

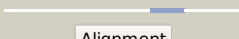

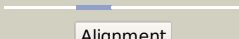

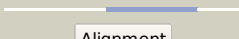


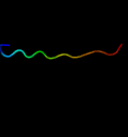
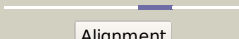
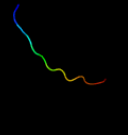
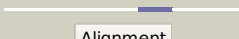
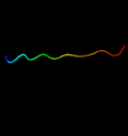
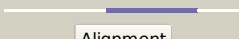




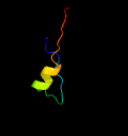




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2696c_(-)_3012839_3013618
Date	Wed Aug 7 12:50:35 BST 2019
Unique Job ID	9f9888456a65c2be

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3dktD_</a>	 Alignment		55.1	23	<b>PDB header:</b> structural protein/virus like particle <b>Chain:</b> D; <b>PDB Molecule:</b> maritimacin; <b>PDBTitle:</b> crystal structure of thermotoga maritima encapsulin
2	<a href="#">d1xa1a_</a>	 Alignment		28.7	11	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
3	<a href="#">c2ytxA_</a>	 Alignment		28.6	20	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> cold shock domain-containing protein e1; <b>PDBTitle:</b> solution structure of the second cold-shock domain of the human2 kiaa0885 protein (unr protein)
4	<a href="#">d1f0ya2</a>	 Alignment		23.1	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
5	<a href="#">c3r1jB_</a>	 Alignment		19.4	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> alpha-ketoglutarate-dependent taurine dioxygenase; <b>PDBTitle:</b> crystal structure of alpha-ketoglutarate-dependent taurine dioxygenase2 from mycobacterium avium, native form
6	<a href="#">d1otja_</a>	 Alignment		18.8	31	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Clavaminate synthase-like <b>Family:</b> TauD/TfdA-like
7	<a href="#">c5vn6B_</a>	 Alignment		18.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> taurine dioxygenase; <b>PDBTitle:</b> crystal structure of taurine dioxygenase from burkholderia ambifaria
8	<a href="#">d1wdka3</a>	 Alignment		16.4	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
9	<a href="#">c5i65A_</a>	 Alignment		15.7	47	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> nonstructural proteins orf1a; <b>PDBTitle:</b> porcine reproductive and respiratory syndrome virus nonstructural2 protein 7 alpha (nsp7 alpha)
10	<a href="#">d1v8ca2</a>	 Alignment		15.6	38	<b>Fold:</b> TBP-like <b>Superfamily:</b> MoaD-related protein, C-terminal domain <b>Family:</b> MoaD-related protein, C-terminal domain
11	<a href="#">c3nctC_</a>	 Alignment		15.3	31	<b>PDB header:</b> dna binding protein, chaperone <b>Chain:</b> C; <b>PDB Molecule:</b> protein psib; <b>PDBTitle:</b> x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca

12	<a href="#">c5hsxB_</a>	Alignment		14.9	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative alpha-ketoglutarate-dependent taurine dioxygenase; <b>PDBTitle:</b> crystal structure of a putative alpha-ketoglutarate-dependent taurine2 dioxygenase from burkholderia xenovorans
13	<a href="#">d2fr1a2</a>	Alignment		13.8	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
14	<a href="#">c5bkeF_</a>	Alignment		13.0	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate <b>PDBTitle:</b> crystal structure of aad-2 in complex with mn(ii) and n-oxalyglycine
15	<a href="#">c4pt2B_</a>	Alignment		12.7	18	<b>PDB header:</b> virus like particle <b>Chain:</b> B: <b>PDB Molecule:</b> encapsulin protein; <b>PDBTitle:</b> myxococcus xanthus encapsulin protein (enca)
16	<a href="#">c5ghaF_</a>	Alignment		12.5	29	<b>PDB header:</b> transferase/transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> sulfur carrier ttub; <b>PDBTitle:</b> sulfur transferase ttua in complex with sulfur carrier ttub
17	<a href="#">c3pvjB_</a>	Alignment		11.8	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-ketoglutarate-dependent taurine dioxygenase; <b>PDBTitle:</b> crystal structure of the fe(ii)/alpha-ketoglutarate dependent taurine2 dioxygenase from pseudomonas putida kt2440
18	<a href="#">d1e8ga1</a>	Alignment		11.5	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Vanillyl-alcohol oxidase-like
19	<a href="#">c5kpeA_</a>	Alignment		11.4	17	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo beta sheet design protein or664; <b>PDBTitle:</b> solution nmr structure of denovo beta sheet design protein, northeast2 structural genomics consortium (nesh) target or664
20	<a href="#">c6dawA_</a>	Alignment		9.9	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> non-heme iron hydroxylase; <b>PDBTitle:</b> x-ray crystal structure of napi l-arginine desaturase bound to fe(ii), 2 l-arginine, and acetate
21	<a href="#">c2wbqA_</a>	Alignment	not modelled	9.4	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-arginine beta-hydroxylase; <b>PDBTitle:</b> crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine
22	<a href="#">d1gmua2</a>	Alignment	not modelled	8.8	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Urease metallochaperone UreE, C-terminal domain <b>Family:</b> Urease metallochaperone UreE, C-terminal domain
23	<a href="#">c6nhuD_</a>	Alignment	not modelled	8.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of the beta lactamase class d ybxi from2 agrobacterium fabrum
24	<a href="#">c5yxaC_</a>	Alignment	not modelled	8.7	19	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> non-structural protein 1; <b>PDBTitle:</b> crystal structure of the c-terminal fragment of ns1 protein from2 yellow fever virus
25	<a href="#">c4hpmA_</a>	Alignment	not modelled	8.3	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bcl-6 corepressor-like protein 1; <b>PDBTitle:</b> pcgf1 ub fold (rawul)/bcor1 pufd complex
26	<a href="#">c4ne0B_</a>	Alignment	not modelled	8.2	38	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> l-arginine beta-hydroxylase; <b>PDBTitle:</b> crystal structure of non-heme iron oxygenase orfp d157a mutant in2 complex with (3s)-hydroxy-l-arg
27	<a href="#">c4hplA_</a>	Alignment	not modelled	8.1	43	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bcl-6 corepressor; <b>PDBTitle:</b> pcgf1 ub fold (rawul)/bcor pufd complex
28	<a href="#">c3s5bB_</a>	Alignment	not modelled	8.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endonuclease g; <b>PDBTitle:</b> crystal structure of ced-3 protease suppressor-6 (cps-6) from2 caenorhabditis elegans <b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> alpha-ketoqlutarate-dependent taurine

