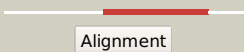

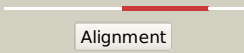
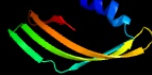


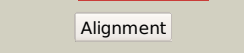



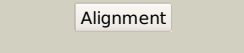

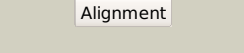



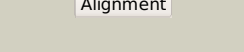

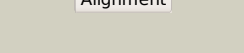

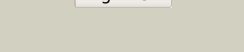












# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2390c_(-) _2683719_2684276
Date	Mon Aug 5 13:25:54 BST 2019
Unique Job ID	c23d8e5fce42c5c5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5d9rA_</a>	 Alignment		97.3	16	<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
2	<a href="#">c3a76B_</a>	 Alignment		97.2	9	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> gamma-hexachlorocyclohexane dehydrochlorinase; <b>PDBTitle:</b> the crystal structure of lina
3	<a href="#">d2ux0a1</a>	 Alignment		97.0	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
4	<a href="#">c5cniA_</a>	 Alignment		96.9	10	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> icml-like; <b>PDBTitle:</b> crystal structure of an icml-like type iv secretion system protein2 (lpg0120) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1 at 2.65 a resolution
5	<a href="#">c3wz4F_</a>	 Alignment		96.8	9	<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)
6	<a href="#">c5u9oD_</a>	 Alignment		96.6	10	<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
7	<a href="#">d1hkxa_</a>	 Alignment		96.5	11	<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="#">c3wz3A_</a>	 Alignment		96.5	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tram protein; <b>PDBTitle:</b> structure of a periplasmic fragment of tram
9	<a href="#">d3stda_</a>	 Alignment		96.5	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
10	<a href="#">d3b8la1</a>	 Alignment		96.5	6	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
11	<a href="#">c4i4kB_</a>	 Alignment		96.4	8	<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

12	<a href="#">d3d9ra1</a>	Alignment		96.3	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> ECA1476-like
13	<a href="#">d3ef8a1</a>	Alignment		96.1	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
14	<a href="#">d2rffa1</a>	Alignment		96.0	5	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
15	<a href="#">d3cu3a1</a>	Alignment		96.0	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
16	<a href="#">c3h51A</a>	Alignment		96.0	13	<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
17	<a href="#">d1idpa</a>	Alignment		95.9	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
18	<a href="#">c3gzrA</a>	Alignment		95.8	10	<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
19	<a href="#">d2f86b1</a>	Alignment		95.2	10	<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
20	<a href="#">d3ebya1</a>	Alignment		95.1	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
21	<a href="#">c3robC</a>	Alignment	not modelled	94.8	11	<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
22	<a href="#">c4ovmE</a>	Alignment	not modelled	94.7	13	<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
23	<a href="#">c4nhfF</a>	Alignment	not modelled	94.6	15	<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
24	<a href="#">c5ig5E</a>	Alignment	not modelled	94.6	9	<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
25	<a href="#">d2rgga1</a>	Alignment	not modelled	94.3	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
26	<a href="#">c5ig4A</a>	Alignment	not modelled	94.2	11	<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
27	<a href="#">c4lehA</a>	Alignment	not modelled	94.2	5	<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
28	<a href="#">c5i97C</a>	Alignment	not modelled	93.6	15	<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 traec from the pkm101 type iv2 secretion system

29	<a href="#">c3f7sA</a>	Alignment	not modelled	92.9	12	<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
30	<a href="#">d2chca1</a>	Alignment	not modelled	92.8	7	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
31	<a href="#">d3b7ca1</a>	Alignment	not modelled	92.3	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
32	<a href="#">d2b1xb1</a>	Alignment	not modelled	92.1	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
33	<a href="#">d2cc3a1</a>	Alignment	not modelled	91.9	8	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> VirB8-like
34	<a href="#">c6of9G</a>	Alignment	not modelled	91.4	16	<b>PDB header:</b> unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> camkii hub; <b>PDBTitle:</b> structure of the chlamydomonas reinhardtii camkii hub homology domain
35	<a href="#">c4gb5A</a>	Alignment	not modelled	90.1	10	<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
36	<a href="#">c2gbxF</a>	Alignment	not modelled	89.2	12	<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
37	<a href="#">d2bhma1</a>	Alignment	not modelled	89.0	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> VirB8-like
38	<a href="#">c2bhmE</a>	Alignment	not modelled	88.1	11	<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
39	<a href="#">c3soyA</a>	Alignment	not modelled	87.8	17	<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
40	<a href="#">c3hx8A</a>	Alignment	not modelled	87.0	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 (np_103587.1) from2 mesorhizobium loti at 1.45 a resolution
41	<a href="#">c4hzbE</a>	Alignment	not modelled	84.4	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
42	<a href="#">d3ejva1</a>	Alignment	not modelled	83.7	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
43	<a href="#">c3k7cC</a>	Alignment	not modelled	81.7	14	<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
44	<a href="#">c5ig0A</a>	Alignment	not modelled	81.4	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
45	<a href="#">c4meiA</a>	Alignment	not modelled	81.1	12	<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
46	<a href="#">d3cnxa1</a>	Alignment	not modelled	80.1	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SAV4671-like
47	<a href="#">c3bb9D</a>	Alignment	not modelled	79.6	11	<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
48	<a href="#">c4o3vA</a>	Alignment	not modelled	79.2	12	<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
49	<a href="#">d2r4ia1</a>	Alignment	not modelled	78.3	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> CHU142-like
50	<a href="#">d3blza1</a>	Alignment	not modelled	75.6	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Sbal0622-like
51	<a href="#">c6bjuD</a>	Alignment	not modelled	74.3	11	<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
52	<a href="#">d3bb9a1</a>	Alignment	not modelled	73.7	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
53	<a href="#">c2rsxA</a>	Alignment	not modelled	71.6	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
54	<a href="#">c3gwrA</a>	Alignment	not modelled	69.2	10	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> putative calcium/calmodulin-dependent protein kinase type

54	<a href="#">c9gw1A</a>	Alignment	not modelled	65.2	10	<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
55	<a href="#">d2owpa1</a>	Alignment	not modelled	65.2	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
56	<a href="#">c5uwaB</a>	Alignment	not modelled	65.1	16	<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
57	<a href="#">d3e99a1</a>	Alignment	not modelled	59.4	7	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
58	<a href="#">c3fkaD</a>	Alignment	not modelled	57.5	17	<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
59	<a href="#">c4fczB</a>	Alignment	not modelled	53.5	14	<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
60	<a href="#">c4ce4i</a>	Alignment	not modelled	50.5	8	<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
61	<a href="#">c1mwuA</a>	Alignment	not modelled	48.4	17	<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.
62	<a href="#">c3fsdA</a>	Alignment	not modelled	44.5	8	<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
63	<a href="#">d1vqqa1</a>	Alignment	not modelled	40.9	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Penicillin binding protein 2a (PBP2A), N-terminal domain
64	<a href="#">c2qguA</a>	Alignment	not modelled	37.9	19	<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
65	<a href="#">c4ouqA</a>	Alignment	not modelled	37.1	19	<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
66	<a href="#">c4or1A</a>	Alignment	not modelled	36.8	19	<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
67	<a href="#">c3kspA</a>	Alignment	not modelled	35.4	13	<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 exigubacterium sibiricum 255-153 at 2.59 a resolution
68	<a href="#">c3dukD</a>	Alignment	not modelled	34.4	13	<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
69	<a href="#">c4r4gA</a>	Alignment	not modelled	33.3	17	<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
70	<a href="#">d2rcda1</a>	Alignment	not modelled	30.7	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
71	<a href="#">c5ve9C</a>	Alignment	not modelled	24.1	50	<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
72	<a href="#">d1v5ra1</a>	Alignment	not modelled	22.0	50	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> GAS2 domain-like <b>Family:</b> GAS2 domain
73	<a href="#">c2jpwA</a>	Alignment	not modelled	19.3	35	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> troponin i, cardiac muscle; <b>PDBTitle:</b> solution structure of the bisphosphorylated cardiac2 specific n-extension of cardiac troponin i
74	<a href="#">c3hzaA</a>	Alignment	not modelled	19.0	14	<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
75	<a href="#">c3ke7A</a>	Alignment	not modelled	19.0	21	<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
76	<a href="#">c5ts4A</a>	Alignment	not modelled	16.6	30	<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 <b>PDB header:</b> de novo protein

77	<a href="#">c5up5A_</a>	Alignment	not modelled	15.9	38	<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
78	<a href="#">c2n6uA_</a>	Alignment	not modelled	15.1	29	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> astexin2-dc4; <b>PDBTitle:</b> solution study of astexin2-dc4
79	<a href="#">d1wqlb1</a>	Alignment	not modelled	12.2	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
80	<a href="#">c3j6vl_</a>	Alignment	not modelled	10.8	7	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 28s ribosomal protein s9, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
81	<a href="#">c3gzxB_</a>	Alignment	not modelled	10.0	12	<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
82	<a href="#">c2micB_</a>	Alignment	not modelled	8.7	20	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 16; <b>PDBTitle:</b> nmr structure of p75 transmembrane domain in dpc micelles
83	<a href="#">c2micA_</a>	Alignment	not modelled	8.7	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 16; <b>PDBTitle:</b> nmr structure of p75 transmembrane domain in dpc micelles
84	<a href="#">c3r2cJ_</a>	Alignment	not modelled	8.4	28	<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
85	<a href="#">c5djQO_</a>	Alignment	not modelled	7.9	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase.
86	<a href="#">c5djQ_</a>	Alignment	not modelled	7.9	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase.
87	<a href="#">c5djQP_</a>	Alignment	not modelled	7.9	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> P: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase.
88	<a href="#">c5djQN_</a>	Alignment	not modelled	7.9	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> N: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase.
89	<a href="#">c6f0kA_</a>	Alignment	not modelled	7.5	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c family protein; <b>PDBTitle:</b> alternative complex iii
90	<a href="#">c3efyB_</a>	Alignment	not modelled	6.9	24	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cif (cell cycle inhibiting factor); <b>PDBTitle:</b> structure of the cyclomodulin cif from pathogenic2 escherichia coli
91	<a href="#">d1ulib_</a>	Alignment	not modelled	6.7	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
92	<a href="#">c3rgaA_</a>	Alignment	not modelled	6.6	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase; <b>PDBTitle:</b> crystal structure of epoxide hydrolase for polyether lasalocid a2 biosynthesis
93	<a href="#">c1zeqX_</a>	Alignment	not modelled	6.5	5	<b>PDB header:</b> metal binding protein <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
94	<a href="#">c2ml6A_</a>	Alignment	not modelled	6.3	19	<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
95	<a href="#">d2cw9a1</a>	Alignment	not modelled	6.3	6	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> TIM44-like
96	<a href="#">c2mewA_</a>	Alignment	not modelled	6.3	30	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> 30s ribosomal protein s10; <b>PDBTitle:</b> solution structure of nuse (s10) from thermotoga maritima
97	<a href="#">d2bmob1</a>	Alignment	not modelled	6.3	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
98	<a href="#">c5x9jB_</a>	Alignment	not modelled	5.9	7	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> prhc; <b>PDBTitle:</b> structre of prhc from penicillium brasilianum nbrc 6234
99	<a href="#">c5v6fA_</a>	Alignment	not modelled	5.6	27	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hemolysin-related protein; <b>PDBTitle:</b> crystal structure of the second beta-prism domain of rbmc from v.2 cholerae bound to manntriose