
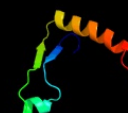

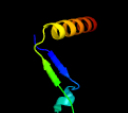



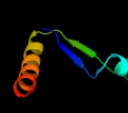



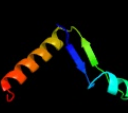



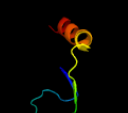



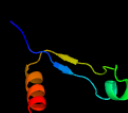


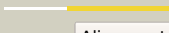

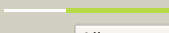
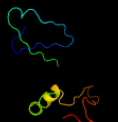

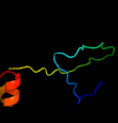
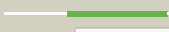



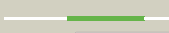


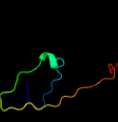

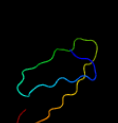


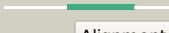




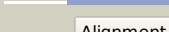
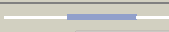
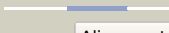


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0396 (-)_475353_475745
Date	Tue Jul 23 14:50:46 BST 2019
Unique Job ID	9658b1d5b295d7da

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ehil_</a>	 Alignment		96.3	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> I: <b>PDB Molecule:</b> nuclease nuct; <b>PDBTitle:</b> nuct from helicobacter pylori
2	<a href="#">c4ggkA_</a>	 Alignment		96.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial cardiolipin hydrolase; <b>PDBTitle:</b> crystal structure of zucchini from mouse (mzuc / pld6 / mitopld) bound2 to tungstate
3	<a href="#">d1xdpa3</a>	 Alignment		94.3	15	<b>Fold:</b> Phospholipase D/nuclease <b>Superfamily:</b> Phospholipase D/nuclease <b>Family:</b> Polyphosphate kinase C-terminal domain
4	<a href="#">d1byra_</a>	 Alignment		93.4	26	<b>Fold:</b> Phospholipase D/nuclease <b>Superfamily:</b> Phospholipase D/nuclease <b>Family:</b> Nuclease
5	<a href="#">c4urjA_</a>	 Alignment		93.0	26	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein fam83a; <b>PDBTitle:</b> crystal structure of human bj-tsa-9
6	<a href="#">c4gelA_</a>	 Alignment		91.7	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial cardiolipin hydrolase; <b>PDBTitle:</b> crystal structure of zucchini
7	<a href="#">c3hsiC_</a>	 Alignment		87.8	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphatidylserine synthase; <b>PDBTitle:</b> crystal structure of phosphatidylserine synthase haemophilus2 influenzae rd kw20
8	<a href="#">c1v0sA_</a>	 Alignment		83.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase d; <b>PDBTitle:</b> uninhibited form of phospholipase d from streptomyces sp.2 strain pmf
9	<a href="#">c5lzkB_</a>	 Alignment		82.6	23	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> protein fam83b; <b>PDBTitle:</b> structure of the domain of unknown function duf1669 from human fam83b
10	<a href="#">c4genA_</a>	 Alignment		77.3	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial cardiolipin hydrolase; <b>PDBTitle:</b> crystal structure of zucchini (monomer)
11	<a href="#">d1v0wa2</a>	 Alignment		77.0	16	<b>Fold:</b> Phospholipase D/nuclease <b>Superfamily:</b> Phospholipase D/nuclease <b>Family:</b> Phospholipase D

12	<a href="#">c2opwA</a>	 Alignment		73.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phyhd1 protein; <b>PDBTitle:</b> crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo)
13	<a href="#">c5daqA</a>	 Alignment		64.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phytanoyl-coa dioxygenase family protein (afu_orthologue) <b>PDBTitle:</b> fe(ii)/(alpha)ketoglutarate-dependent dioxygenase asqj in complex with2 4-methoxycycloptin
14	<a href="#">c5zm4B</a>	 Alignment		58.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dioxygenase anda; <b>PDBTitle:</b> fe(ii)/(alpha)ketoglutarate-dependent dioxygenase anda with2 preandiloid c
15	<a href="#">c4naoA</a>	 Alignment		57.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxygenase; <b>PDBTitle:</b> crystal structure of eash
16	<a href="#">d1xdpa4</a>	 Alignment		52.4	28	<b>Fold:</b> Phospholipase D/nuclease <b>Superfamily:</b> Phospholipase D/nuclease <b>Family:</b> Polyphosphate kinase C-terminal domain
17	<a href="#">c4mhuB</a>	 Alignment		50.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ectoine hydroxylase; <b>PDBTitle:</b> crystal structure of ectd from s. alaskensis with bound fe
18	<a href="#">c3emrA</a>	 Alignment		46.2	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ectd; <b>PDBTitle:</b> crystal structure analysis of the ectoine hydroxylase ectd from2 salibacillus salexigens
19	<a href="#">c5epaE</a>	 Alignment		44.0	20	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> snok; <b>PDBTitle:</b> crystal structure of non-heme alpha ketoglutarate dependent2 carbocyclase snok from nogalamycin biosynthesis
20	<a href="#">c3nnbB</a>	 Alignment		43.0	12	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> cura; <b>PDBTitle:</b> halogenase domain from cura module (crystal form iii)
21	<a href="#">d2a1xa1</a>	 Alignment	not modelled	41.6	18	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Clavaminatase synthase-like <b>Family:</b> PhyH-like
22	<a href="#">c4rctB</a>	 Alignment	not modelled	39.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> restriction endonuclease r.ngovii; <b>PDBTitle:</b> crystal structure of r-protein of ngoavii restriction endonuclease
23	<a href="#">c5m0tA</a>	 Alignment	not modelled	34.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-ketoglutarate-dependent non-heme iron oxygenase eash; <b>PDBTitle:</b> alpha-ketoglutarate-dependent non-heme iron oxygenase eash
24	<a href="#">c5yboA</a>	 Alignment	not modelled	32.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> prha; <b>PDBTitle:</b> fe(ii)/(alpha)ketoglutarate-dependent dioxygenase prha in complex with2 preaustinoid a1
25	<a href="#">c4xaaA</a>	 Alignment	not modelled	32.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxygenase; <b>PDBTitle:</b> crystal structure of avio1 from streptomyces viridochromogenes tue57
26	<a href="#">c5erID</a>	 Alignment	not modelled	29.3	13	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> snon,snon; <b>PDBTitle:</b> crystal structure of the epimerase snon in complex with ni2+,2 succinate and nogalamycin ro
27	<a href="#">c4xabA</a>	 Alignment	not modelled	28.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> evdo2; <b>PDBTitle:</b> crystal structure of evdo2 from micromonospora carbonacea var.2 aurantiaca
28	<a href="#">c4xc9B</a>	 Alignment	not modelled	25.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidase/hydroxylase; <b>PDBTitle:</b> crystal structure of apo hygx from streptomyces hygroscopicus

