



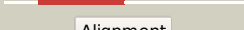











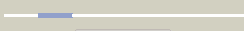


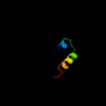

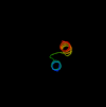


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0736 (-) _828143_828895
Date	Fri Jul 26 01:50:31 BST 2019
Unique Job ID	6238c17580a1d072

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hugJ_	 Alignment		99.6	100	PDB header: transcription/membrane protein Chain: J; PDB Molecule: probable conserved membrane protein; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rslA2 in complex with -35 promoter binding domain of sigI
2	c3vdoB_	 Alignment		99.4	19	PDB header: dna binding protein/protein binding Chain: B; PDB Molecule: anti-sigma-k factor rskA; PDBTitle: structure of extra-cytoplasmic function(ecf) sigma factor sigK in2 complex with its negative regulator rskA from mycobacterium3 tuberculosis
3	c2z2sD_	 Alignment		99.3	21	PDB header: transcription Chain: D; PDB Molecule: anti-sigma factor chrr, transcriptional activator chrr; PDBTitle: crystal structure of rhodobacter sphaeroides sigE in complex with the2 anti-sigma chrr
4	c5wuqD_	 Alignment		99.1	18	PDB header: metal binding protein Chain: D; PDB Molecule: anti-sigma-w factor rsiw; PDBTitle: crystal structure of sigW in complex with its anti-sigma rsiw, a zinc2 binding form
5	c5frhA_	 Alignment		98.8	13	PDB header: transcription Chain: A; PDB Molecule: anti-sigma factor rsra; PDBTitle: solution structure of oxidised rsra
6	c5camC_	 Alignment		91.4	16	PDB header: transcription Chain: C; PDB Molecule: pupr protein; PDBTitle: crystal structure of the cytoplasmic domain of the pseudomonas putida2 anti-sigma factor pupr (semet)
7	c6cp8B_	 Alignment		42.5	24	PDB header: toxin/antitoxin Chain: B; PDB Molecule: cdia; PDBTitle: contact-dependent growth inhibition toxin-immunity protein complex2 from from e. coli 3006
8	c4ehpB_	 Alignment		29.7	35	PDB header: cell adhesion Chain: B; PDB Molecule: catenin alpha-1; PDBTitle: crystal structure of human vinculin head domain (residues 1-252) in2 complex with alpha-catenin (residues 277-382)
9	d2ou3a1	 Alignment		26.5	9	Fold: TerB-like Superfamily: TerB-like Family: COG3793-like
10	c5ze4A_	 Alignment		25.8	26	PDB header: lyase Chain: A; PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the structure of holo- structure of dhad complex with [2fe-2s] cluster
11	c3im9A_	 Alignment		23.6	13	PDB header: transferase Chain: A; PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from staphylococcus aureus

12	c4jd9B_	Alignment		21.4	21	PDB header: protein binding Chain: B: PDB Molecule: 14.5 kda salivary protein; PDBTitle: contact pathway inhibitor from a sand fly
13	d1ryba_	Alignment		20.1	17	Fold: Phosphorylase/hydrolase-like Superfamily: Peptidyl-tRNA hydrolase-like Family: Peptidyl-tRNA hydrolase-like
14	c2jxuA_	Alignment		19.9	14	PDB header: unknown function Chain: A: PDB Molecule: terb; PDBTitle: nmr solution structure of kp-terb, a tellurite resistance2 protein from klebsiella pneumoniae
15	c4ynhA_	Alignment		18.9	19	PDB header: structural protein Chain: A: PDB Molecule: spindle assembly abnormal protein 5; PDBTitle: structure of the c. elegans sas-5 implico dimerization domain
16	c5oynB_	Alignment		18.3	11	PDB header: lyase Chain: B: PDB Molecule: dehydratase, ilvd/edd family; PDBTitle: crystal structure of d-xylonate dehydratase in holo-form
17	c2mjIA_	Alignment		18.0	25	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: solution structure of peptidyl-trna hyrolase from vibrio cholerae
18	c3isyA_	Alignment		17.7	11	PDB header: protein binding Chain: A: PDB Molecule: intracellular proteinase inhibitor; PDBTitle: crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
19	d1wjva1	Alignment		16.5	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: C2HC finger
20	c5j84A_	Alignment		15.9	19	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase; PDBTitle: crystal structure of l-arabinonate dehydratase in holo-form
21	c4n71A_	Alignment	not modelled	15.7	12	PDB header: oxidoreductase Chain: A: PDB Molecule: predicted hd phosphohydrolase phnz; PDBTitle: x-ray crystal structure of 2-amino-1-hydroxyethylphosphonate-bound2 phnz
22	c6iytA_	Alignment	not modelled	15.1	35	PDB header: transferase Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: crystal structure of the acyltransferase domain from second module 142 of salinomycin polyketide synthase
23	d1ejxb_	Alignment	not modelled	14.5	15	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
24	d1mlaa1	Alignment	not modelled	14.3	17	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
25	d1nm2a1	Alignment	not modelled	13.3	22	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
26	c3neaA_	Alignment	not modelled	13.2	20	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of peptidyl-trna hydrolase from francisella2 tularensis
27	d4ubpb_	Alignment	not modelled	12.7	5	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
28	d1z6na1	Alignment	not modelled	12.7	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
						Fold: Phosphorylase/hydrolase-like

