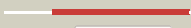






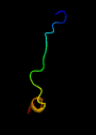

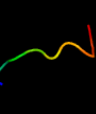



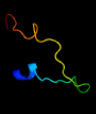

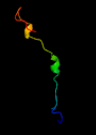








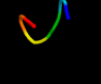



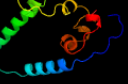
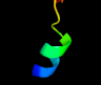
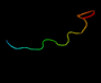


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1814_(erg3)_2056528_2057430
Date	Fri Aug 2 13:30:42 BST 2019
Unique Job ID	d05881b6dae93177

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4zr0A_</a>	 Alignment		99.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ceramide very long chain fatty acid hydroxylase scs7; <b>PDBTitle:</b> full length scs7p (only hydroxylase domain visible)
2	<a href="#">c2yf3F_</a>	 Alignment		34.1	29	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> mazg-like nucleoside triphosphate pyrophosphohydrolase; <b>PDBTitle:</b> crystal structure of dr2231, the mazg-like protein from deinococcus2 radiodurans, complex with manganese
3	<a href="#">c4hdtA_</a>	 Alignment		30.4	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyisobutyryl-coa hydrolase; <b>PDBTitle:</b> crystal structure of a carnitiny-coa dehydratase from mycobacterium2 thermoresistibile
4	<a href="#">c3p4hA_</a>	 Alignment		23.1	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent dna ligase, n-terminal domain protein; <b>PDBTitle:</b> structures of archaeal members of the ligd 3'-phosphoesterase dna2 repair enzyme superfamily
5	<a href="#">c2rfpA_</a>	 Alignment		22.2	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ntp pyrophosphohydrolase; <b>PDBTitle:</b> crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
6	<a href="#">c5nb9A_</a>	 Alignment		22.1	26	<b>PDB header:</b> rna <b>Chain:</b> A: <b>PDB Molecule:</b> rna chaperone proq; <b>PDBTitle:</b> structure of the n-terminal domain of the escherichia coli proq rna2 binding protein
7	<a href="#">c3p43A_</a>	 Alignment		20.9	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure and activities of archaeal members of the ligd 3'2 phosphoesterase dna repair enzyme superfamily
8	<a href="#">c5dmpA_</a>	 Alignment		19.2	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of the archaeal nhej phosphoesterase from methanocella2 paludicola.
9	<a href="#">d2ftxb1</a>	 Alignment		18.3	47	<b>Fold:</b> Kinetochore globular domain-like <b>Superfamily:</b> Kinetochore globular domain <b>Family:</b> Spc24-like
10	<a href="#">c2fv4B_</a>	 Alignment		18.0	47	<b>PDB header:</b> structural protein, protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical 24.6 kda protein in ilv2-ade17 <b>PDBTitle:</b> nmr solution structure of the yeast kinetochore spc24/spc252 globular domain
11	<a href="#">c2e55D_</a>	 Alignment		17.0	50	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> uracil phosphoribosyltransferase; <b>PDBTitle:</b> structure of aq2163 protein from aquifex aeolicus

12	<a href="#">c5td8C_</a>	Alignment		16.3	47	<b>PDB header:</b> replication <b>Chain:</b> C: <b>PDB Molecule:</b> kinetochore protein spc24; <b>PDBTitle:</b> crystal structure of an extended dwarf ndc80 complex
13	<a href="#">d1i5ea_</a>	Alignment		15.7	83	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
14	<a href="#">d1v9sa1</a>	Alignment		15.5	50	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
15	<a href="#">d1bd3a_</a>	Alignment		15.3	67	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
16	<a href="#">d1o5oa_</a>	Alignment		14.8	67	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
17	<a href="#">c2ehja_</a>	Alignment		14.8	50	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil phosphoribosyltransferase; <b>PDBTitle:</b> structure of uracil phosphoribosyl transferase
18	<a href="#">c4ymkA_</a>	Alignment		13.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa desaturase 1; <b>PDBTitle:</b> crystal structure of stearyl-coenzyme a desaturase 1
19	<a href="#">d1rxta1</a>	Alignment		12.8	38	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-myristoyl transferase, NMT
20	<a href="#">c3n9dA_</a>	Alignment		11.9	33	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent dna ligase; <b>PDBTitle:</b> monoclinic structure of p. aeruginosa ligd phosphoesterase domain
21	<a href="#">c4r9iA_</a>	Alignment	not modelled	11.6	37	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> serpin-18; <b>PDBTitle:</b> crystal structure of cysteine proteinase inhibitor serpin18 from2 bombyx mori
22	<a href="#">d1i8na_</a>	Alignment	not modelled	11.1	23	<b>Fold:</b> Hairpin loop containing domain-like <b>Superfamily:</b> Hairpin loop containing domain-like <b>Family:</b> Anti-platelet protein
23	<a href="#">c1i8nA_</a>	Alignment	not modelled	11.1	23	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> anti-platelet protein; <b>PDBTitle:</b> crystal structure of leech anti-platelet protein
24	<a href="#">c4uetA_</a>	Alignment	not modelled	10.8	33	<b>PDB header:</b> retinol-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nematode fatty acid retinoid binding protein; <b>PDBTitle:</b> diversity in the structures and ligand binding sites among2 the fatty acid and retinol binding proteins of nematodes3 revealed by na-far-1 from necator americanus
25	<a href="#">c5i25A_</a>	Alignment	not modelled	10.3	6	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> boron transporter 1; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana bor1
26	<a href="#">c2vgpD_</a>	Alignment	not modelled	9.6	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> inner centromere protein a; <b>PDBTitle:</b> crystal structure of aurora b kinase in complex with a2 aminothiazole inhibitor
27	<a href="#">c5mjrA_</a>	Alignment	not modelled	9.4	28	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> protein thf1; <b>PDBTitle:</b> structure of psb29 at 1.55a
28	<a href="#">c3njcA_</a>	Alignment	not modelled	9.3	40	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> yslb protein; <b>PDBTitle:</b> crystal structure of the yslb protein from bacillus subtilis.2 northeast structural genomics consortium target sr460.

