






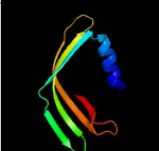









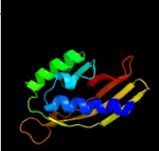

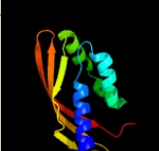




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0200 (-) _237206_237895
Date	Tue Jul 23 14:50:25 BST 2019
Unique Job ID	ac58f5b00d77057f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4i4kB_</a>	 Alignment		97.3	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein sgcj; <b>PDBTitle:</b> streptomyces globisporus c-1027 9-membered enediyne conserved protein2 sgce6
2	<a href="#">d2ux0a1</a>	 Alignment		97.2	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
3	<a href="#">d2rffa1</a>	 Alignment		97.1	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
4	<a href="#">d3b8la1</a>	 Alignment		96.9	8	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
5	<a href="#">d1hkxa_</a>	 Alignment		96.9	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
6	<a href="#">c5d9rA_</a>	 Alignment		96.5	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> protein accumulation and replication of chloroplasts 6, <b>PDBTitle:</b> crystal structure of a conserved domain in the intermembrane space2 region of the plastid division protein arc6
7	<a href="#">d2f86b1</a>	 Alignment		96.3	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
8	<a href="#">c3h51A_</a>	 Alignment		96.3	15	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> putative calcium/calmodulin dependent protein kinase ii <b>PDBTitle:</b> crystal structure of putative calcium/calmodulin dependent protein2 kinase ii association domain (np_636218.1) from xanthomonas3 campestris at 1.70 a resolution
9	<a href="#">d3cu3a1</a>	 Alignment		96.3	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
10	<a href="#">c5cnlA_</a>	 Alignment		96.2	9	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> icmI-like; <b>PDBTitle:</b> crystal structure of an icmI-like type iv secretion system protein2 (lpg0120) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1 at 2.65 a resolution
11	<a href="#">c3wz4F_</a>	 Alignment		96.2	12	<b>PDB header:</b> unknown function <b>Chain:</b> F; <b>PDB Molecule:</b> doti; <b>PDBTitle:</b> structure of the periplasmic domain of doti (crystal form i)

12	<a href="#">c4nhfF_</a>	Alignment		96.1	10	<b>PDB header:</b> protein transport <b>Chain:</b> F: <b>PDB Molecule:</b> trwg protein; <b>PDBTitle:</b> crystal structure of the soluble domain of trwg type iv secretion2 machinery from bartonella grahamii
13	<a href="#">c5ig4A_</a>	Alignment		96.1	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted protein; <b>PDBTitle:</b> crystal structure of n. vectensis camkii-a hub
14	<a href="#">d2cc3a1</a>	Alignment		95.8	8	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> VirB8-like
15	<a href="#">d3d9ra1</a>	Alignment		95.7	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> ECA1476-like
16	<a href="#">c3gzaA_</a>	Alignment		95.6	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein with a ntf2-like fold; <b>PDBTitle:</b> crystal structure of an uncharacterized protein with a cystatin-like2 fold (cc_2572) from caulobacter vibrioides at 1.40 a resolution
17	<a href="#">c3a76B_</a>	Alignment		95.5	7	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> gamma-hexachlorocyclohexane dehydrochlorinase; <b>PDBTitle:</b> the crystal structure of lina
18	<a href="#">c4ovmE_</a>	Alignment		95.5	16	<b>PDB header:</b> unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein sgcj; <b>PDBTitle:</b> crystal structure of sgcj protein from streptomyces carzinostaticus
19	<a href="#">c3hx8A_</a>	Alignment		95.4	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ketosteroid isomerase; <b>PDBTitle:</b> crystal structure of putative ketosteroid isomerase (np_103587.1) from2 mesorhizobium loti at 1.45 a resolution
