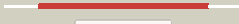



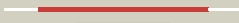
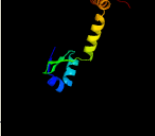
















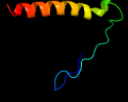
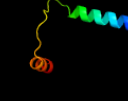
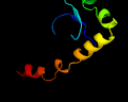

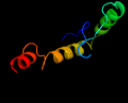
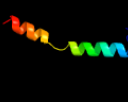
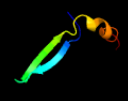
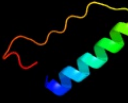



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1247C_(-) _1388981_1389250
Date	Wed Jul 31 22:05:34 BST 2019
Unique Job ID	a550ab6132dbee6a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3g5oA	 Alignment		99.9	43	PDB header: toxin/antitoxin Chain: A: PDB Molecule: uncharacterized protein rv2865; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
2	c3oeiB	 Alignment		99.9	34	PDB header: toxin, protein binding Chain: B: PDB Molecule: relj (antitoxin rv3357); PDBTitle: crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
3	d2a6qa1	 Alignment		99.9	29	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
4	c3d55A	 Alignment		99.8	33	PDB header: toxin inhibitor Chain: A: PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
5	d2a6qb1	 Alignment		99.7	35	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
6	c3hs2H	 Alignment		99.6	29	PDB header: antitoxin Chain: H: PDB Molecule: prevent host death protein; PDBTitle: crystal structure of phd truncated to residue 57 in an orthorhombic2 space group
7	c3hryA	 Alignment		99.5	31	PDB header: antitoxin Chain: A: PDB Molecule: prevent host death protein; PDBTitle: crystal structure of phd in a trigonal space group and partially2 disordered
8	c2odkD	 Alignment		99.4	22	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: putative prevent-host-death protein from nitrosomonas europaea
9	d2odka1	 Alignment		99.3	22	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
10	c3k6qB	 Alignment		94.6	15	PDB header: ligand binding protein Chain: B: PDB Molecule: putative ligand binding protein; PDBTitle: crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
11	c3bpgA	 Alignment		44.6	28	PDB header: toxin Chain: A: PDB Molecule: antitoxin relb3; PDBTitle: crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii

12	d1ez4a2	Alignment		34.4	13	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
13	c5cegC_	Alignment		33.2	18	PDB header: toxin Chain: C: PDB Molecule: addiction module antidote protein, copg/arc/metj family; PDBTitle: x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum
14	c2qzsA_	Alignment		30.0	11	PDB header: transferase Chain: A: PDB Molecule: glycogen synthase; PDBTitle: crystal structure of wild-type e.coli gs in complex with adp and2 glucose(wtgsb)
15	c3bpqC_	Alignment		24.9	28	PDB header: toxin Chain: C: PDB Molecule: antitoxin relb3; PDBTitle: crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
16	c3okaA_	Alignment		23.8	19	PDB header: transferase Chain: A: PDB Molecule: gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol PDBTitle: crystal structure of corynebacterium glutamicum pimb' in complex with2 gdp-man (triclinic crystal form)
17	d1grja1	Alignment		22.3	22	Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain
18	c6nkID_	Alignment		22.2	15	PDB header: antitoxin Chain: D: PDB Molecule: antitoxin vapb1; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
19	c4ochA_	Alignment		21.6	22	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease muts2; PDBTitle: apo structure of smr domain of muts2 from deinococcus radiodurans
20	c1n0fF_	Alignment		21.0	16	PDB header: biosynthetic protein Chain: F: PDB Molecule: protein mrAZ; PDBTitle: crystal structure of a cell division and cell wall2 biosynthesis protein upf0040 from mycoplasma pneumoniae:3 indication of a novel fold with a possible new conserved4 sequence motif
21	d1n0ea_	Alignment	not modelled	20.6	17	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: Hypothetical protein MraZ
22	d1pzga2	Alignment	not modelled	20.3	16	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
23	c6ct6B_	Alignment	not modelled	19.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate dehydrogenase; PDBTitle: crystal structure of lactate dehydrogenase from eimeria maxima with2 nadh and oxamate
24	c5yhha_	Alignment	not modelled	18.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized conserved protein yiim; PDBTitle: crystal structure of yiim from geobacillus stearothermophilus
25	c4xsuB_	Alignment	not modelled	17.4	9	PDB header: transferase Chain: B: PDB Molecule: alr3699 protein; PDBTitle: crystal structure of anabaena alr3699/hepe in complex with udp and2 glucose
26	c6d9tA_	Alignment	not modelled	17.1	13	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase; PDBTitle: bsha from staphylococcus aureus complexed with udp
27	c2zqeA_	Alignment	not modelled	16.7	14	PDB header: dna binding protein Chain: A: PDB Molecule: smts2 protein; PDBTitle: crystal structure of the smr domain of thermus thermophilus smts2
28	c6gneB_	Alignment	not modelled	16.6	12	PDB header: transferase Chain: B: PDB Molecule: probable starch synthase 4, chloroplastic/amyloplastic; PDBTitle: catalytic domain of starch synthase iv from arabidopsis thaliana bound2 to adp and acarbose