29	d2ptha_	Alignment	not modelled	12.6	24	Superfamily: Peptidyl-tRNA hydrolase-like Family: Peptidyl-tRNA hydrolase-like
30	d2f8aa1	Alignment	not modelled	12.2	10	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
31	c5icuA_	Alignment	not modelled	12.1	12	PDB header: chaperone Chain: A: PDB Molecule: copc; PDBTitle: the crystal structure of copc from methylosinus trichosporium ob3b
32	c3tzzA_	Alignment	not modelled	11.9	23	PDB header: transferase Chain: A: PDB Molecule: polyketide synthase pks13; PDBTitle: crystal structure of a fragment containing the acyltransferase domain2 of pks13 from mycobacterium tuberculosis in the carboxypalmitoylated3 form at 2.5 a
33	c2n59A_	Alignment	not modelled	11.8	9	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein csgh; PDBTitle: solution structure of r. palustris csgh
34	d1or7c_	Alignment	not modelled	11.7	14	Fold: N-terminal, cytoplasmic domain of anti-sigmaE factor RseA Superfamily: N-terminal, cytoplasmic domain of anti-sigmaE factor RseA Family: N-terminal, cytoplasmic domain of anti-sigmaE factor RseA
35	c1or7C_	Alignment	not modelled	11.7	14	PDB header: transcription Chain: C: PDB Molecule: sigma-e factor negative regulatory protein; PDBTitle: crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
36	d1e9ya1	Alignment	not modelled	11.4	7	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
37	c4tr3A_	Alignment	not modelled	11.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: type iii iodothyronine deiodinase; PDBTitle: mouse iodothyronine deiodinase 3 catalytic core, semet-labeled active2 site mutant secys->cys
38	c4z42B_	Alignment	not modelled	11.2	11	PDB header: hydrolase Chain: B: PDB Molecule: urease subunit beta; PDBTitle: crystal structure of urease from yersinia enterocolitica
39	c2yreA_	Alignment	not modelled	11.2	38	PDB header: protein binding Chain: A: PDB Molecule: f-box only protein 30; PDBTitle: solution structure of the zinc finger domains (1-87) from2 human f-box only protein
40	c2jfkD_	Alignment	not modelled	11.1	19	PDB header: transferase Chain: D: PDB Molecule: fatty acid synthase; PDBTitle: structure of the mat domain of human fas with malonyl-coa
41	c6npaD_	Alignment	not modelled	11.0	20	PDB header: oxidoreductase Chain: D: PDB Molecule: tmbp, (r)-1-hydroxy-2-trimethylaminoethylphosphonate PDBTitle: x-ray crystal structure of tmbp, (r)-1-hydroxy-2-2 trimethylaminoethylphosphonate oxygenase, with (r)-1-hydroxy-2-3 trimethylaminoethylphosphonate
42	c6iyoA_	Alignment	not modelled	11.0	35	PDB header: transferase Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: crystal structure of the acyltransferase domain from the second module2 of the salinomycin polyketide synthase
43	c3rgiA_	Alignment	not modelled	10.9	10	PDB header: transferase Chain: A: PDB Molecule: disd protein; PDBTitle: trans-acting transferase from disorazole synthase
44	c5czcA_	Alignment	not modelled	10.6	33	PDB header: transferase Chain: A: PDB Molecule: malonyl-coa-[acyl-carrier-protein] transacylase; PDBTitle: the structure of vink
45	c2z2jA_	Alignment	not modelled	9.5	25	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of peptidyl-trna hydrolase from mycobacterium2 tuberculosis
46	d1o73a_	Alignment	not modelled	9.2	38	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
47	c3im8A_	Alignment	not modelled	8.9	21	PDB header: transferase Chain: A: PDB Molecule: malonyl acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from streptococcus pneumoniae
48	c6gc1A_	Alignment	not modelled	8.8	21	PDB header: unknown function Chain: A: PDB Molecule: nhl repeat-containing protein 2; PDBTitle: crystal structure of trx-like and nhl repeat containing domains of2 human nhlrc2
49	c2hh7A_	Alignment	not modelled	8.7	32	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein csor; PDBTitle: crystal structure of cu(i) bound csor from mycobacterium tuberculosis.
50	c4rr5A_	Alignment	not modelled	8.5	17	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: the crystal structure of synechocystis sp. pcc 6803 malonyl-coa: acp2 transacylase
51	c5d6sB_	Alignment	not modelled	8.4	22	PDB header: oxidoreductase Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: structure of epoxyqueuosine reductase from streptococcus thermophilus.
52	c2c2nA_	Alignment	not modelled	8.4	17	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of human mitochondrial malonyltransferase
53	c4yodA_	Alignment	not modelled	8.3	28	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-like protein; PDBTitle: crystal structure of a thioredoxin-like protein (baccac_02376) from2 bacteroides caccae atcc 43185 at 1.90 a resolution
						PDB header: viral protein