20	<a href="#">c5u9oD_</a>	Alignment		95.3	13	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> plastid division protein cdp1, chloroplastic,plastid <b>PDBTitle:</b> cocrystal structure of the intermembrane space region of the plastid2 division proteins parc6 and pdv1
21	<a href="#">c5i97C_</a>	Alignment	not modelled	95.3	9	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> conjugal transfer protein; <b>PDBTitle:</b> structural analysis and inhibition of trae from the pkm101 type iv2 secretion system
22	<a href="#">c5ig5E_</a>	Alignment	not modelled	95.2	15	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> camkii-b hub; <b>PDBTitle:</b> crystal structure of n. vectensis camkii-b hub at ph 4.2
23	<a href="#">c3robC_</a>	Alignment	not modelled	95.1	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> the crystal structure of a conserved protein from planctomyces2 limnophilus dsm 3776
24	<a href="#">c3f7sA_</a>	Alignment	not modelled	94.9	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized ntf2-like protein; <b>PDBTitle:</b> crystal structure of a ntf2-like protein of unknown function (pp_4556)2 from pseudomonas putida kt2440 at 2.11 a resolution
25	<a href="#">d2rqqa1</a>	Alignment	not modelled	94.9	6	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
26	<a href="#">d2chca1</a>	Alignment	not modelled	94.3	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
27	<a href="#">d1idpa_</a>	Alignment	not modelled	94.3	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
28	<a href="#">c6of9G_</a>	Alignment	not modelled	93.5	13	<b>PDB header:</b> unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> camkii hub; <b>PDBTitle:</b> structure of the chlamydamonas reinhardtii camkii hub homology domain

29	<a href="#">c2bhmE</a>	Alignment	not modelled	93.4	9	<b>PDB header:</b> bacterial protein <b>Chain:</b> E: <b>PDB Molecule:</b> type iv secretion system protein virb8; <b>PDBTitle:</b> crystal structure of virb8 from brucella suis
30	<a href="#">c3wz3A</a>	Alignment	not modelled	93.4	10	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> stram protein; <b>PDBTitle:</b> structure of a periplasmic fragment of tram
31	<a href="#">d2r4ia1</a>	Alignment	not modelled	93.4	8	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> CHU142-like
32	<a href="#">d3ef8a1</a>	Alignment	not modelled	93.3	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
33	<a href="#">d3cnxa1</a>	Alignment	not modelled	93.2	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SAV4671-like
34	<a href="#">d3stda</a>	Alignment	not modelled	92.8	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
35	<a href="#">d2bhma1</a>	Alignment	not modelled	92.7	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> VirB8-like
36	<a href="#">d3ebya1</a>	Alignment	not modelled	92.5	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
37	<a href="#">c4meiA</a>	Alignment	not modelled	92.3	11	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> virb8 protein; <b>PDBTitle:</b> crystal structure of a virb8 type iv secretion system machinery2 soluble domain from bartonella tribocorum
38	<a href="#">d3ejva1</a>	Alignment	not modelled	92.0	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
39	<a href="#">c3bb9D</a>	Alignment	not modelled	90.9	12	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative orphan protein; <b>PDBTitle:</b> crystal structure of a putative ketosteroid isomerase (sfri_1973) from2 shewanella frigidimarina ncimb 400 at 1.80 a resolution
40	<a href="#">c4lehA</a>	Alignment	not modelled	89.2	7	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> bile acid 7-alpha dehydratase, baie; <b>PDBTitle:</b> crystal structure of a bile-acid 7-alpha dehydratase (closci_03134)2 from clostridium scindens atcc 35704 at 2.90 a resolution
41	<a href="#">c4gb5A</a>	Alignment	not modelled	88.6	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of kfla4162 protein from kribbella flavida
42	<a href="#">d3blza1</a>	Alignment	not modelled	88.4	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Sbal0622-like
43	<a href="#">c2gbxF</a>	Alignment	not modelled	87.7	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> biphenyl 2,3-dioxygenase beta subunit; <b>PDBTitle:</b> crystal structure of biphenyl 2,3-dioxygenase from sphingomonas2 yanoikuyae b1 bound to biphenyl
44	<a href="#">c3k7cC</a>	Alignment	not modelled	87.1	16	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> putative ntf2-like transpeptidase; <b>PDBTitle:</b> crystal structure of putative ntf2-like transpeptidase (np_281412.1)2 from campylobacter jejuni at 2.00 a resolution
45	<a href="#">d2b1xb1</a>	Alignment	not modelled	87.1	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
46	<a href="#">c4hzbE</a>	Alignment	not modelled	86.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> putative periplasmic protein; <b>PDBTitle:</b> crystal structure of the type vi semet effector-immunity complex tae3-2 tai3 from ralstonia pickettii
47	<a href="#">c3gwrA</a>	Alignment	not modelled	85.6	12	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> putative calcium/calmodulin-dependent protein kinase type <b>PDBTitle:</b> crystal structure of putative calcium/calmodulin-dependent protein2 kinase type ii association domain (yp_315894.1) from thiobacillus3 denitrificans atcc 25259 at 2.00 a resolution
48	<a href="#">c3soyA</a>	Alignment	not modelled	83.2	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> ntf2-like superfamily protein; <b>PDBTitle:</b> nuclear transport factor 2 (ntf2-like) superfamily protein from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
49	<a href="#">c6bjuD</a>	Alignment	not modelled	81.7	14	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> atzh; <b>PDBTitle:</b> the structure of atzh: a little known member of the atrazine breakdown2 pathway
50	<a href="#">d3e99a1</a>	Alignment	not modelled	81.6	6	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
51	<a href="#">c4fczB</a>	Alignment	not modelled	80.5	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> toluene-tolerance protein; <b>PDBTitle:</b> crystal structure of toluene-tolerance protein from pseudomonas putida2 (strain kt2440), northeast structural genomics consortium (nesg)3 target ppr99
52	<a href="#">d3b7ca1</a>	Alignment	not modelled	80.3	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
53	<a href="#">c5ig0A</a>	Alignment	not modelled	79.2	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> camk/camk2 protein kinase; <b>PDBTitle:</b> crystal structure of s. rosetta camkii hub
						<b>PDB header:</b> transport protein

54	<a href="#">c3ub1C_</a>	Alignment	not modelled	72.5	16	<b>Chain:</b> C: <b>PDB Molecule:</b> orf13-like protein; <b>PDBTitle:</b> ntf2 like protein involved in plasmid conjugation
55	<a href="#">d1vqqa1</a>	Alignment	not modelled	72.1	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Penicillin binding protein 2a (PBP2A), N-terminal domain
56	<a href="#">c2rsxA_</a>	Alignment	not modelled	66.3	26	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yoeb; <b>PDBTitle:</b> solution structure of isea, an inhibitor protein of dl- endopeptidases2 from bacillus subtilis
57	<a href="#">c2qguA_</a>	Alignment	not modelled	64.6	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable signal peptide protein; <b>PDBTitle:</b> three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
58	<a href="#">c1mwuA_</a>	Alignment	not modelled	63.5	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 2a; <b>PDBTitle:</b> structure of methicillin acyl-penicillin binding protein 2a from2 methicillin resistant staphylococcus aureus strain 27r at 2.60 a3 resolution.
