


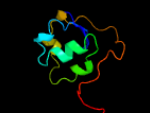
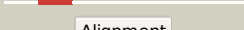

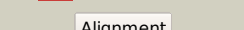

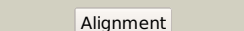







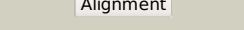
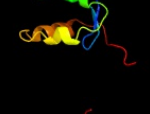
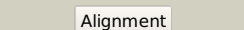







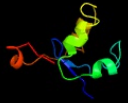






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1371 (-) _1543365_1544834
Date	Wed Jul 31 22:05:47 BST 2019
Unique Job ID	54a5e7edf17f3c28

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4zyoA_	 Alignment		99.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: acyl-coa desaturase; PDBTitle: crystal structure of human integral membrane stearyl-coa desaturase2 with substrate
2	clfcbA_	 Alignment		99.8	28	PDB header: oxidoreductase (ch-oh(d)-cytochrome(a)) Chain: A: PDB Molecule: flavocytochrome b2; PDBTitle: molecular structure of flavocytochrome b2 at 2.4 angstroms resolution
3	d1iccc_	 Alignment		99.8	25	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
4	d1kbia2	 Alignment		99.8	32	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
5	d1aqaa_	 Alignment		99.8	19	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
6	d1cyoa_	 Alignment		99.7	16	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
7	d1hkoa_	 Alignment		99.7	15	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
8	c3lf5B_	 Alignment		99.7	28	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome b5 reductase 4; PDBTitle: structure of human nadh cytochrome b5 oxidoreductase (ncb5or) b52 domain to 1.25a resolution
9	d1m2ia_	 Alignment		99.7	18	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
10	c4b8nC_	 Alignment		99.7	29	PDB header: electron transport Chain: C: PDB Molecule: cytochrome b5-host origin; PDBTitle: cytochrome b5 of ostreococcus tauri virus 2
11	d1do9a_	 Alignment		99.7	15	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5

12	c2ibjA	Alignment		99.7	17	PDB header: electron transport Chain: A: PDB Molecule: cytochrome b5; PDBTitle: structure of house fly cytochrome b5
13	d1soxa2	Alignment		99.7	20	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
14	d1lj0a	Alignment		99.7	24	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
15	d1euea	Alignment		99.7	25	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
16	d1axxa	Alignment		99.7	18	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
17	c2keoA	Alignment		99.7	12	PDB header: ligase Chain: A: PDB Molecule: probable e3 ubiquitin-protein ligase herc2; PDBTitle: solution nmr structure of human protein hs00059, cytochrome-b5-like2 domain of the herc2 e3 ligase. northeast structural genomics3 consortium (nesg) target ht98a
18	d1mj4a	Alignment		99.7	21	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
19	d1cxya	Alignment		99.7	33	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
20	c1x3xA	Alignment		99.6	25	PDB header: electron transport Chain: A: PDB Molecule: cytochrome b5; PDBTitle: crystal structure of cytochrome b5 from ascaris suum
21	c1soxB	Alignment	not modelled	99.5	21	PDB header: oxidoreductase Chain: B: PDB Molecule: sulfite oxidase; PDBTitle: sulfite oxidase from chicken liver
22	c4ymkA	Alignment	not modelled	99.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: acyl-coa desaturase 1; PDBTitle: crystal structure of stearoyl-coenzyme a desaturase 1
23	c6nzxA	Alignment	not modelled	99.3	22	PDB header: metal binding protein Chain: A: PDB Molecule: cytochrome b5; PDBTitle: hadesarchaea ynp_n21 cytochrome b5 domain protein (kuo41884.1)
24	c4x8yA	Alignment	not modelled	98.6	15	PDB header: membrane protein Chain: A: PDB Molecule: membrane-associated progesterone receptor component 1; PDBTitle: crystal structure of human pgrmc1 cytochrome b5-like domain
25	d1j03a	Alignment	not modelled	98.5	18	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Steroid-binding domain
26	d1t0ga	Alignment	not modelled	98.4	18	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Steroid-binding domain
27	c3frrA	Alignment	not modelled	87.3	17	PDB header: protein binding Chain: A: PDB Molecule: uncharacterized protein kiaa0174; PDBTitle: structure of human ist1(ntd) - (residues 1-189)(p21)
28	d1ho8a	Alignment	not modelled	61.5	14	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Regulatory subunit H of the V-type ATPase PDB header: protein transport, endocytosis