54	c4indR_	Alignment	not modelled	8.2	17	Chain: R: PDB Molecule: c381 turret protein; PDBTitle: the triple jelly roll fold and turret assembly in an archaeal virus
55	c4qbuA_	Alignment	not modelled	8.2	12	PDB header: transferase Chain: A: PDB Molecule: zmaa; PDBTitle: structure of the acyl transferase domain of zmaa
56	c3aaiB_	Alignment	not modelled	8.1	26	PDB header: transcription Chain: B: PDB Molecule: copper homeostasis operon regulatory protein; PDBTitle: x-ray crystal structure of csor from thermus thermophilus hb8
57	d1i5ga_	Alignment	not modelled	7.8	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
58	c3lwaA_	Alignment	not modelled	7.8	25	PDB header: isomerase Chain: A: PDB Molecule: secreted thiol-disulfide isomerase; PDBTitle: the crystal structure of a secreted thiol-disulfide isomerase from2 corynebacterium glutamicum to 1.75a
59	c5dz6A_	Alignment	not modelled	7.8	10	PDB header: transferase Chain: A: PDB Molecule: polyketide biosynthesis malonyl coa-acyl carrier protein PDBTitle: acyl transferase from bacillaene pks
60	d2fsqa1	Alignment	not modelled	7.5	17	Fold: LigT-like Superfamily: LigT-like Family: Atu0111-like
61	d1z3ea1	Alignment	not modelled	7.3	29	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: ArsC-like
62	c3myxA_	Alignment	not modelled	7.3	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pspto_0244; PDBTitle: crystal structure of a pspto_0244 (protein with unknown function which2 belongs to pfam duf861 family) from pseudomonas syringae pv. tomato3 str. dc3000 at 1.30 a resolution
63	c2m46A_	Alignment	not modelled	7.2	24	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase, putative; PDBTitle: solution nmr structure of sacol0876 from staphylococcus aureus col,2 nesg target zr353 and csgid target idp00841
64	c2kokA_	Alignment	not modelled	7.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase; PDBTitle: solution structure of an arsenate reductase (arsc) related protein2 from brucella melitensis. seattle structural genomics center for3 infectious disease target braba.00007.a
65	c3razA_	Alignment	not modelled	7.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-related protein; PDBTitle: the crystal structure of thioredoxin-related protein from neisseria2 meningitidis serogroup b
66	c2g2oA_	Alignment	not modelled	7.0	17	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of e.coli fabd complexed with sulfate
67	d1rw1a_	Alignment	not modelled	7.0	24	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: ArsC-like
68	c3f0iA_	Alignment	not modelled	6.9	24	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase; PDBTitle: arsenate reductase from vibrio cholerae.
69	c5n3uA_	Alignment	not modelled	6.8	19	PDB header: lyase Chain: A: PDB Molecule: phycocyanobilin lyase subunit alpha; PDBTitle: the structure of the complex of cpce and cpcf of phycocyanin lyase2 from nostoc sp. pcc7120
70	c1ij3B_	Alignment	not modelled	6.8	17	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
71	c1ij3C_	Alignment	not modelled	6.8	17	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
72	c4etrA_	Alignment	not modelled	6.8	23	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: x-ray structure of pa2169 from pseudomonas aeruginosa
73	c4dhwA_	Alignment	not modelled	6.7	21	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of peptidyl-trna hydrolase from pseudomonas2 aeruginosa with adipic acid at 2.4 angstrom resolution
74	c3hhdC_	Alignment	not modelled	6.6	19	PDB header: transferase, hydrolase Chain: C: PDB Molecule: fatty acid synthase; PDBTitle: structure of the human fatty acid synthase ks-mat didomain as a2 framework for inhibitor design.
75	c4fopA_	Alignment	not modelled	6.6	10	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of peptidyl-trna hydrolase from acinetobacter2 baumannii at 1.86 a resolution
76	c3k7zB_	Alignment	not modelled	6.4	17	PDB header: dna binding protein Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
77	c1rb1B_	Alignment	not modelled	6.4	17	PDB header: dna binding protein Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
78	c1rb6C_	Alignment	not modelled	6.4	17	PDB header: dna binding protein Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: antiparallel trimer of gcn4-leucine zipper core mutant as n16a2 tetragonal form
79	c1rb1A_	Alignment	not modelled	6.4	17	PDB header: dna binding protein Chain: A: PDB Molecule: general control protein gcn4;