29	<a href="#">c2kvvA</a>	Alignment	not modelled	9.2	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative excisionase; <b>PDBTitle:</b> solution nmr of putative excisionase from klebsiella pneumoniae,2 northeast structural genomics consortium target kpr49
30	<a href="#">d2ysca1</a>	Alignment	not modelled	9.2	80	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
31	<a href="#">c2n4pA</a>	Alignment	not modelled	9.1	50	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> tar dna-binding protein 43; <b>PDBTitle:</b> solution structure of the n-terminal domain of tdp-43
32	<a href="#">c2js3B</a>	Alignment	not modelled	8.9	40	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr structure of protein q6n9a4_rhopa. northeast structural genomics2 consortium target rpt8
33	<a href="#">c6appB</a>	Alignment	not modelled	8.8	31	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> anti-marburgvirus nucleoprotein single domain antibody a complexed2 with nucleoprotein c-terminal domain
34	<a href="#">d1mzga</a>	Alignment	not modelled	8.7	10	<b>Fold:</b> SufE/NifU <b>Superfamily:</b> SufE/NifU <b>Family:</b> SufE-like
35	<a href="#">c2hfvA</a>	Alignment	not modelled	7.9	40	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein rpa1041; <b>PDBTitle:</b> solution nmr structure of protein rpa1041 from pseudomonas2 aeruginosa. northeast structural genomics consortium3 target pat90.
36	<a href="#">c2mdwA</a>	Alignment	not modelled	7.9	100	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> designed protein; <b>PDBTitle:</b> nmr structure of a strand-swapped dimer of the ww domain
37	<a href="#">d1i94m</a>	Alignment	not modelled	7.8	32	<b>Fold:</b> S13-like H2TH domain <b>Superfamily:</b> S13-like H2TH domain <b>Family:</b> Ribosomal protein S13
38	<a href="#">c5y22A</a>	Alignment	not modelled	7.6	38	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> 22aa-pstd peptide; <b>PDBTitle:</b> nmr-based model of the 22 amino acid peptide in polysialyltransferase2 domain (pstd) of the polysialyltransferase st8sia iv
39	<a href="#">c5mrgA</a>	Alignment	not modelled	7.5	50	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> tar dna-binding protein 43; <b>PDBTitle:</b> solution structure of tdp-43 (residues 1-102)
40	<a href="#">c5eqwE</a>	Alignment	not modelled	7.4	22	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> putative major coat protein; <b>PDBTitle:</b> structure of the major structural protein d135 of acidianus tailed2 spindle virus (atsv)
41	<a href="#">c5l9pA</a>	Alignment	not modelled	7.2	56	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein; <b>PDBTitle:</b> crystal structure of the pbp mota from a. tumefaciens b6
42	<a href="#">d2ho2a1</a>	Alignment	not modelled	7.1	60	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
43	<a href="#">c3uiyA</a>	Alignment	not modelled	6.7	19	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> chimera protein of sefd and sefa; <b>PDBTitle:</b> crystal structure of sefd_dscA in h2o
44	<a href="#">d1ni7a</a>	Alignment	not modelled	6.7	9	<b>Fold:</b> SufE/NifU <b>Superfamily:</b> SufE/NifU <b>Family:</b> SufE-like
45	<a href="#">c4or1B</a>	Alignment	not modelled	6.7	17	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> invasin homolog aafb, major fimbrial subunit of aggregative <b>PDBTitle:</b> structure and mechanism of fibronectin binding and biofilm formation2 of enteroaggregative escherischia coli aaf fimbriae
46	<a href="#">c4yztA</a>	Alignment	not modelled	6.7	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose hydrolase; <b>PDBTitle:</b> crystal structure of a tri-modular gh5 (subfamily 4) endo-beta-1, 4-2 glucanase from bacillus licheniformis complexed with cellotetraose
47	<a href="#">c5nsjB</a>	Alignment	not modelled	6.6	27	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> pre-glycoprotein polyprotein gp complex; <b>PDBTitle:</b> gp1 receptor-binding domain from whitewater arroyo mammarenavirus
48	<a href="#">c5mqfQ</a>	Alignment	not modelled	6.6	30	<b>PDB header:</b> splicing <b>Chain:</b> Q: <b>PDB Molecule:</b> protein bud31 homolog; <b>PDBTitle:</b> cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
49	<a href="#">c2k4mA</a>	Alignment	not modelled	6.5	42	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0146 protein mth_1000; <b>PDBTitle:</b> solution nmr structure of m. thermoautotrophicum protein mth_1000,2 northeast structural genomics consortium target tr8
50	<a href="#">d1iyka1</a>	Alignment	not modelled	6.2	25	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-myristoyl transferase, NMT
51	<a href="#">c2k4zA</a>	Alignment	not modelled	6.1	38	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dsrr; <b>PDBTitle:</b> solution nmr structure of allochromatium vinosum dsrr:2 northeast structural genomics consortium target op5
52	<a href="#">c3bbnM</a>	Alignment	not modelled	5.9	32	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> ribosomal protein s13; <b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
53	<a href="#">d2gzoa1</a>	Alignment	not modelled	5.8	16	<b>Fold:</b> VC0467-like <b>Superfamily:</b> VC0467-like <b>Family:</b> VC0467-like

