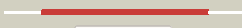

















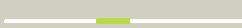
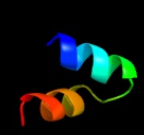


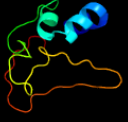


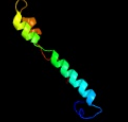



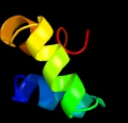



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2275 (-)_2546893_2547762
Date	Mon Aug 5 13:25:41 BST 2019
Unique Job ID	8789505e0955d49f

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2x9qA_	 Alignment		100.0	98	PDB header: ligase Chain: A; PDB Molecule: cyclodipeptide synthetase; PDBTitle: structure of the mycobacterium tuberculosis protein, rv2275,2 demonstrates that cyclodipeptide synthetases are related3 to type i trna-synthetases.
2	c3oqhB_	 Alignment		100.0	26	PDB header: ligase Chain: B; PDB Molecule: putative uncharacterized protein yvmc; PDBTitle: crystal structure of b. licheniformis cdps yvmc-blic
3	c6ez3C_	 Alignment		100.0	23	PDB header: rna binding protein Chain: C; PDB Molecule: cyclo(l-leucyl-l-leucyl) synthase; PDBTitle: structure of cdps from staphylococcus haemolyticus
4	c3oqvA_	 Alignment		100.0	35	PDB header: protein binding Chain: A; PDB Molecule: albc; PDBTitle: albc, a cyclodipeptide synthase from streptomyces noursei
5	c5ocdD_	 Alignment		98.6	12	PDB header: rna binding protein Chain: D; PDB Molecule: cyclodipeptide synthase; PDBTitle: structure of a cdps from fluoribacter dumoffii
6	c5mlqA_	 Alignment		98.0	20	PDB header: ligase Chain: A; PDB Molecule: cdps; PDBTitle: structure of cdps from nocardia brasiliensis
7	c5mlpA_	 Alignment		94.7	19	PDB header: ligase Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: structure of cdps from rickettsiella grylli
8	d2nw8a1	 Alignment		71.6	22	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Bacterial tryptophan 2,3-dioxygenase
9	c2noxP_	 Alignment		70.1	20	PDB header: oxidoreductase Chain: P; PDB Molecule: tryptophan 2,3-dioxygenase; PDBTitle: crystal structure of tryptophan 2,3-dioxygenase from ralstonia2 metallidurans
10	d1cuka1	 Alignment		67.0	30	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
11	d1ugpa_	 Alignment		58.8	14	Fold: Nitrile hydratase alpha chain Superfamily: Nitrile hydratase alpha chain Family: Nitrile hydratase alpha chain

12	c3qyhG	Alignment		57.9	18	PDB header: lyase Chain: G: PDB Molecule: co-type nitrile hydratase alpha subunit; PDBTitle: crystal structure of co-type nitrile hydratase beta-h711 from2 pseudomonas putida.
13	c3ol0C	Alignment		51.7	52	PDB header: de novo protein Chain: C: PDB Molecule: de novo designed monomer trefoil-fold sub-domain which PDBTitle: crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
14	c2gwcE	Alignment		43.5	11	PDB header: ligase Chain: E: PDB Molecule: glutamate cysteine ligase; PDBTitle: crystal structure of plant glutamate cysteine ligase in complex with a2 transition state analogue
15	c4hkaA	Alignment		42.4	12	PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophan 2,3-dioxygenase; PDBTitle: crystal structure of drosophila melanogaster tryptophan 2,3-2 dioxygenase in complex with heme
16	d1ufza	Alignment		31.4	13	Fold: RuvA C-terminal domain-like Superfamily: HBS1-like domain Family: HBS1-like domain
17	d1wiva	Alignment		31.0	13	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
18	d2coba1	Alignment		25.9	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
19	d1veka	Alignment		25.9	14	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
20	c3ogfA	Alignment		25.4	52	PDB header: de novo protein Chain: A: PDB Molecule: de novo designed dimeric trefoil-fold sub-domain which PDBTitle: crystal structure of difoil-4p homo-trimer: de novo designed dimeric2 trefoil-fold sub-domain which forms homo-trimer assembly
21	d3bzka5	Alignment	not modelled	25.3	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
22	c2rkjM	Alignment	not modelled	21.9	9	PDB header: ligase/rna Chain: M: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: cocrystal structure of a tyrosyl-trna synthetase splicing factor with2 a group i intron rna
23	c3nwpA	Alignment	not modelled	21.3	21	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of a 6-phosphogluconolactonase (sbal_2240) from2 shewanella baltica os155 at 1.40 a resolution
24	c6n0wA	Alignment	not modelled	21.2	10	PDB header: ligase Chain: A: PDB Molecule: tyrosine--trna ligase; PDBTitle: crystal structure of a tyrosine--trna ligase from elizabethkingia2 anophelis
25	d1qcsa1	Alignment	not modelled	21.2	29	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
26	d1prta	Alignment	not modelled	20.9	25	Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: ADP-ribosylating toxins
27	c2fy2A	Alignment	not modelled	20.5	15	PDB header: transferase Chain: A: PDB Molecule: choline o-acetyltransferase; PDBTitle: structures of ligand bound human choline acetyltransferase provide2 insight into regulation of acetylcholine synthesis
28	c2dagA	Alignment	not modelled	20.4	14	PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin carboxyl-terminal hydrolase 5; PDBTitle: solution structure of the first uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)