29	<a href="#">d2o8ra4</a>	Alignment	not modelled	23.8	31	<b>Fold:</b> Phospholipase D/nuclease <b>Superfamily:</b> Phospholipase D/nuclease <b>Family:</b> Polyphosphate kinase C-terminal domain
30	<a href="#">c3dt5A_</a>	Alignment	not modelled	20.8	100	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein af_0924; <b>PDBTitle:</b> c_terminal domain of protein of unknown function af_0924 from2 archaeoglobus fulgidus.
31	<a href="#">c4zonB_</a>	Alignment	not modelled	18.6	23	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> verruculogen synthase; <b>PDBTitle:</b> structure of ftmox1 with fumitremorgen b complex
32	<a href="#">c5ncjB_</a>	Alignment	not modelled	17.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> leucine hydroxylase; <b>PDBTitle:</b> grie in complex with manganese, succinate and (2s,4r)-5-hydroxyleucine
33	<a href="#">c6ec3C_</a>	Alignment	not modelled	15.9	17	<b>PDB header:</b> transferase, oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> methyltransferase domain-containing protein; <b>PDBTitle:</b> crystal structure of evdm1
34	<a href="#">c2rdsA_</a>	Alignment	not modelled	13.6	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-deoxypentalenic acid 11-beta hydroxylase; fe(ii)/alpha- <b>PDBTitle:</b> crystal structure of ptlh with fe/oxalylglycine and ent-1-2 deoxypentalenic acid bound
35	<a href="#">d1jy1a2</a>	Alignment	not modelled	9.6	40	<b>Fold:</b> Phospholipase D/nuclease <b>Superfamily:</b> Phospholipase D/nuclease <b>Family:</b> Tyrosyl-DNA phosphodiesterase TDP1
36	<a href="#">d1qzqa1</a>	Alignment	not modelled	9.6	19	<b>Fold:</b> Phospholipase D/nuclease <b>Superfamily:</b> Phospholipase D/nuclease <b>Family:</b> Tyrosyl-DNA phosphodiesterase TDP1
37	<a href="#">d2f3ci1</a>	Alignment	not modelled	9.5	50	<b>Fold:</b> Kazal-type serine protease inhibitors <b>Superfamily:</b> Kazal-type serine protease inhibitors <b>Family:</b> Ovomucoid domain III-like
38	<a href="#">d1zata2</a>	Alignment	not modelled	7.5	10	<b>Fold:</b> L,D-transpeptidase pre-catalytic domain-like <b>Superfamily:</b> L,D-transpeptidase pre-catalytic domain-like <b>Family:</b> L,D-transpeptidase pre-catalytic domain-like
39	<a href="#">c5m86C_</a>	Alignment	not modelled	7.2	33	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> ta1207; <b>PDBTitle:</b> crystal structure of the thermoplasma acidophilum protein ta1207
40	<a href="#">c5jnbE_</a>	Alignment	not modelled	7.1	45	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> rnp (rrm rna binding domain) containing; <b>PDBTitle:</b> structure of gld-2/rnp-8 complex
41	<a href="#">c4ploA_</a>	Alignment	not modelled	6.3	19	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> netrin-1; <b>PDBTitle:</b> crystal structure of chicken netrin-1 (ln-le3) in complex with mouse2 dcc (fn4-5)
42	<a href="#">c4xbzB_</a>	Alignment	not modelled	6.1	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> evdo1; <b>PDBTitle:</b> crystal structure of evdo1 from micromonospora carbonacea var.2 aurantiaca
43	<a href="#">c6epkB_</a>	Alignment	not modelled	5.6	36	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> precursor membrane protein; <b>PDBTitle:</b> crystal structure of the precursor membrane protein-envelope protein2 heterodimer from the yellow fever virus
44	<a href="#">c1q8hA_</a>	Alignment	not modelled	5.6	56	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> osteocalcin; <b>PDBTitle:</b> crystal structure of porcine osteocalcin
45	<a href="#">d1q8ha_</a>	Alignment	not modelled	5.6	56	<b>Fold:</b> GLA-domain <b>Superfamily:</b> GLA-domain <b>Family:</b> GLA-domain
46	<a href="#">d2p8ta2</a>	Alignment	not modelled	5.6	55	<b>Fold:</b> DCoH-like <b>Superfamily:</b> GAD domain-like <b>Family:</b> PH0730 C-terminal domain-like
47	<a href="#">c4b03D_</a>	Alignment	not modelled	5.6	22	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> dengue virus 1 prm protein; <b>PDBTitle:</b> 6a electron cryomicroscopy structure of immature dengue virus serotype2 1