54	<a href="#">c5y3uA</a>	Alignment	not modelled	5.7	38	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> pstd-22aa-polysia; <b>PDBTitle:</b> nmr-based model of the 22 amino acid peptide in polysialyltransferase2 domain (pstd) of the polysialyltransferase st8sia iv in the presence3 of polysialic acid (polysia)
55	<a href="#">c1rxtB</a>	Alignment	not modelled	5.7	38	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> glycylpeptide n-tetradecanoyltransferase 1; <b>PDBTitle:</b> crystal structure of human myristoyl-coa:protein n-2 myristoyltransferase.
56	<a href="#">d1uh6a</a>	Alignment	not modelled	5.6	36	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
57	<a href="#">d2do8a1</a>	Alignment	not modelled	5.6	13	<b>Fold:</b> VC0467-like <b>Superfamily:</b> VC0467-like <b>Family:</b> VC0467-like
58	<a href="#">c5lfiA</a>	Alignment	not modelled	5.6	36	<b>PDB header:</b> immune system <b>Chain:</b> A; <b>PDB Molecule:</b> lactococcin-a immunity protein; <b>PDBTitle:</b> lactococcin a immunity protein
59	<a href="#">c1iyC</a>	Alignment	not modelled	5.5	25	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> myristoyl-coa:protein n-myristoyltransferase; <b>PDBTitle:</b> crystal structure of candida albicans n-myristoyltransferase with non-2 peptidic inhibitor
60	<a href="#">d2ew0a1</a>	Alignment	not modelled	5.3	13	<b>Fold:</b> VC0467-like <b>Superfamily:</b> VC0467-like <b>Family:</b> VC0467-like
61	<a href="#">c2lxeA</a>	Alignment	not modelled	5.2	42	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> histone-lysine n-methyltransferase suvr4; <b>PDBTitle:</b> s4wyild
62	<a href="#">c2muiA</a>	Alignment	not modelled	5.1	15	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> upf0301 protein algh; <b>PDBTitle:</b> solution structure of the algh protein from pseudomonas aeruginosa,2 pa0405, upf0301
63	<a href="#">c5up1A</a>	Alignment	not modelled	5.1	42	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> eehee_rd3_1049; <b>PDBTitle:</b> solution structure of the de novo mini protein eehee_rd3_1049
64	<a href="#">c2laza</a>	Alignment	not modelled	5.0	60	<b>PDB header:</b> signaling protein/transcription <b>Chain:</b> A; <b>PDB Molecule:</b> e3 ubiquitin-protein ligase smurf1; <b>PDBTitle:</b> structure of the first ww domain of human smurf1 in complex with a2 mono-phosphorylated human smad1 derived peptide
65	<a href="#">c2lb0A</a>	Alignment	not modelled	5.0	60	<b>PDB header:</b> signaling protein/transcription <b>Chain:</b> A; <b>PDB Molecule:</b> e3 ubiquitin-protein ligase smurf1; <b>PDBTitle:</b> structure of the first ww domain of human smurf1 in complex with a di-2 phosphorylated human smad1 derived peptide
66	<a href="#">c5cpcA</a>	Alignment	not modelled	5.0	6	<b>PDB header:</b> cell invasion <b>Chain:</b> A; <b>PDB Molecule:</b> secreted effector protein sopd; <b>PDBTitle:</b> crystal structure of sopd, a type iii secreted virulence effector from2 salmonella enterica