29	c5h75B	Alignment	not modelled	20.3	17	PDB header: lyase Chain: B: PDB Molecule: mersacidin decarboxylase,immunoglobulin g-binding protein PDBTitle: crystal structure of the mrsd-protein a fusion protein
30	d1whca	Alignment	not modelled	18.8	14	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
31	c3gg9C	Alignment	not modelled	18.6	17	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase oxidoreductase protein; PDBTitle: crystal structure of putative d-3-phosphoglycerate dehydrogenase2 oxidoreductase from ralstonia solanacearum
32	d1qzua	Alignment	not modelled	18.6	22	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
33	d1nuna	Alignment	not modelled	18.5	24	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
34	c5aonB	Alignment	not modelled	17.5	20	PDB header: signaling protein Chain: B: PDB Molecule: peroxin 14; PDBTitle: crystal structure of the conserved n-terminal domain of2 pex14 from trypanosoma brucei
35	c4jvcA	Alignment	not modelled	17.3	9	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator mvfr; PDBTitle: crystal structure of pqsr co-inducer binding domain
36	c3o4aC	Alignment	not modelled	17.2	48	PDB header: de novo protein Chain: C: PDB Molecule: de novo designed beta-trefoil architecture with symmetric PDBTitle: crystal structure of symfoil-2: de novo designed beta-trefoil2 architecture with symmetric primary structure
37	c5i87A	Alignment	not modelled	16.3	20	PDB header: membrane protein Chain: A: PDB Molecule: peroxin 14; PDBTitle: targeting the pex14-pex5 interaction by small molecules provides novel2 therapeutic routes to treat trypanosomiasis.
38	d1q1ua	Alignment	not modelled	16.0	33	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
39	d1v29a	Alignment	not modelled	16.0	14	Fold: Nitrile hydratase alpha chain Superfamily: Nitrile hydratase alpha chain Family: Nitrile hydratase alpha chain
40	c2qk4A	Alignment	not modelled	16.0	14	PDB header: ligase Chain: A: PDB Molecule: trifunctional purine biosynthetic protein adenosine-3; PDBTitle: human glycinamide ribonucleotide synthetase
41	c3ff5B	Alignment	not modelled	15.6	18	PDB header: protein transport Chain: B: PDB Molecule: peroxisomal biogenesis factor 14; PDBTitle: crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
42	d1ry7a	Alignment	not modelled	15.4	43	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
43	c3hbwA	Alignment	not modelled	15.4	38	PDB header: hormone Chain: A: PDB Molecule: fibroblast growth factor 13; PDBTitle: crystal structure of human fibroblast growth factor2 homologous factor 2a (fhf2a), also referred to as3 fibroblast growth factor 13a (fgf13a)
44	c1pwaA	Alignment	not modelled	15.2	30	PDB header: hormone/growth factor Chain: A: PDB Molecule: fibroblast growth factor-19; PDBTitle: crystal structure of fibroblast growth factor 19
45	d1pwaa	Alignment	not modelled	15.2	30	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
46	d1qqka	Alignment	not modelled	15.0	14	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
47	d1pc6a	Alignment	not modelled	14.9	20	Fold: NinB Superfamily: NinB Family: NinB
48	c1pbtA	Alignment	not modelled	14.7	15	PDB header: hydrolase, oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: the crystal structure of tm1154, oxidoreductase, sol/devb2 family from thermotoga maritima
49	c2eklA	Alignment	not modelled	14.6	10	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: structure of st1218 protein from sulfolobus tokodaii
50	d1vega	Alignment	not modelled	14.5	9	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
51	c1y89B	Alignment	not modelled	14.4	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: devb protein; PDBTitle: crystal structure of devb protein
52	d1tt4a	Alignment	not modelled	14.2	15	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase family 2 (GCS2)
53	c4bofA	Alignment	not modelled	14.0	17	PDB header: hydrolase Chain: A: PDB Molecule: arginine deiminase; PDBTitle: crystal structure of arginine deiminase from group a streptococcus
54	c1xyr6	Alignment	not modelled	13.8	26	PDB header: virus Chain: 6: PDB Molecule: genome polyprotein, coat protein vp3; PDB Fragment: residues 620-630 PDBTitle: poliovirus 135s cell

						entry intermediate
55	d1gqea_	Alignment	not modelled	13.7	17	Fold: Release factor Superfamily: Release factor Family: Release factor
56	c6h9dB_	Alignment	not modelled	13.5	9	PDB header: hydrolase Chain: B: PDB Molecule: lysozyme; PDBTitle: muramidase domain of spmx from asticcacaulis excentricus
57	c3f1rA_	Alignment	not modelled	13.4	29	PDB header: hormone Chain: A: PDB Molecule: fibroblast growth factor 20; PDBTitle: crystal structure of fgf20 dimer
58	c3lhiA_	Alignment	not modelled	13.2	19	PDB header: hydrolase Chain: A: PDB Molecule: putative 6-phosphogluconolactonase; PDBTitle: crystal structure of putative 6-phosphogluconolactonase(yj_207848.1)2 from neisseria gonorrhoeae fa 1090 at 1.33 a resolution
59	c2fyoA_	Alignment	not modelled	13.1	11	PDB header: transferase Chain: A: PDB Molecule: carnitine o-palmitoyltransferase ii, mitochondrial; PDBTitle: crystal structure of rat carnitine palmitoyltransferase 2 in space2 group p43212
60	c1q6xA_	Alignment	not modelled	13.0	17	PDB header: transferase Chain: A: PDB Molecule: choline o-acetyltransferase; PDBTitle: crystal structure of rat choline acetyltransferase
61	d1jj2l_	Alignment	not modelled	12.8	38	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: L15e
62	d1ihka_	Alignment	not modelled	12.7	24	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
63	c2crnA_	Alignment	not modelled	12.5	17	PDB header: immune system Chain: A: PDB Molecule: ubash3a protein; PDBTitle: solution structure of the uba domain of human ubash3a2 protein
64	c2w85A_	Alignment	not modelled	12.5	20	PDB header: protein transport Chain: A: PDB Molecule: peroxisomal membrane anchor protein pex14; PDBTitle: structure of pex14 in complex with pex19
65	d1bara_	Alignment	not modelled	12.4	38	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
66	d1fmms_	Alignment	not modelled	12.4	43	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
67	c2bkxB_	Alignment	not modelled	12.3	21	PDB header: hydrolase Chain: B: PDB Molecule: glucosamine-6-phosphate deaminase; PDBTitle: structure and kinetics of a monomeric glucosamine-6-2 phosphate deaminase: missing link of the nagb superfamily PDB header: transcription Chain: A: PDB Molecule: nua4 complex subunit eaf3 homolog; PDBTitle: chemical shift assignment and solution structure of fr822a from 2 drosophila melanogaster. northeast structural genomics consortium3 target fr822a
68	c2lrqA_	Alignment	not modelled	12.2	20	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
69	d1qqla_	Alignment	not modelled	12.2	14	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
70	d2crna1	Alignment	not modelled	11.9	17	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
71	c5zxeA_	Alignment	not modelled	11.9	38	PDB header: cell cycle Chain: A: PDB Molecule: consensus sequence based basic form of fibroblast growth PDBTitle: structure of a consensus sequence derived from the fgf family
72	c5aj3h_	Alignment	not modelled	11.8	23	PDB header: ribosome Chain: H: PDB Molecule: PDBTitle: structure of the small subunit of the mammalian mitoribosome
73	d1blaa_	Alignment	not modelled	11.4	38	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
74	d1dv0a_	Alignment	not modelled	11.4	20	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
75	d1ffki_	Alignment	not modelled	11.3	25	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: L15e
76	d2cpwa1	Alignment	not modelled	11.3	11	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
77	d1hkna_	Alignment	not modelled	11.3	43	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
78	d1vqom1	Alignment	not modelled	11.3	25	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: L15e
79	c2k3yA_	Alignment	not modelled	11.2	14	PDB header: transcription regulator Chain: A: PDB Molecule: chromatin modification-related protein eaf3; PDBTitle: solution structure of eaf3 chromo barrel domain bound to2 histone h3 with a dimethyllysine analog h3k36me2 PDB header: hydrolase

80	c2dakA_	Alignment	not modelled	11.1	11	Chain: A: PDB Molecule: ubiquitin carboxyl-terminal hydrolase 5; PDBTitle: solution structure of the second uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
81	d1p3y1_	Alignment	not modelled	11.1	20	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
82	c2px2B_	Alignment	not modelled	11.1	12	PDB header: transferase Chain: B: PDB Molecule: genome polyprotein [contains: capsid protein c (core) PDBTitle: crystal structure of the murray valley encephalitis virus ns5 2'-o2 methyltransferase domain in complex with sah (monoclinic form 1)
83	d1bfga_	Alignment	not modelled	11.0	38	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
84	c3ieiD_	Alignment	not modelled	11.0	24	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
85	d1oqya2	Alignment	not modelled	10.9	20	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
86	c2n37A_	Alignment	not modelled	10.9	40	PDB header: unknown function Chain: A: PDB Molecule: avr-pia protein; PDBTitle: solution structure of avr-pia
87	c5h77B_	Alignment	not modelled	10.6	12	PDB header: signaling protein, immune system Chain: B: PDB Molecule: camp-dependent protein kinase type ii-alpha regulatory PDBTitle: crystal structure of the pka-protein a fusion protein
88	d1rg8a_	Alignment	not modelled	10.2	43	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
89	c2cpwA_	Alignment	not modelled	10.2	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cbl-interacting protein sts-1 variant; PDBTitle: solution structure of rsgi ruh-031, a uba domain from human2 cdna
90	c3qatB_	Alignment	not modelled	10.2	13	PDB header: transferase Chain: B: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of acyl-carrier-protein-s-malonyltransferase from2 bartonella henselae
91	c4ag9B_	Alignment	not modelled	10.0	15	PDB header: transferase Chain: B: PDB Molecule: glucosamine-6-phosphate n-acetyltransferase; PDBTitle: c. elegans glucosamine-6-phosphate n-acetyltransferase (gna1):2 ternary complex with coenzyme a and glcna
92	c1tt4B_	Alignment	not modelled	10.0	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative cytoplasmic protein; PDBTitle: structure of np459575, a predicted glutathione synthase from2 salmonella typhimurium
93	c2nw7C_	Alignment	not modelled	9.7	57	PDB header: oxidoreductase Chain: C: PDB Molecule: tryptophan 2,3-dioxygenase; PDBTitle: crystal structure of tryptophan 2,3-dioxygenase (tdo) from2 xanthomonas campestris in complex with ferric heme.3 northeast structural genomics target xcr13
94	c4gx9A_	Alignment	not modelled	9.6	13	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii subunit epsilon,dna polymerase iii PDBTitle: crystal structure of a dna polymerase iii alpha-epsilon chimera
95	c6jlsA_	Alignment	not modelled	9.6	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative flavoprotein decarboxylase; PDBTitle: crystal structure of fmn-dependent cysteine decarboxylases tvaf from2 thioviridamide biosynthesis
96	c3mntA_	Alignment	not modelled	9.5	24	PDB header: transferase Chain: A: PDB Molecule: leucine carboxyl methyltransferase 1; PDBTitle: crystal structure of human leucine carboxyl methyltransferase 1
97	c2p23A_	Alignment	not modelled	9.5	30	PDB header: signaling protein Chain: A: PDB Molecule: fibroblast growth factor 19; PDBTitle: crystal structure of human fgf19
98	c2h1fB_	Alignment	not modelled	9.4	13	PDB header: transferase Chain: B: PDB Molecule: lipopolysaccharide heptosyltransferase-1; PDBTitle: e. coli heptosyltransferase waac with adp
99	c3abqA_	Alignment	not modelled	9.3	23	PDB header: lyase Chain: A: PDB Molecule: ethanolamine ammonia-lyase heavy chain; PDBTitle: crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and 2-amino-1-propanol