59	<a href="#">c5uwaB_</a>	Alignment	not modelled	55.4	8	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable phospholipid-binding protein mlac; <b>PDBTitle:</b> structure of e. coli phospholipid binding protein mlac
60	<a href="#">d2cw9a1</a>	Alignment	not modelled	55.2	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> TIM44-like
61	<a href="#">d2owpa1</a>	Alignment	not modelled	52.1	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
62	<a href="#">c3ke7A_</a>	Alignment	not modelled	49.6	9	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ketosteroid isomerase; <b>PDBTitle:</b> crystal structure of putative ketosteroid isomerase (yp_001303366.1)2 from parabacteroides distasonis atcc 8503 at 1.45 a resolution
63	<a href="#">c3dukD_</a>	Alignment	not modelled	48.7	21	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> ntf2-like protein of unknown function; <b>PDBTitle:</b> crystal structure of a ntf2-like protein of unknown function2 (mfla_0564) from methylobacillus flagellatus kt at 2.200 a resolution
64	<a href="#">c4ce4i_</a>	Alignment	not modelled	48.1	13	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> mrpl9; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
65	<a href="#">c3fkaD_</a>	Alignment	not modelled	41.1	14	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized ntf-2 like protein; <b>PDBTitle:</b> crystal structure of a ntf-2 like protein of unknown function2 (spo1084) from silicibacter pomeroyi dss-3 at 1.69 a resolution
66	<a href="#">d3bb9a1</a>	Alignment	not modelled	40.0	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
67	<a href="#">c3hzaA_</a>	Alignment	not modelled	40.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ntf2-like protein of unknown function; <b>PDBTitle:</b> crystal structure of ntf2-like protein of unknown function mn2a_05052 from prochlorococcus marinus (yp_291699.1) from prochlorococcus sp.3 nat12a at 1.40 a resolution
68	<a href="#">c4o3vA_</a>	Alignment	not modelled	35.3	7	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> virb8-like protein of type iv secretion system; <b>PDBTitle:</b> crystal structure of a virb8-like protein of type iv secretion system2 from rickettsia typhi
69	<a href="#">c6humQ_</a>	Alignment	not modelled	33.8	24	<b>PDB header:</b> proton transport <b>Chain:</b> Q: <b>PDB Molecule:</b> proton-translocating nadh-quinone dehydrogenase subunit q <b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus
70	<a href="#">c4y4vB_</a>	Alignment	not modelled	33.6	6	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical secreted protein; <b>PDBTitle:</b> structure of helicobacter pylori csd6 in the d-ala-bound state
71	<a href="#">c4r4gA_</a>	Alignment	not modelled	28.4	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative lipoprotein ycda; <b>PDBTitle:</b> crystal structure of a putative lipoprotein (ycda) from bacillus2 subtilis subsp. subtilis str. 168 at 2.62 a resolution
72	<a href="#">c3fsdA_</a>	Alignment	not modelled	24.5	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ntf2-like protein of unknown function in nutrient uptake; <b>PDBTitle:</b> crystal structure of ntf2-like protein of unknown function in nutrient2 uptake (yp_427473.1) from rhodospirillum rubrum atcc 11170 at 1.70 a3 resolution
73	<a href="#">c3kspA_</a>	Alignment	not modelled	24.3	10	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> calcium/calmodulin-dependent kinase ii association domain; <b>PDBTitle:</b> crystal structure of a putative ca/calmodulin-dependent kinase ii2 association domain (exig_1688) from exiguobacterium sibiricum 255-153 at 2.59 a resolution
74	<a href="#">c3gzxB_</a>	Alignment	not modelled	22.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> biphenyl dioxygenase subunit beta; <b>PDBTitle:</b> crystal structure of the biphenyl dioxygenase in complex with biphenyl2 from comamonas testosteroni sp. strain b-356
75	<a href="#">c5up5A_</a>	Alignment	not modelled	20.3	43	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> ehee_rd1_0284; <b>PDBTitle:</b> solution structure of the de novo mini protein ehee_rd1_0284
76	<a href="#">d1ulib_</a>	Alignment	not modelled	17.4	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit <b>PDB header:</b> metal binding protein