29	d1h8ba_	Alignment	not modelled	16.4	12	Fold: EF Hand-like Superfamily: EF-hand Family: EF-hand modules in multidomain proteins
30	d2bisa1	Alignment	not modelled	16.4	21	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
31	d1g8ma1	Alignment	not modelled	15.2	9	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
32	c2m4hA_	Alignment	not modelled	15.0	26	PDB header: viral protein Chain: A: PDB Molecule: feline calicivirus vpg protein; PDBTitle: solution structure of the core domain (10-76) of the feline2 calicivirus vpg protein
33	c6ihdA_	Alignment	not modelled	14.3	11	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of malate dehydrogenase from metallosphaera sedula
34	c1ez4B_	Alignment	not modelled	14.2	13	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate dehydrogenase; PDBTitle: crystal structure of non-allosteric l-lactate dehydrogenase2 from lactobacillus pentosus at 2.3 angstrom resolution
35	d1a5za2	Alignment	not modelled	13.9	14	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
36	c2jimH_	Alignment	not modelled	13.6	16	PDB header: transferase Chain: H: PDB Molecule: glycosyl transferase, group 1 family protein; PDBTitle: crystal structure of a family gt4 glycosyltransferase from bacillus2 anthracis orf ba1558.
37	c3wadA_	Alignment	not modelled	12.9	14	PDB header: transferase Chain: A: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of glycosyltransferase vinc involved in the2 biosynthesis of vicenistatin
38	c2p4vA_	Alignment	not modelled	12.9	10	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor greb; PDBTitle: crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
39	c1griA_	Alignment	not modelled	12.6	16	PDB header: transcription regulation Chain: A: PDB Molecule: grea protein; PDBTitle: grea transcript cleavage factor from escherichia coli
40	c4q2uM_	Alignment	not modelled	12.5	10	PDB header: toxin/toxin repressor Chain: M: PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
41	d1pkxa1	Alignment	not modelled	11.9	6	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
42	c2v9vA_	Alignment	not modelled	11.8	14	PDB header: transcription Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: crystal structure of moorella thermoacetica selb(377-511)
43	c5d00A_	Alignment	not modelled	11.8	16	PDB header: transferase Chain: A: PDB Molecule: n-acetyl-alpha-d-glucosaminyl l-malate synthase; PDBTitle: crystal structure of bsha from b. subtilis complexed with n-2 acetylglucosaminyl-malate and ump
44	c6nkoA_	Alignment	not modelled	11.7	17	PDB header: unknown function Chain: A: PDB Molecule: forh; PDBTitle: crystal structure of forh
45	c3vufA_	Alignment	not modelled	11.4	18	PDB header: transferase Chain: A: PDB Molecule: granule-bound starch synthase 1, PDBTitle: crystal structure of rice granule bound starch synthase i catalytic2 domain in complex with adp
46	c6ejjA_	Alignment	not modelled	10.7	13	PDB header: transferase Chain: A: PDB Molecule: wlac protein; PDBTitle: structure of a glycosyltransferase
47	d1uxja2	Alignment	not modelled	10.6	13	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
48	c4d0kC_	Alignment	not modelled	10.1	14	PDB header: gene regulation Chain: C: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit PDBTitle: complex of chaetomium thermophilum pan2 (wd40-cs1) with pan3 (c-term)
49	c4rbdD_	Alignment	not modelled	10.0	23	PDB header: transferase Chain: D: PDB Molecule: sucrose synthase:glycosyl transferases group 1; PDBTitle: the crystal structure of nitrosomonas europaea sucrose synthase:2 insights into the evolutionary origin of sucrose metabolism in3 prokaryotes
50	c5l6mA_	Alignment	not modelled	9.4	25	PDB header: hydrolase Chain: A: PDB Molecule: vapb family protein; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
51	c3nepX_	Alignment	not modelled	9.3	9	PDB header: oxidoreductase Chain: X: PDB Molecule: malate dehydrogenase; PDBTitle: 1.55a resolution structure of malate dehydrogenase from salinibacter2 ruber
52	c3c4vB_	Alignment	not modelled	9.2	14	PDB header: transferase Chain: B: PDB Molecule: predicted glycosyltransferases; PDBTitle: structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
53	c2r60A_	Alignment	not modelled	9.0	21	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2