29	c3ggzC_	Alignment	not modelled	47.1	13	Chain: C; PDB Molecule: increased sodium tolerance protein 1; PDBTitle: crystal structure of s.cerevisiae ist1 n-terminal domain in complex2 with did2 mim motif
30	d1bdsa_	Alignment	not modelled	27.7	44	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
31	c1bdsA_	Alignment	not modelled	27.7	44	PDB header: anti-hypertensive, anti-viral protein Chain: A; PDB Molecule: bds-i; PDBTitle: determination of the three-dimensional solution structure of the2 antihypertensive and antiviral protein bds-i from the sea anemone3 anemonia sulcata. a study using nuclear magnetic resonance and hybrid4 distance geometry-dynamical simulated annealing
32	c2lufA_	Alignment	not modelled	24.2	25	PDB header: de novo protein Chain: A; PDB Molecule: retro trp-cage peptide; PDBTitle: retro trp-cage peptide
33	c5mtdD_	Alignment	not modelled	24.0	12	PDB header: chaperone Chain: D; PDB Molecule: secb-like chaperone rv1957; PDBTitle: mycobacterium tuberculosis rv1957 secb-like chaperone in complex with2 a chad peptide from rv1956 higa1 antitoxin
34	d1wpla_	Alignment	not modelled	23.6	28	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
35	c1is7F_	Alignment	not modelled	22.6	28	PDB header: hydrolase/protein binding Chain: F; PDB Molecule: gtp cyclohydrolase i; PDBTitle: crystal structure of rat gtpchi/gfrp stimulatory complex
36	c1wm9D_	Alignment	not modelled	21.6	22	PDB header: hydrolase Chain: D; PDB Molecule: gtp cyclohydrolase i; PDBTitle: structure of gtp cyclohydrolase i from thermus thermophilus hb8
37	d1wura1	Alignment	not modelled	21.6	22	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
38	d1a8ra_	Alignment	not modelled	20.6	20	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
39	c3utmC_	Alignment	not modelled	19.9	57	PDB header: transferase/signaling protein Chain: C; PDB Molecule: axin-1; PDBTitle: crystal structure of a mouse tankyrase-axin complex
40	c4uqfB_	Alignment	not modelled	19.3	26	PDB header: hydrolase Chain: B; PDB Molecule: gtp cyclohydrolase 1; PDBTitle: crystal structure of listeria monocytogenes gtp cyclohydrolase i
41	c5eybB_	Alignment	not modelled	18.4	20	PDB header: dna binding protein/dna Chain: B; PDB Molecule: dna-binding protein reb1; PDBTitle: x-ray structure of reb1-ter complex
42	c5zojE_	Alignment	not modelled	18.0	10	PDB header: dna binding protein Chain: E; PDB Molecule: inner nuclear membrane protein man1; PDBTitle: crystal structure of human smad2-man1 complex
43	c3ieiD_	Alignment	not modelled	17.7	12	PDB header: transferase Chain: D; PDB Molecule: leucine carboxyl methyltransferase 1; PDBTitle: crystal structure of human leucine carboxylmethyltransferase-1 in2 complex with s-adenosyl homocysteine
44	c2ckcA_	Alignment	not modelled	17.5	55	PDB header: hydrolase Chain: A; PDB Molecule: chromodomain-helicase-dna-binding protein 7; PDBTitle: solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
45	d2ckca1	Alignment	not modelled	17.5	55	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
46	d2v0ea1	Alignment	not modelled	16.1	55	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
47	c3mntA_	Alignment	not modelled	15.7	12	PDB header: transferase Chain: A; PDB Molecule: leucine carboxyl methyltransferase 1; PDBTitle: crystal structure of human leucine carboxyl methyltransferase 1
48	d2ckaa1	Alignment	not modelled	15.7	36	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
49	c2ckaA_	Alignment	not modelled	15.7	36	PDB header: hydrolase Chain: A; PDB Molecule: chromodomain-helicase-dna-binding protein 8; PDBTitle: solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
50	c6edjD_	Alignment	not modelled	15.6	100	PDB header: virus like particle Chain: D; PDB Molecule: external core antigen; PDBTitle: cryo-em structure of woodchuck hepatitis virus capsid
51	c3bzjA_	Alignment	not modelled	15.1	27	PDB header: hydrolase Chain: A; PDB Molecule: uv endonuclease; PDBTitle: uvde k229l
52	c3dfdA_	Alignment	not modelled	14.7	31	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: protein yqbn; PDBTitle: crystal structure of the protein yqbn. northeast structural2 genomics consortium target sr445.
53	c2daeA_	Alignment	not modelled	14.3	18	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: kiiaa0733 protein; PDBTitle: solution structure of the n-terminal cue domain in the2 human mitogen-activated protein kinase kinase kinase 73 interacting