77	<a href="#">c1zeqX_</a>	Alignment	not modelled	15.1	14	<b>Chain:</b> X: <b>PDB Molecule:</b> cation efflux system protein cusf; <b>PDBTitle:</b> 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
78	<a href="#">d1wqlb1</a>	Alignment	not modelled	14.5	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
79	<a href="#">c2yewl_</a>	Alignment	not modelled	13.6	23	<b>PDB header:</b> virus <b>Chain:</b> I: <b>PDB Molecule:</b> e2 envelope glycoprotein; <b>PDBTitle:</b> modeling barmah forest virus structural proteins
80	<a href="#">c4or1A_</a>	Alignment	not modelled	13.5	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf4783 family protein (bacova_04304) from2 bacteroides ovatus atcc 8483 at 1.40 a resolution
81	<a href="#">c4ouqA_</a>	Alignment	not modelled	13.1	5	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf4783 family protein (bf1468) from2 bacteroides fragilis ych46 at 1.55 a resolution
82	<a href="#">c5ve9C_</a>	Alignment	not modelled	12.2	38	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> microtubule-actin cross-linking factor 1, isoforms 1/2/3/5; <b>PDBTitle:</b> structure of hacf7 ef1-ef2-gar domains
83	<a href="#">d1g6pa_</a>	Alignment	not modelled	11.5	10	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
84	<a href="#">c3qk9B_</a>	Alignment	not modelled	11.4	14	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> mitochondrial import inner membrane translocase subunit <b>PDBTitle:</b> yeast tim44 c-terminal domain complexed with cymal-3
85	<a href="#">c2l3oA_</a>	Alignment	not modelled	10.8	50	<b>PDB header:</b> cytokine <b>Chain:</b> A: <b>PDB Molecule:</b> interleukin 3; <b>PDBTitle:</b> solution structure of murine interleukin 3
86	<a href="#">d1v5ra1</a>	Alignment	not modelled	10.3	38	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> GAS2 domain-like <b>Family:</b> GAS2 domain
87	<a href="#">c6bzfG_</a>	Alignment	not modelled	9.7	33	<b>PDB header:</b> dna binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> sporulation-specific protein 16; <b>PDBTitle:</b> structure of s. cerevisiae zip2:spo16 complex, c2 form
88	<a href="#">c5vf3Z_</a>	Alignment	not modelled	9.6	67	<b>PDB header:</b> virus <b>Chain:</b> Z: <b>PDB Molecule:</b> highly immunogenic outer capsid protein; <b>PDBTitle:</b> bacteriophage t4 isometric capsid
89	<a href="#">c3wxxF_</a>	Alignment	not modelled	9.0	6	<b>PDB header:</b> membrane protein/chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> aoopb; <b>PDBTitle:</b> crystal structure of a t3ss complex from aeromonas hydrophila
90	<a href="#">c3cvqC_</a>	Alignment	not modelled	8.5	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> putative metal binding protein; <b>PDBTitle:</b> crystal structure of a periplasmic putative metal binding protein
91	<a href="#">c2ml6A_</a>	Alignment	not modelled	7.8	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr structure of protein zp_02069618.1 from bacteroides uniformis atcc2 8492
92	<a href="#">c4jzaB_</a>	Alignment	not modelled	7.0	5	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a legionella phosphoinositide phosphatase:2 insights into lipid metabolism in pathogen host interaction
93	<a href="#">c2lxcB_</a>	Alignment	not modelled	5.7	15	<b>PDB header:</b> protein binding/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> small glutamine-rich tetratricopeptide repeat-containing <b>PDBTitle:</b> solution structure of the complex between the sgt2 homodimerization2 domain and the get5 ubl domain
94	<a href="#">c5ts4A_</a>	Alignment	not modelled	5.7	5	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> denovo ntf2; <b>PDBTitle:</b> crystal structure of a de novo designed protein with curved beta-sheet
95	<a href="#">c5uyvA_</a>	Alignment	not modelled	5.3	18	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic chelated iron-binding protein yfea; <b>PDBTitle:</b> yfea ancillary sites that do not co-load with site 2
96	<a href="#">c3r2cJ_</a>	Alignment	not modelled	5.2	6	<b>PDB header:</b> transcription/rna <b>Chain:</b> J: <b>PDB Molecule:</b> 30s ribosomal protein s10; <b>PDBTitle:</b> crystal structure of antitermination factors nusB and nusE in complex2 with boxA rna
97	<a href="#">d2rcda1</a>	Alignment	not modelled	5.1	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like