						halothermothrix orenii PDB header: viral protein,transferase Chain: A: PDB Molecule: glycosyltransferase b736l; PDBTitle: crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
54	c3oy2A_	Alignment	not modelled	8.8	26	PDB header: hydrolase Chain: F: PDB Molecule: dhurrinase; PDBTitle: crystal structure of the sorghum bicolor dhurrinase 1
55	c1v02F_	Alignment	not modelled	8.7	9	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Family 1 of glycosyl hydrolase
56	d1v02a_	Alignment	not modelled	8.7	9	PDB header: transferase Chain: C: PDB Molecule: sucrose synthase 1; PDBTitle: the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.
57	c3s29C_	Alignment	not modelled	8.7	16	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
58	d1rzua_	Alignment	not modelled	8.6	15	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase; PDBTitle: x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
59	c2p6pB_	Alignment	not modelled	8.6	7	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol mannosyltransferase (pima); PDBTitle: crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
60	c2gejA_	Alignment	not modelled	8.5	11	PDB header: viral protein Chain: A: PDB Molecule: gp6; PDBTitle: crystal structure of bacteriophage hk97 gp6
61	c3jvoA_	Alignment	not modelled	8.4	15	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
62	c3b4uB_	Alignment	not modelled	8.2	9	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
63	d2csua2	Alignment	not modelled	8.0	17	PDB header: dna binding protein Chain: A: PDB Molecule: ttha0139; PDBTitle: crystal structure of ttha0139 I34a from thermus thermophilus hb8
64	c5ytpA_	Alignment	not modelled	7.7	22	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
65	d1gv0a2	Alignment	not modelled	7.6	13	PDB header: structural genomics Chain: B: PDB Molecule: supf0297 protein ef_1202; PDBTitle: solution structure of the ireb homodimer
66	c5us5B_	Alignment	not modelled	7.5	13	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
67	d1lda2	Alignment	not modelled	7.3	18	PDB header: transferase Chain: A: PDB Molecule: ndp-rhamnosyltransferase; PDBTitle: spinosyn rhamnosyltransferase spng
68	c3tsaA_	Alignment	not modelled	7.2	11	PDB header: hydrolase Chain: E: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit pan3; PDBTitle: structure of the saccharomyces cerevisiae pan2-pan3 core complex
69	c4q8jE_	Alignment	not modelled	7.0	17	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
70	d7mdha2	Alignment	not modelled	7.0	10	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
71	d1hyha2	Alignment	not modelled	6.9	14	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
72	c3ncvB_	Alignment	not modelled	6.9	29	PDB header: hydrolase Chain: B: PDB Molecule: dna mismatch repair protein mutl; PDBTitle: ngol
73	c3mybA_	Alignment	not modelled	6.9	17	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase mycobacterium smegmatis
74	c5b42A_	Alignment	not modelled	6.9	13	PDB header: dna binding protein Chain: A: PDB Molecule: dna mismatch repair protein mutl; PDBTitle: crystal structure of the c-terminal endonuclease domain of aquifex2 aeolicus mutl.
75	d1mlda2	Alignment	not modelled	6.8	21	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
76	d2a7wa1	Alignment	not modelled	6.8	7	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: HisE-like (PRA-PH)
77	c2a7wF_	Alignment	not modelled	6.8	7	PDB header: hydrolase Chain: F: PDB Molecule: phosphoribosyl-atp pyrophosphatase; PDBTitle: crystal structure of phosphoribosyl-atp pyrophosphatase2 from chromobacterium violaceum (atcc 12472). nesg target3 cvr7
78	d1i10a2	Alignment	not modelled	6.7	15	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
79	d9ldta2	Alignment	not modelled	6.6	10	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain

80	c1a5zA_	Alignment	not modelled	6.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase; PDBTitle: lactate dehydrogenase from thermotoga maritima (tmdlh)
81	c3gabC_	Alignment	not modelled	6.4	13	PDB header: hydrolase Chain: C: PDB Molecule: dna mismatch repair protein mutl; PDBTitle: c-terminal domain of bacillus subtilis mutl crystal form i
82	c2rreA_	Alignment	not modelled	6.4	9	PDB header: nuclear protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structure and function of the n-terminal nucleolin binding domain of 2 nuclear valocine containing protein like 2 (nvl2) harboring a3 nucleolar localization signal
83	d1t2da2	Alignment	not modelled	6.3	9	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
84	d1ldna2	Alignment	not modelled	6.2	15	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
85	c3ahyD_	Alignment	not modelled	6.2	11	PDB header: hydrolase Chain: D: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of beta-glucosidase 2 from fungus trichoderma reesei2 in complex with tris
86	c2e37B_	Alignment	not modelled	5.9	20	PDB header: oxidoreductase Chain: B: PDB Molecule: l-lactate dehydrogenase; PDBTitle: structure of tt0471 protein from thermus thermophilus
87	c6fqbE_	Alignment	not modelled	5.9	6	PDB header: ligase Chain: E: PDB Molecule: cobyrinic acid synthase; PDBTitle: murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
88	d1o6za2	Alignment	not modelled	5.8	15	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
89	c5he8J_	Alignment	not modelled	5.6	9	PDB header: protein binding Chain: J: PDB Molecule: helicase loader; PDBTitle: bacterial initiation protein
90	c4uupB_	Alignment	not modelled	5.5	12	PDB header: oxidoreductase Chain: B: PDB Molecule: malate dehydrogenase; PDBTitle: reconstructed ancestral trichomonad malate dehydrogenase in2 complex with nadh, so4, and po4
91	c2lsoA_	Alignment	not modelled	5.5	11	PDB header: nuclear protein Chain: A: PDB Molecule: histone h1x; PDBTitle: solution nmr structure of the globular domain of human histone h1x,2 northeast structural genomics consortium (nesg) target hr7057a
92	d1qc7a_	Alignment	not modelled	5.4	21	Fold: alpha-alpha superhelix Superfamily: FliG Family: FliG
93	d2cmda2	Alignment	not modelled	5.4	21	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
94	d1zcza1	Alignment	not modelled	5.4	6	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
95	c5d17L_	Alignment	not modelled	5.4	8	PDB header: dna binding protein Chain: L: PDB Molecule: transposon tn7 transposition protein tnse; PDBTitle: structure of the c-terminal domain of tnse at 2.85 resolution
96	c5ngwA_	Alignment	not modelled	5.2	9	PDB header: hydrolase Chain: A: PDB Molecule: opgh99a; PDBTitle: glycoside hydrolase-like protein
97	d1i0za2	Alignment	not modelled	5.2	13	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
98	c5ghaF_	Alignment	not modelled	5.1	23	PDB header: transferase/transport protein Chain: F: PDB Molecule: sulfur carrier ttub; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
99	c4hlnA_	Alignment	not modelled	5.1	10	PDB header: transferase Chain: A: PDB Molecule: starch synthase i; PDBTitle: structure of barley starch synthase i in complex with2 maltooligosaccharide