






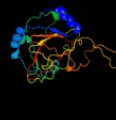








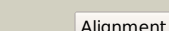
















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0193c_(-)_224722_226569
Date	Tue Jul 23 14:50:24 BST 2019
Unique Job ID	c4af6eedca89a72a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5erID_	 Alignment		98.8	19	PDB header: isomerase Chain: D; PDB Molecule: snon, snon; PDBTitle: crystal structure of the epimerase snon in complex with ni2+, 2 succinate and nogalamycin ro
2	c5ncjB_	 Alignment		98.6	10	PDB header: oxidoreductase Chain: B; PDB Molecule: leucine hydroxylase; PDBTitle: grie in complex with manganese, succinate and (2s,4r)-5-hydroxyleucine
3	c4naoA_	 Alignment		97.8	16	PDB header: oxidoreductase Chain: A; PDB Molecule: putative oxygenase; PDBTitle: crystal structure of eash
4	c5m0tA_	 Alignment		97.7	17	PDB header: oxidoreductase Chain: A; PDB Molecule: alpha-ketoglutarate-dependent non-heme iron oxygenase eash; PDBTitle: alpha-ketoglutarate-dependent non-heme iron oxygenase eash
5	c5epaE_	 Alignment		97.6	18	PDB header: lyase Chain: E; PDB Molecule: snok; PDBTitle: crystal structure of non-heme alpha ketoglutarate dependent 2 carbocyclase snok from nogalamycin biosynthesis
6	c4mhuB_	 Alignment		97.6	14	PDB header: oxidoreductase Chain: B; PDB Molecule: ectoine hydroxylase; PDBTitle: crystal structure of ectd from s. alaskensis with bound fe
7	c5yboA_	 Alignment		97.6	18	PDB header: oxidoreductase Chain: A; PDB Molecule: prha; PDBTitle: fe(ii)/(alpha)ketoglutarate-dependent dioxygenase prha in complex with 2 preaustinoid a1
8	c3emrA_	 Alignment		97.5	13	PDB header: oxidoreductase Chain: A; PDB Molecule: ectd; PDBTitle: crystal structure analysis of the ectoine hydroxylase ectd from 2 salibacillus salexigens
9	c4zonB_	 Alignment		97.5	19	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: B; PDB Molecule: verruculogen synthase; PDBTitle: structure of ftmxo1 with fumitremorgen b complex
10	c2opwA_	 Alignment		97.4	15	PDB header: oxidoreductase Chain: A; PDB Molecule: phyhd1 protein; PDBTitle: crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo)
11	c6ec3C_	 Alignment		97.3	21	PDB header: transferase, oxidoreductase Chain: C; PDB Molecule: methyltransferase domain-containing protein; PDBTitle: crystal structure of evdmo1

12	c4xc9B_	Alignment		97.2	18	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidase/hydroxylase; PDBTitle: crystal structure of apo hygX from streptomyces hygroscopicus
13	d2a1xa1	Alignment		97.2	16	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: PhyH-like
14	c2rdsA_	Alignment		97.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxypentalenic acid 11-beta hydroxylase; Fe(II)/alpha- PDBTitle: crystal structure of pTlh with Fe(II)/alpha-ketoglutarate-dependent dioxygenase and ent-1-2 deoxypentalenic acid bound
15	c5zm4B_	Alignment		97.1	14	PDB header: oxidoreductase Chain: B: PDB Molecule: dioxygenase and a; PDBTitle: Fe(II)/alpha-ketoglutarate-dependent dioxygenase and a with 2 preaniloid c
16	c4xabA_	Alignment		97.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: evdo2; PDBTitle: crystal structure of evdo2 from micromonospora carbonacea var.2 aurantiaca
17	c5daqA_	Alignment		97.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: phytanoyl-coa dioxygenase family protein (afu_orthologue PDBTitle: Fe(II)/alpha-ketoglutarate-dependent dioxygenase asqj in complex with 2 4-methoxycycloptin
18	c3qjbA_	Alignment		97.0	10	PDB header: biosynthetic protein Chain: A: PDB Molecule: cytc3; PDBTitle: cytc3 with Fe(II) and alpha-ketoglutarate
19	c4xaaA_	Alignment		97.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxygenase; PDBTitle: crystal structure of avio1 from streptomyces viridochromogenes tue57
20	c4xbzB_	Alignment		96.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: evdo1; PDBTitle: crystal structure of evdo1 from micromonospora carbonacea var.2 aurantiaca
21	d2fcta1	Alignment	not modelled	96.8	12	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: PhyH-like
22	c3nnlB_	Alignment	not modelled	82.6	14	PDB header: biosynthetic protein Chain: B: PDB Molecule: cura; PDBTitle: halogenase domain from cura module (crystal form iii)
23	c2lvIA_	Alignment	not modelled	59.6	52	PDB header: lantibiotic-binding-protein Chain: A: PDB Molecule: spai; PDBTitle: nmr structure the lantibiotic immunity protein spai
24	c6h3cC_	Alignment	not modelled	50.5	18	PDB header: signaling protein Chain: C: PDB Molecule: brisc and brca1-a complex member 2; PDBTitle: cryo-em structure of the brisc complex bound to shmt2
25	c1bvvyF_	Alignment	not modelled	45.9	15	PDB header: oxidoreductase Chain: F: PDB Molecule: protein (cytochrome p450 bm-3); PDBTitle: complex of the heme and fmN-binding domains of the2 cytochrome p450(bm-3)
26	d1bvvyf_	Alignment	not modelled	45.9	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
27	d1ueka2	Alignment	not modelled	45.2	14	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: 4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE
28	c3iaxB_	Alignment	not modelled	44.4	60	PDB header: protein transport Chain: B: PDB Molecule: colicin-a; PDBTitle: the crystal structure of the tolB box of colicin a in complex with 2 tolB reveals important differences in the recruitment of the common3 tolB translocation portal used by group a colicins
						PDB header: electron transport

29	c2m6rA	Alignment	not modelled	42.6	9	Chain: A: PDB Molecule: flavodoxin; PDBTitle: apo_yqca
30	c4h2dB	Alignment	not modelled	42.1	23	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-dependent diflavin oxidoreductase 1; PDBTitle: crystal structure of ndor1
31	c4mndA	Alignment	not modelled	37.4	22	PDB header: transferase Chain: A: PDB Molecule: ctp l-myo-inositol-1-phosphate cytidyltransferase/cdp-l- PDBTitle: crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
32	c4oxxA	Alignment	not modelled	33.1	21	PDB header: electron transport Chain: A: PDB Molecule: cindoxin; PDBTitle: crystal structure of cindoxin, surface entropy reduction mutant
33	c1ex1A	Alignment	not modelled	32.7	19	PDB header: hydrolase Chain: A: PDB Molecule: protein (beta-d-glucan exohydrolase isoenzyme exo1); PDBTitle: beta-d-glucan exohydrolase from barley
34	d1ykgA1	Alignment	not modelled	31.3	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
35	c1t98B	Alignment	not modelled	30.1	21	PDB header: cell cycle Chain: B: PDB Molecule: chromosome partition protein mukf; PDBTitle: crystal structure of mukf(1-287)
36	c3re2A	Alignment	not modelled	30.0	25	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
37	c3u88B	Alignment	not modelled	29.8	23	PDB header: transcription Chain: B: PDB Molecule: menin; PDBTitle: crystal structure of human menin in complex with mll1 and ledgf
38	c4gq6A	Alignment	not modelled	28.3	23	PDB header: transcription/transcription inhibitor Chain: A: PDB Molecule: menin; PDBTitle: human menin in complex with mll peptide
39	d1rlja	Alignment	not modelled	27.3	21	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavoprotein NrdI
40	d2azeb1	Alignment	not modelled	24.8	18	Fold: E2F-DP heterodimerization region Superfamily: E2F-DP heterodimerization region Family: E2F dimerization segment
41	c4kkkA	Alignment	not modelled	24.5	21	PDB header: hydrolase Chain: A: PDB Molecule: exoglucanase s; PDBTitle: complex structure of catalytic domain of clostridium cellulovorans2 exgs and cellotetraose
42	c5d50E	Alignment	not modelled	23.9	18	PDB header: dna binding protein Chain: E: PDB Molecule: anti-repressor protein; PDBTitle: crystal structure of rep-ant complex from salmonella-temperate phage
43	c2z4tA	Alignment	not modelled	20.8	13	PDB header: transferase Chain: A: PDB Molecule: beta-galactoside alpha-2,6-sialyltransferase; PDBTitle: crystal structure of vibronaceae photobacterium sp. jt-ish-224 2,6-2 sialyltransferase in a ternary complex with donor product cmp and3 acceptor substrate lactose
44	d1ja1a2	Alignment	not modelled	20.4	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
45	c2a8vA	Alignment	not modelled	20.4	17	PDB header: protein/rna Chain: A: PDB Molecule: rna binding domain of rho transcription PDBTitle: rho transcription termination factor/rna complex
46	c6r8fE	Alignment	not modelled	20.3	22	PDB header: signaling protein Chain: E: PDB Molecule: brisc and brca1-a complex member 2,brcc45 (bre, brisc and PDBTitle: cryo-em structure of the human brisc-shmt2 complex
47	c6r8fG	Alignment	not modelled	20.3	22	PDB header: signaling protein Chain: G: PDB Molecule: brisc and brca1-a complex member 2,brcc45 (bre, brisc and PDBTitle: cryo-em structure of the human brisc-shmt2 complex
48	d1w7pd2	Alignment	not modelled	19.7	36	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
49	c5ulmB	Alignment	not modelled	19.5	19	PDB header: transferase Chain: B: PDB Molecule: mitogen-activated protein kinase kinase kinase 5; PDBTitle: structure of the ask1 central regulatory region
50	c4r84B	Alignment	not modelled	19.2	13	PDB header: transferase Chain: B: PDB Molecule: sialyltransferase 0160; PDBTitle: crystal structure of sialyltransferase from photobacterium damsela2 with cmp-3f(a)neu5ac bound
51	c5b3kA	Alignment	not modelled	18.7	15	PDB header: electron transport Chain: A: PDB Molecule: uncharacterized protein pa3435; PDBTitle: c101a mutant of flavodoxin from pseudomonas aeruginosa
52	c4nf9A	Alignment	not modelled	18.1	22	PDB header: cell cycle Chain: A: PDB Molecule: protein casc5; PDBTitle: structure of the knl1/nsl1 complex
53	d1x38a1	Alignment	not modelled	17.2	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: NagZ-like
54	c4d2kB	Alignment	not modelled	17.0	16	PDB header: apoptosis Chain: B: PDB Molecule: drep2; PDBTitle: crystal structure of drep2 cide domain
						Fold: Histone-fold

55	d1wwja1	Alignment	not modelled	16.8	18	Superfamily: Histone-fold Family: Bacterial histone-fold protein
56	d1e52a	Alignment	not modelled	15.6	20	Fold: Long alpha-hairpin Superfamily: C-terminal UvrC-binding domain of UvrB Family: C-terminal UvrC-binding domain of UvrB
57	c6ekrA	Alignment	not modelled	15.5	21	PDB header: hydrolase Chain: A: PDB Molecule: type ii site-specific deoxyribonuclease; PDBTitle: crystal structure of type iip restriction endonuclease kpn2i
58	d1jr7a	Alignment	not modelled	15.0	18	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Gab protein (hypothetical protein YgaT)
59	c3u3iA	Alignment	not modelled	14.8	35	PDB header: rna binding protein Chain: A: PDB Molecule: nucleocapsid protein; PDBTitle: a rna binding protein from crimean-congo hemorrhagic fever virus
60	c3bq9A	Alignment	not modelled	14.7	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted rossmann fold nucleotide-binding domain- PDBTitle: crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
61	c6go1A	Alignment	not modelled	14.6	32	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase-like protein; PDBTitle: crystal structure of a bacillus anthracis peptidoglycan deacetylase
62	d1b1ca	Alignment	not modelled	14.3	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
63	c4ct7A	Alignment	not modelled	14.0	14	PDB header: transcription Chain: A: PDB Molecule: ccr4-not transcription complex subunit 1; PDBTitle: cnot9-cnot1 complex with bound tryptophan
64	c3o2iB	Alignment	not modelled	13.8	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of a functionally unknown protein from2 leptospirillum sp. group ii uba
65	c4iw3j	Alignment	not modelled	13.8	15	PDB header: metal binding protein/translation Chain: J: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a pseudomonas putida prolyl-4-hydroxylase (p4h)2 in complex with elongation factor tu (ef-tu)
66	c2hnbA	Alignment	not modelled	13.7	17	PDB header: electron transport Chain: A: PDB Molecule: protein mioc; PDBTitle: solution structure of a bacterial holo-flavodoxin
67	c3riuC	Alignment	not modelled	13.2	30	PDB header: hydrolase Chain: C: PDB Molecule: translin associated factor x, isoform b; PDBTitle: crystal structure of drosophila hexameric c3po formed by truncated2 translin and trax
68	c1bcrA	Alignment	not modelled	12.6	21	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: serine carboxypeptidase ii; PDBTitle: complex of the wheat serine carboxypeptidase, cpdw-ii, with the2 microbial peptide aldehyde inhibitor, antipain, and arginine at room3 temperature
69	c4j5iH	Alignment	not modelled	12.3	20	PDB header: oxidoreductase Chain: H: PDB Molecule: alpha-ketoglutarate-dependent taurine dioxygenase; PDBTitle: crystal structure of an alpha-ketoglutarate-dependent taurine2 dioxygenase from mycobacterium smegmatis
70	d1zpsa1	Alignment	not modelled	12.1	22	Fold: Hisl-like Superfamily: Hisl-like Family: Hisl-like
71	c3gr1A	Alignment	not modelled	11.9	17	PDB header: membrane protein Chain: A: PDB Molecule: protein prgh; PDBTitle: periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-392)
72	d1eexa	Alignment	not modelled	11.8	33	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: Diol dehydratase, alpha subunit
73	c2vcbA	Alignment	not modelled	11.7	21	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylglucosaminidase; PDBTitle: family 89 glycoside hydrolase from clostridium perfringens2 in complex with pugnac
74	c3cw4A	Alignment	not modelled	11.7	29	PDB header: transferase Chain: A: PDB Molecule: polymerase basic protein 2; PDBTitle: large c-terminal domain of influenza a virus rna-dependent polymerase2 pb2
75	c2g19A	Alignment	not modelled	11.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: egl nine homolog 1; PDBTitle: cellular oxygen sensing: crystal structure of hypoxia-inducible factor2 prolyl hydroxylase (phd2)
76	c3hmjB	Alignment	not modelled	11.6	33	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: saccharomyces cerevisiae fas type i
77	c2e2sA	Alignment	not modelled	11.6	44	PDB header: toxin Chain: A: PDB Molecule: agelenin; PDBTitle: solution structure of agelenin, an insecticidal peptide2 from the venom of agelena opulenta
78	c2vkzC	Alignment	not modelled	11.6	33	PDB header: transferase Chain: C: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
79	c5zt3A	Alignment	not modelled	11.5	27	PDB header: plant protein Chain: A: PDB Molecule: wa352; PDBTitle: crystal structure of wa352 from oryza sativa
80	c2hpcH	Alignment	not modelled	11.5	18	PDB header: blood clotting Chain: H: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of fragment d from human fibrinogen complexed with2 gly-pro-arg-pro-amide.

81	d2hlya1	Alignment	not modelled	11.4	25	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Atu2299-like
82	c5hwiA	Alignment	not modelled	11.3	37	PDB header: transferase Chain: A: PDB Molecule: glutathione-specific gamma-glutamylcyclotransferase; PDBTitle: crystal structure of selenomethionine labelled gamma glutamyl2 cyclotransferase specific to glutathione from yeast
83	c5tuvB	Alignment	not modelled	11.1	21	PDB header: transcription Chain: B: PDB Molecule: transcription factor e2f5; PDBTitle: crystal structure of the e2f5-dp1-p107 ternary complex
84	c3cgxA	Alignment	not modelled	11.0	31	PDB header: transferase Chain: A: PDB Molecule: putative nucleotide-diphospho-sugar transferase; PDBTitle: crystal structure of putative nucleotide-diphospho-sugar transferase2 (yp_389115.1) from desulfovibrio desulfuricans g20 at 1.90 a3 resolution
85	c3if4C	Alignment	not modelled	10.9	31	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: integron cassette protein hfx_cass5; PDBTitle: structure from the mobile metagenome of north west arm sewage outfall:2 integron cassette protein hfx_cass5
86	c6bmeB	Alignment	not modelled	10.9	15	PDB header: heme binding protein Chain: B: PDB Molecule: truncated hemoglobin 4; PDBTitle: crystal structure of chlamydomonas reinhardtii thb4
87	c3bvhe	Alignment	not modelled	10.9	16	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of recombinant gammad364a fibrinogen fragment d with2 the peptide ligand gly-pro-arg-pro-amide
88	c2uv8C	Alignment	not modelled	10.7	33	PDB header: transferase Chain: C: PDB Molecule: fatty acid synthase subunit alpha (fas2); PDBTitle: crystal structure of yeast fatty acid synthase with stalled2 acyl carrier protein at 3.1 angstrom resolution
89	c3hr4C	Alignment	not modelled	10.7	22	PDB header: oxidoreductase/metal binding protein Chain: C: PDB Molecule: nitric oxide synthase, inducible; PDBTitle: human inos reductase and calmodulin complex
90	d1eysh2	Alignment	not modelled	10.6	17	Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region
91	c4az3A	Alignment	not modelled	10.4	24	PDB header: hydrolase Chain: A: PDB Molecule: lysosomal protective protein 32 kda chain; PDBTitle: crystal structure of cathepsin a, complexed with 15a
92	c5odvB	Alignment	not modelled	10.4	22	PDB header: virus Chain: B: PDB Molecule: coat protein; PDBTitle: structure of watermelon mosaic virus potyvirus.
93	d1wg8a1	Alignment	not modelled	10.4	24	Fold: SAM domain-like Superfamily: Putative methyltransferase TM0872, insert domain Family: Putative methyltransferase TM0872, insert domain
94	d1xbpg2	Alignment	not modelled	10.3	75	Fold: Ribosomal L11/L12e N-terminal domain Superfamily: Ribosomal L11/L12e N-terminal domain Family: Ribosomal L11/L12e N-terminal domain
95	d1mmsa2	Alignment	not modelled	10.3	75	Fold: Ribosomal L11/L12e N-terminal domain Superfamily: Ribosomal L11/L12e N-terminal domain Family: Ribosomal L11/L12e N-terminal domain
96	d1r31a1	Alignment	not modelled	10.3	30	Fold: Ferredoxin-like Superfamily: NAD-binding domain of HMG-CoA reductase Family: NAD-binding domain of HMG-CoA reductase
97	c4yokA	Alignment	not modelled	10.2	16	PDB header: unknown function Chain: A: PDB Molecule: putative flagellar protein flis; PDBTitle: crystal structure of a duf3823 family protein (parmer_04126) from2 parabacteroides merdae atcc 43184 at 1.80 a resolution
98	d2gpia1	Alignment	not modelled	10.2	26	Fold: Shew3726-like Superfamily: Shew3726-like Family: Shew3726-like
99	c2zwiA	Alignment	not modelled	10.0	20	PDB header: transferase Chain: A: PDB Molecule: alpha-/beta-galactoside alpha-2,3-sialyltransferase; PDBTitle: crystal structure of alpha/beta-galactoside alpha-2,3-2 sialyltransferase from a luminous marine bacterium, <i>photobacterium3 phosphoreum</i>