79	c1f0zA_	Alignment	not modelled	6.4	17	PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution PDB header: dna binding protein
80	c3k7zA_	Alignment	not modelled	6.4	17	Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
81	c1swiA_	Alignment	not modelled	6.4	17	PDB header: leucine zipper Chain: A: PDB Molecule: gcn4p1; PDBTitle: gcn4-leucine zipper core mutant as n16a complexed with benzene
82	c3gwnA_	Alignment	not modelled	6.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: probable fad-linked sulfhydryl oxidase r596; PDBTitle: crystal structure of the fad binding domain from mimivirus sulfhydryl2 oxidase r596
83	c3ewlA_	Alignment	not modelled	6.4	28	Chain: A: PDB Molecule: uncharacterized conserved protein bf1870; PDBTitle: crystal structure of conserved protein bf1870 of unknown function from2 bacteroides fragilis
84	c5dz7A_	Alignment	not modelled	6.3	13	PDB header: transferase Chain: A: PDB Molecule: polyketide biosynthesis protein pkse; PDBTitle: structural basis of acyl transfer in a trans-at polyketide synthase
85	c1e9zA_	Alignment	not modelled	6.3	7	PDB header: hydrolase Chain: A: PDB Molecule: urease subunit alpha; PDBTitle: crystal structure of helicobacter pylori urease
86	c3fz4A_	Alignment	not modelled	6.3	35	PDB header: oxidoreductase Chain: A: PDB Molecule: putative arsenate reductase; PDBTitle: the crystal structure of a possible arsenate reductase from2 streptococcus mutans ua159
87	c1ij2C_	Alignment	not modelled	6.3	17	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvt1 coiled-coil trimer with threonine at the a(16)2 position
88	c6ar7C_	Alignment	not modelled	6.3	26	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 burkholderia thailandensis
89	c3mhsC_	Alignment	not modelled	6.3	44	PDB header: hydrolase/transcription regulator/protei Chain: C: PDB Molecule: saga-associated factor 11; PDBTitle: structure of the saga ubp8/sgf11/sus1/sgf73 dub module bound to2 ubiquitin aldehyde
90	c3es4B_	Alignment	not modelled	6.2	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein duf861 with a rmlc-like cupin fold; PDBTitle: crystal structure of protein of unknown function (duf861) with a rmlc-2 like cupin fold (17741406) from agrobacterium tumefaciens str. c583 (dupont) at 1.64 a resolution
91	c2lusA_	Alignment	not modelled	6.1	35	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: nmr structure of carnoscorpius rotundicauda thioredoxin related2 protein 16 and its role in regulating transcription factor nf-kb3 activity
92	c5bp1A_	Alignment	not modelled	6.1	31	PDB header: transferase Chain: A: PDB Molecule: mycocerosic acid synthase; PDBTitle: condensing di-domain (ks-at) of a mycocerosic acid synthase-like (mas-2 like) pks
93	c3qgaD_	Alignment	not modelled	6.1	7	PDB header: hydrolase Chain: D: PDB Molecule: fusion of urease beta and gamma subunits; PDBTitle: 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae
94	c2hyxA_	Alignment	not modelled	6.0	29	PDB header: unknown function Chain: A: PDB Molecule: protein dipz; PDBTitle: structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
95	c3fkfC_	Alignment	not modelled	6.0	20	PDB header: oxidoreductase Chain: C: PDB Molecule: thiol-disulfide oxidoreductase; PDBTitle: thiol-disulfide oxidoreductase from bacteroides fragilis nctc 9343
96	c2he3A_	Alignment	not modelled	5.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione peroxidase 2; PDBTitle: crystal structure of the selenocysteine to cysteine mutant of human2 glutathione peroxidase 2 (gp2)
97	d1xvqa_	Alignment	not modelled	5.9	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
98	c3emxB_	Alignment	not modelled	5.9	27	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from aeropyrum pernix
99	c3gv1A_	Alignment	not modelled	5.9	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: disulfide interchange protein; PDBTitle: crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae