
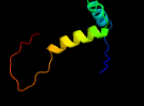

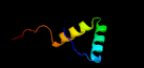



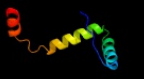



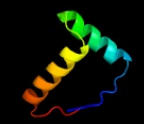

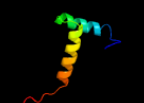



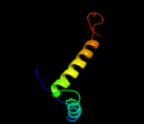




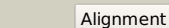

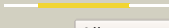







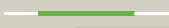
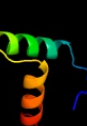






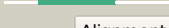



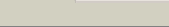
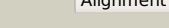


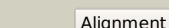


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3321c_(-)_3708245_3708487
Date	Thu Aug 8 16:20:53 BST 2019
Unique Job ID	74bba0970ed54d90

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1q5vB_</a>	 Alignment		95.1	27	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> apo-nikr
2	<a href="#">c5x3tA_</a>	 Alignment		95.1	24	<b>PDB header:</b> antitoxin/toxin <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin vapb26; <b>PDBTitle:</b> vapbc from mycobacterium tuberculosis
3	<a href="#">c2bj3D_</a>	 Alignment		94.9	14	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> nikr-apo
4	<a href="#">c2k5jB_</a>	 Alignment		94.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yiif; <b>PDBTitle:</b> solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
5	<a href="#">d2bsqe1</a>	 Alignment		93.7	17	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Trafficking protein A-like
6	<a href="#">c3kk4B_</a>	 Alignment		93.6	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein bp1543; <b>PDBTitle:</b> uncharacterized protein bp1543 from bordetella pertussis tohama i
7	<a href="#">c2h1oH_</a>	 Alignment		93.3	17	<b>PDB header:</b> gene regulation/dna complex <b>Chain:</b> H: <b>PDB Molecule:</b> trafficking protein a; <b>PDBTitle:</b> structure of fitab bound to ir36 dna fragment
8	<a href="#">d2bj7a1</a>	 Alignment		92.9	20	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
9	<a href="#">c2ca9B_</a>	 Alignment		91.8	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative nickel-responsive regulator; <b>PDBTitle:</b> apo-nikr from helicobacter pylori in closed trans-2 conformation
10	<a href="#">d2hzaa1</a>	 Alignment		90.1	30	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
11	<a href="#">d2hzab1</a>	 Alignment		87.7	30	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like

12	<a href="#">c6a7vU</a>	 Alignment		87.2	23	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> U: <b>PDB Molecule:</b> antitoxin vapb11; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
13	<a href="#">c1xrxD</a>	 Alignment		73.2	29	<b>PDB header:</b> replication inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> seqa protein; <b>PDBTitle:</b> crystal structure of a dna-binding protein
14	<a href="#">d1xrx1</a>	 Alignment		73.2	29	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> SeqA N-terminal domain-like
15	<a href="#">c3h87D</a>	 Alignment		69.1	29	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> D: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
16	<a href="#">c2k29A</a>	 Alignment		67.4	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin relb; <b>PDBTitle:</b> structure of the dbd domain of e. coli antitoxin relb
17	<a href="#">c6g1nB</a>	 Alignment		53.3	26	<b>PDB header:</b> antitoxin <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin hicb; <b>PDBTitle:</b> crystal structure of the burkholderia pseudomallei antitoxin hicb
18	<a href="#">c2an7A</a>	 Alignment		47.9	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein pard; <b>PDBTitle:</b> solution structure of the bacterial antidote pard
19	<a href="#">d1mnta</a>	 Alignment		43.0	22	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
20	<a href="#">c3fmtF</a>	 Alignment		42.9	16	<b>PDB header:</b> replication inhibitor/dna <b>Chain:</b> F: <b>PDB Molecule:</b> protein seqa; <b>PDBTitle:</b> crystal structure of seqa bound to dna
21	<a href="#">d2cpga</a>	 Alignment	not modelled	40.2	23	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
22	<a href="#">c1ea4K</a>	 Alignment	not modelled	40.2	23	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> K: <b>PDB Molecule:</b> transcriptional repressor copg; <b>PDBTitle:</b> transcriptional repressor copg/22bp dsdna complex
23	<a href="#">c1u9pA</a>	 Alignment	not modelled	24.9	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> parc; <b>PDBTitle:</b> permuted single-chain arc
24	<a href="#">c4fxeB</a>	 Alignment	not modelled	24.8	20	<b>PDB header:</b> toxin/toxin inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin relb; <b>PDBTitle:</b> crystal structure of the intact e. coli relbe toxin-antitoxin complex
25	<a href="#">c4p7dA</a>	 Alignment	not modelled	23.4	21	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin hicb3; <b>PDBTitle:</b> antitoxin hicb3 crystal structure
26	<a href="#">c2mdvB</a>	 Alignment	not modelled	21.9	25	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> designed protein; <b>PDBTitle:</b> nmr structure of beta alpha alpha 38
27	<a href="#">c1t01B</a>	 Alignment	not modelled	20.9	47	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> talin 1; <b>PDBTitle:</b> vinculin complexed with the vbs1 helix from talin
28	<a href="#">d1wuda1</a>	 Alignment	not modelled	19.8	17	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> HRDC-like <b>Family:</b> HRDC domain from helicases
29	<a href="#">c6a6xC</a>	 Alignment	not modelled	19.0	26	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> antitoxin maze7;

						<b>PDBTitle:</b> the crystal structure of the mtb maze-mazf-mt9 complex
30	<a href="#">d1s4ka_</a>	Alignment	not modelled	19.0	22	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> YdiL-like
31	<a href="#">c1syqB_</a>	Alignment	not modelled	18.3	47	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> talin 1; <b>PDBTitle:</b> human vinculin head domain vh1, residues 1-258, in complex with human2 talin's vinculin binding site 1, residues 607-636
32	<a href="#">d1a2za_</a>	Alignment	not modelled	17.9	15	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) <b>Family:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
33	<a href="#">c3qoqC_</a>	Alignment	not modelled	16.6	16	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> alginate and motility regulator z; <b>PDBTitle:</b> crystal structure of the transcription factor amrz in complex with the2 18 base pair amrz1 binding site
34	<a href="#">c4q2uM_</a>	Alignment	not modelled	16.1	10	<b>PDB header:</b> toxin/toxin repressor <b>Chain:</b> M: <b>PDB Molecule:</b> antitoxin dinj; <b>PDBTitle:</b> crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
35	<a href="#">d1iofa_</a>	Alignment	not modelled	13.9	19	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) <b>Family:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
36	<a href="#">d1zq1c2</a>	Alignment	not modelled	13.5	21	<b>Fold:</b> DCoH-like <b>Superfamily:</b> GAD domain-like <b>Family:</b> GAD domain
37	<a href="#">d1iu8a_</a>	Alignment	not modelled	13.4	20	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) <b>Family:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
38	<a href="#">c4a1qB_</a>	Alignment	not modelled	13.1	28	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> orf e73; <b>PDBTitle:</b> solution structure of e73 protein from sulfolobus spindle-2 shaped virus ragged hills, a hyperthermophilic3 crenarchaeal virus from yellowstone national park
39	<a href="#">c4aa1B_</a>	Alignment	not modelled	13.1	28	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> orf e73; <b>PDBTitle:</b> thermostable protein from hyperthermophilic virus ssv-rh
40	<a href="#">c3lacA_</a>	Alignment	not modelled	12.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrrolidone-carboxylate peptidase; <b>PDBTitle:</b> crystal structure of bacillus anthracis pyrrolidone-carboxylate2 peptidase, pcp
41	<a href="#">c3giuA_</a>	Alignment	not modelled	12.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrrolidone-carboxylate peptidase; <b>PDBTitle:</b> 1.25 angstrom crystal structure of pyrrolidone-carboxylate peptidase2 (pcp) from staphylococcus aureus
42	<a href="#">c2jr6A_</a>	Alignment	not modelled	11.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0434 protein nma0874; <b>PDBTitle:</b> solution structure of upf0434 protein nma0874. northeast structural2 genomics target mr32
43	<a href="#">c5htiA_</a>	Alignment	not modelled	11.8	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> msha biogenesis protein mshe; <b>PDBTitle:</b> structure of mshe with cdg
44	<a href="#">c3t98C_</a>	Alignment	not modelled	11.5	24	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> nuclear pore complex protein nup54; <b>PDBTitle:</b> molecular architecture of the transport channel of the nuclear pore2 complex: nup54/nup58
45	<a href="#">d1d8wa_</a>	Alignment	not modelled	11.4	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> L-rhamnose isomerase
46	<a href="#">c4gxhC_</a>	Alignment	not modelled	10.4	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> pyrrolidone-carboxylate peptidase; <b>PDBTitle:</b> crystal structure of a pyrrolidone-carboxylate peptidase 1 (target id2 nysgrc-012831) from xenorhabdus bovienii ss-2004
47	<a href="#">c6ejfQ_</a>	Alignment	not modelled	10.4	11	<b>PDB header:</b> motor protein <b>Chain:</b> Q: <b>PDB Molecule:</b> type iv pilus assembly protein pilf; <b>PDBTitle:</b> thermus thermophilus pilf atpase (apoprotein form)
48	<a href="#">d1auga_</a>	Alignment	not modelled	9.8	27	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) <b>Family:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
49	<a href="#">d2d6fc2</a>	Alignment	not modelled	9.6	23	<b>Fold:</b> DCoH-like <b>Superfamily:</b> GAD domain-like <b>Family:</b> GAD domain
50	<a href="#">d1xrsa_</a>	Alignment	not modelled	9.1	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Cobalamin (vitamin B12)-dependent enzymes <b>Family:</b> D-lysine 5,6-aminomutase alpha subunit, KamD
51	<a href="#">c3t98A_</a>	Alignment	not modelled	9.1	24	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear pore complex protein nup54; <b>PDBTitle:</b> molecular architecture of the transport channel of the nuclear pore2 complex: nup54/nup58
52	<a href="#">c6iyaD_</a>	Alignment	not modelled	8.8	19	<b>PDB header:</b> antitoxin <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator copg family; <b>PDBTitle:</b> structure of the dna binding domain of antitoxin copaso
53	<a href="#">c1zw2B_</a>	Alignment	not modelled	8.4	33	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> talin; <b>PDBTitle:</b> vinculin head (0-258) in complex with the talin rod2 residues 2345-2369
54	<a href="#">c2gpyB_</a>	Alignment	not modelled	8.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of putative o-methyltransferase from

						bacillus2 halodurans
55	<a href="#">c2ebjB_</a>	Alignment	not modelled	7.6	40	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> pyrrolidone carboxyl peptidase; <b>PDBTitle:</b> crystal structure of pyrrolidone carboxyl peptidase from thermus2 thermophilus
56	<a href="#">d1ltqa1</a>	Alignment	not modelled	7.6	0	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> phosphatase domain of polynucleotide kinase
57	<a href="#">c4d8jD_</a>	Alignment	not modelled	7.5	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> macrodomain ter protein; <b>PDBTitle:</b> structure of e. coli matp-mats complex
58	<a href="#">c4hv0B_</a>	Alignment	not modelled	7.0	13	<b>PDB header:</b> transcription, viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> avtr; <b>PDBTitle:</b> structure and function of avtr, a novel transcriptional regulator from2 a hyperthermophilic archaeal lipothrivirus
59	<a href="#">d1p94a_</a>	Alignment	not modelled	5.8	16	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
60	<a href="#">d1a4ia2</a>	Alignment	not modelled	5.7	19	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Tetrahydrofolate dehydrogenase/cyclohydrolase
61	<a href="#">c3kxeD_</a>	Alignment	not modelled	5.7	15	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> antitoxin protein pard-1; <b>PDBTitle:</b> a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
62	<a href="#">c3abqA_</a>	Alignment	not modelled	5.6	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> ethanolamine ammonia-lyase heavy chain; <b>PDBTitle:</b> crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and 2-amino-1-propanol
63	<a href="#">c4xc8B_</a>	Alignment	not modelled	5.4	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> isobutyryl-coa mutase fused; <b>PDBTitle:</b> isobutyryl-coa mutase fused with bound butyryl-coa, gdp, and mg and2 without cobalamin (apo-icmf/gdp)
64	<a href="#">c6dy3G_</a>	Alignment	not modelled	5.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> n-acylethanolamine-hydrolyzing acid amidase alpha-subunit; <b>PDBTitle:</b> caenorhabditis elegans n-acylethanolamine-hydrolyzing acid amidase2 (naaa) ortholog
65	<a href="#">c6dy1A_</a>	Alignment	not modelled	5.4	4	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acylethanolamine acid amidase alpha-subunit; <b>PDBTitle:</b> rabbit n-acylethanolamine-hydrolyzing acid amidase (naaa) with fatty2 acid (myristate), in presence of triton x-100