					protein 2 (map3k7ip2)
54	c3qi7A_	Alignment	not modelled	13.3	14 PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
55	d2dl6a1	Alignment	not modelled	13.2	36 Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
56	d1jmta_	Alignment	not modelled	12.6	29 Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Splicing factor U2AF subunits
57	c1lj2C_	Alignment	not modelled	12.2	40 PDB header: viral protein/ translation Chain: C: PDB Molecule: eukaryotic protein synthesis initiation factor; PDBTitle: recognition of eif4g by rotavirus nsp3 reveals a basis for2 mrna circularization
58	c2j4dA_	Alignment	not modelled	11.4	26 PDB header: dna binding protein Chain: A: PDB Molecule: cryptochrome dash; PDBTitle: cryptochrome 3 from arabidopsis thaliana
59	c1qqp4_	Alignment	not modelled	11.0	20 PDB header: virus Chain: 4: PDB Molecule: protein (genome polyprotein); PDBTitle: foot-and-mouth disease virus/ oligosaccharide receptor complex.
60	c1lj2D_	Alignment	not modelled	10.7	40 PDB header: viral protein/ translation Chain: D: PDB Molecule: eukaryotic protein synthesis initiation factor; PDBTitle: recognition of eif4g by rotavirus nsp3 reveals a basis for2 mrna circularization
61	d1njra_	Alignment	not modelled	10.2	33 Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain
62	c6hxiD_	Alignment	not modelled	10.0	15 PDB header: lyase Chain: D: PDB Molecule: succinyl-coa ligase (adp-forming) subunit alpha; PDBTitle: structure of atp citrate lyase from methanotrix soehngenii in complex2 with citrate and coenzyme a
63	c4d0uD_	Alignment	not modelled	9.7	29 PDB header: viral protein Chain: D: PDB Molecule: fiber protein; PDBTitle: crystal structure of the fiber head domain of the adenovirus snake2 adenovirus 1, selenomethionine-derivative
64	d1ii2a2	Alignment	not modelled	9.2	25 Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain
65	c5zt3A_	Alignment	not modelled	9.1	21 PDB header: plant protein Chain: A: PDB Molecule: wa352; PDBTitle: crystal structure of wa352 from oryza sativa
66	d2dita1	Alignment	not modelled	8.9	31 Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
67	d1ouoa_	Alignment	not modelled	8.5	29 Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: Endonuclease I
68	c5bs1C_	Alignment	not modelled	7.7	24 PDB header: chaperone Chain: C: PDB Molecule: crrbcx-iiia; PDBTitle: crystal structure of rbcx-iiia from chlamydomonas reinhardtii
69	c2inuC_	Alignment	not modelled	7.4	40 PDB header: lyase Chain: C: PDB Molecule: insulin fructotransferase; PDBTitle: crystal structure of insulin fructotransferase in the absence of2 substrate
70	c3isrB_	Alignment	not modelled	7.1	13 PDB header: hydrolase Chain: B: PDB Molecule: transglutaminase-like enzymes, putative cysteine protease; PDBTitle: the crystal structure of a putative cysteine protease from cytophaga2 hutchinsonii to 1.9a
71	c5zlaD_	Alignment	not modelled	6.7	45 PDB header: hydrolase Chain: D: PDB Molecule: dfa-iiiase c387a mutant; PDBTitle: crystal structure of mutant c387a of dfa-iiiase from arthrobacter2 chlorophenicus a6 in complex with dfa-iii
72	c3kojA_	Alignment	not modelled	6.6	27 PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein ycf41; PDBTitle: crystal structure of the ssb domain of q5n255_synp6 protein from2 synechococcus sp. northeast structural genomics consortium target3 snr59a.
73	c3rnbB_	Alignment	not modelled	6.5	25 PDB header: protein binding Chain: B: PDB Molecule: dna mismatch repair protein mlh1; PDBTitle: crystal structure of mutl protein homolog 1 isoform 1 [homo sapiens]
74	d1owla2	Alignment	not modelled	6.5	20 Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
75	c4fmoA_	Alignment	not modelled	6.3	26 PDB header: hydrolase Chain: A: PDB Molecule: dna mismatch repair protein mlh1; PDBTitle: structure of the c-terminal domain of the saccharomyces cerevisiae2 mutl alpha (mlh1/pms1) heterodimer bound to a fragment of exo1
76	c3s2xB_	Alignment	not modelled	6.0	25 PDB header: transferase Chain: B: PDB Molecule: acetyl-coa synthase subunit alpha; PDBTitle: structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain
77	d1bi5a2	Alignment	not modelled	6.0	38 Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
78	d1u0ua2	Alignment	not modelled	6.0	31 Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like