29	<a href="#">c4j5iH_</a>	Alignment	not modelled	8.0	38	dioxygenase; <b>PDBTitle:</b> crystal structure of an alpha-ketoglutarate-dependent taurine2 dioxygenase from mycobacterium smegmatis <b>PDB header:</b> hydrolase, protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> rna-dependent rna polymerase; <b>PDBTitle:</b> crystal structure of the viral otu domain protease from farallon virus <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oxacillinase; <b>PDBTitle:</b> crystal structure of oxa-45, a class d beta-lactamase with extended2 spectrum activity
30	<a href="#">c6dx5B_</a>	Alignment	not modelled	8.0	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Vanillyl-alcohol oxidase-like
31	<a href="#">c4gn2A_</a>	Alignment	not modelled	7.8	22	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> B: <b>PDB Molecule:</b> insulin-like 3; <b>PDBTitle:</b> solution structure of insl3
32	<a href="#">d1wvfa1</a>	Alignment	not modelled	7.7	19	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> tail fiber protein; <b>PDBTitle:</b> crystal structure of acinetobacter baumannii phage am24 tailspike2 protein
33	<a href="#">c2h8bB_</a>	Alignment	not modelled	7.7	75	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
34	<a href="#">c5w5pA_</a>	Alignment	not modelled	7.6	56	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of the beta lactamase class d ybxi from nostoc
35	<a href="#">d1xhca1</a>	Alignment	not modelled	7.6	16	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> zika virus non-structural protein ns1
36	<a href="#">c6nhsA_</a>	Alignment	not modelled	7.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative dioxygenase; <b>PDBTitle:</b> x-ray crystal structure of a putative dioxygenase from mycobacterium2 abscessus
37	<a href="#">c5iy3A_</a>	Alignment	not modelled	7.6	23	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> zika virus protein; <b>PDBTitle:</b> zika virus non-structural protein 1 (ns1)
38	<a href="#">c4y0eB_</a>	Alignment	not modelled	7.2	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative alpha kg dependent 2,4-d dioxygenase; <b>PDBTitle:</b> crystal structure of a putative alpha-ketoglutarate dependent 2,4-d2 dioxygenase from burkholderia xenovorans
39	<a href="#">c5k6kB_</a>	Alignment	not modelled	6.4	23	<b>PDB header:</b> lyase <b>Chain:</b> J: <b>PDB Molecule:</b> cyanate hydratase; <b>PDBTitle:</b> site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase
40	<a href="#">c5j92B_</a>	Alignment	not modelled	6.2	23	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> plectasin derivative nz2114; <b>PDBTitle:</b> solution structure of plectasin derivative nz2114
41	<a href="#">c2iv1J_</a>	Alignment	not modelled	6.1	16	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Clavamate synthase-like <b>Family:</b> TauD/TfdA-like
42	<a href="#">c6k50A_</a>	Alignment	not modelled	6.0	50	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
43	<a href="#">d1oiha_</a>	Alignment	not modelled	5.9	23	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> major vault protein; <b>PDBTitle:</b> crystal structure of the p21 r1-r7 n-terminal domain of murine mvp
44	<a href="#">d2fmra_</a>	Alignment	not modelled	5.9	40	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar hook-length control protein; <b>PDBTitle:</b> solution structure of the c-terminal domain of the flik
45	<a href="#">c3gf5A_</a>	Alignment	not modelled	5.8	56	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> SAM (sterile alpha motif) domain
46	<a href="#">c2rrlA_</a>	Alignment	not modelled	5.8	8	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
47	<a href="#">d1dxsa_</a>	Alignment	not modelled	5.8	63	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of the beta lactamase class d ybxi from burkholderia2 thailandensis
48	<a href="#">d1k38a_</a>	Alignment	not modelled	5.6	17	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> ns1; <b>PDBTitle:</b> west Nile virus non-structural protein 1 (ns1) form 2 crystal
49	<a href="#">c6ni0A_</a>	Alignment	not modelled	5.6	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Z-DNA binding domain
50	<a href="#">c4o6cB_</a>	Alignment	not modelled	5.5	26	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> double-stranded rna-binding protein; <b>PDBTitle:</b> solution structure of the z-dna binding domain of the2 vaccinia virus gene e3l
51	<a href="#">d1oyia_</a>	Alignment	not modelled	5.4	50	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> proline-rich 28 kda antigen; <b>PDBTitle:</b> crystal structure of secreted proline rich antigen mtc28 (rv0040c)2 from mycobacterium tuberculosis
52	<a href="#">c1oyiA_</a>	Alignment	not modelled	5.4	50	<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
53	<a href="#">c4ol4A_</a>	Alignment	not modelled	5.3	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> (r)-phenoxypropionate/alpha-
54	<a href="#">c3qoqC_</a>	Alignment	not modelled	5.3	41	
55	<a href="#">c6d1eD_</a>	Alignment	not modelled	5.2	21	

55	<a href="#">c0u100_</a>	Alignment	not modelled	5.2	31	ketoglutarate-dioxygenase; <b>PDBTitle:</b> ft_5 dioxygenase apoenzyme
56	<a href="#">d1ofcx2</a>	Alignment	not modelled	5.2	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> SLIDE domain
57	<a href="#">d1s7ia_</a>	Alignment	not modelled	5.1	33	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> DGPF domain (Pfam 04946)
58	<a href="#">d1gv4a2</a>	Alignment	not modelled	5.1	11	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains