure of meaban virus nucleoside-2'-o-2 methyltransferase
92	d2awna1	Alignment	not modelled	15.8	38	Fold: OB-fold Superfamily: MOP-like Family: ABC-transporter additional domain
93	c1vi7A_	Alignment	not modelled	15.8	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yigz; PDBTitle: crystal structure of an hypothetical protein
94	d1ppjd1	Alignment	not modelled	15.7	30	Fold: Cytochrome c Superfamily: Cytochrome c Family: Cytochrome bc1 domain
95	c6elsA_	Alignment	not modelled	15.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: polyphenol oxidase, chloroplastic; PDBTitle: structure of latent apple tyrosinase (mdppo1)
96	c4fddB_	Alignment	not modelled	15.5	43	PDB header: transport protein Chain: B: PDB Molecule: rna-binding protein fus; PDBTitle: crystal structure of kap beta2-py-nls
97	c4fq3B_	Alignment	not modelled	15.5	43	PDB header: protein binding Chain: B: PDB Molecule: fusion (involved in t(12;16) in malignant liposarcoma); PDBTitle: crystal structure of transportin/fus-nls
98	c5yvvhB_	Alignment	not modelled	15.5	43	PDB header: protein transport/rna binding protein Chain: B: PDB Molecule: rna-binding protein fus; PDBTitle: crystal structure of karyopherin beta2 in complex with fus(371-526)
99	c5yviB_	Alignment	not modelled	15.5	43	PDB header: protein transport/rna binding protein Chain: B: PDB Molecule: rna-binding protein fus; PDBTitle: crystal structure of karyopherin beta2 in complex with fus(456-526)