79	c3l8dA_	Alignment	not modelled	5.9	0	PDB header: transferase Chain: A; PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyltransferase from bacillus thuringiensis
80	c3s6eB_	Alignment	not modelled	5.6	39	PDB header: rna binding protein Chain: B; PDB Molecule: rna-binding protein 39; PDBTitle: crystal structure of a rna binding motif protein 39 (rbm39) from mus2 musculus at 0.95 a resolution
81	c2l21A_	Alignment	not modelled	5.6	32	PDB header: transport protein Chain: A; PDB Molecule: cation-independent mannose-6-phosphate receptor; PDBTitle: chicken igf2r domain 11
82	d2v0fa1	Alignment	not modelled	5.6	36	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
83	c1pbyA_	Alignment	not modelled	5.6	29	PDB header: oxidoreductase Chain: A; PDB Molecule: quinoxemoprotein amine dehydrogenase 60 kda subunit; PDBTitle: structure of the phenylhydrazine adduct of the quinoxemoprotein amine2 dehydrogenase from paracoccus denitrificans at 1.7 a resolution
84	d1s6la2	Alignment	not modelled	5.4	42	Fold: NosL/MerB-like Superfamily: NosL/MerB-like Family: MerB-like
85	d2j07a2	Alignment	not modelled	5.3	23	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
86	c5jnoA_	Alignment	not modelled	5.3	15	PDB header: cell cycle Chain: A; PDB Molecule: ben domain-containing protein 3; PDBTitle: crystal structure of the bd1-ntpr complex from bend3 and pich
87	d1cwva5	Alignment	not modelled	5.3	22	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Invasin/intimin cell-adhesion fragment, C-terminal domain