



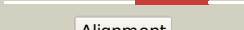
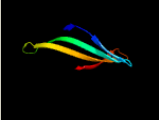
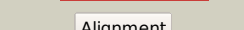

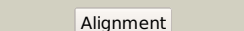





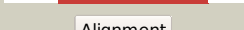

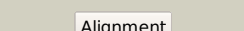

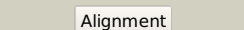





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3492c (- )_3910644_3911126
Date	Fri Aug 9 18:20:16 BST 2019
Unique Job ID	6543fdf113632008

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5d9rA_</a>	 Alignment		97.2	13	<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="#">d2ux0a1</a>	 Alignment		97.2	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
3	<a href="#">d3b8la1</a>	 Alignment		96.9	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
4	<a href="#">c3wz4F_</a>	 Alignment		96.8	16	<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)
5	<a href="#">c5cniA_</a>	 Alignment		96.8	12	<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
6	<a href="#">c4i4kB_</a>	 Alignment		96.8	10	<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
7	<a href="#">d1hkxa_</a>	 Alignment		96.7	13	<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		96.6	11	<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="#">c5u9oD_</a>	 Alignment		96.6	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
10	<a href="#">d2rfra1</a>	 Alignment		96.5	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
11	<a href="#">c3h51A_</a>	 Alignment		96.5	17	<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

12	<a href="#">c4ovmE_</a>	Alignment		96.3	12	<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
13	<a href="#">d3cu3a1</a>	Alignment		96.1	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
14	<a href="#">d1idpa_</a>	Alignment		96.0	20	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
15	<a href="#">d2f86b1</a>	Alignment		95.9	12	<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
16	<a href="#">c3a76B_</a>	Alignment		95.7	8	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> gamma-hexachlorocyclohexane dehydrochlorinase; <b>PDBTitle:</b> the crystal structure of lina
17	<a href="#">d2rgqa1</a>	Alignment		95.6	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
18	<a href="#">d3stda_</a>	Alignment		95.5	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
19	<a href="#">d2chca1</a>	Alignment		95.4	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
20	<a href="#">d3ef8a1</a>	Alignment		95.2	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
21	<a href="#">c5ig5E_</a>	Alignment	not modelled	95.2	11	<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
22	<a href="#">c3robC_</a>	Alignment	not modelled	94.6	15	<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
23	<a href="#">c5ig4A_</a>	Alignment	not modelled	94.5	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
24	<a href="#">c4gb5A_</a>	Alignment	not modelled	94.4	11	<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
25	<a href="#">d3ebye1</a>	Alignment	not modelled	94.1	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
26	<a href="#">c6of9G_</a>	Alignment	not modelled	94.1	18	<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
27	<a href="#">d3ejva1</a>	Alignment	not modelled	93.7	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
28	<a href="#">c4nhfF_</a>	Alignment	not modelled	93.6	13	<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
						<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein with a ntf2-like

29	<a href="#">c3gqrA</a>	Alignment	not modelled	93.2	18	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
30	<a href="#">c3bb9D</a>	Alignment	not modelled	93.1	18	<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
31	<a href="#">c3soyA</a>	Alignment	not modelled	93.1	8	<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
32	<a href="#">c3f7sA</a>	Alignment	not modelled	93.1	10	<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
33	<a href="#">d3d9ra1</a>	Alignment	not modelled	92.9	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> ECA1476-like
34	<a href="#">c3gwrA</a>	Alignment	not modelled	92.8	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
35	<a href="#">c4lehA</a>	Alignment	not modelled	92.6	16	<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 (clocsi_03134)2 from clostridium scindens atcc 35704 at 2.90 a resolution
36	<a href="#">c2gbxF</a>	Alignment	not modelled	92.5	9	<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="#">c3ub1C</a>	Alignment	not modelled	92.0	9	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> orf13-like protein; <b>PDBTitle:</b> ntf2 like protein involved in plasmid conjugation
38	<a href="#">c3hx8A</a>	Alignment	not modelled	91.8	11	<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
39	<a href="#">d2cc3a1</a>	Alignment	not modelled	91.5	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> VirB8-like
40	<a href="#">c5i97C</a>	Alignment	not modelled	91.2	17	<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
41	<a href="#">c4meiA</a>	Alignment	not modelled	91.0	17	<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
42	<a href="#">d2b1xb1</a>	Alignment	not modelled	90.7	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
43	<a href="#">c4hzbE</a>	Alignment	not modelled	89.7	27	<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
44	<a href="#">d3e99a1</a>	Alignment	not modelled	89.7	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
45	<a href="#">d3cxa1</a>	Alignment	not modelled	88.5	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SAV4671-like
46	<a href="#">d2bhma1</a>	Alignment	not modelled	86.6	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> VirB8-like
47	<a href="#">c3k7cC</a>	Alignment	not modelled	85.3	21	<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
48	<a href="#">c2qguA</a>	Alignment	not modelled	85.2	21	<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
49	<a href="#">c2bhmE</a>	Alignment	not modelled	85.2	16	<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
50	<a href="#">d3b7ca1</a>	Alignment	not modelled	84.1	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
51	<a href="#">d2r4ia1</a>	Alignment	not modelled	83.2	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> CHU142-like
52	<a href="#">c5ig0A</a>	Alignment	not modelled	82.4	11	<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 <b>Chain:</b> B: <b>PDB Molecule:</b> toluene-tolerance protein;

53	<a href="#">c4fczB_</a>	Alignment	not modelled	81.7	13	<b>PDBTitle:</b> crystal structure of toluene-tolerance protein from pseudomonas putida2 (strain kt2440), northeast structural genomics consortium (nesg)3 target ppr99
54	<a href="#">d3blza1</a>	Alignment	not modelled	81.6	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Sbal0622-like
55	<a href="#">c5uwaB_</a>	Alignment	not modelled	81.5	13	<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
56	<a href="#">d3bb9a1</a>	Alignment	not modelled	79.9	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
57	<a href="#">c2rsxA_</a>	Alignment	not modelled	76.2	19	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yoeb; <b>PDBTitle:</b> solution structure of izea, an inhibitor protein of dl-endopeptidases2 from bacillus subtilis
58	<a href="#">c3fkaD_</a>	Alignment	not modelled	62.2	25	<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="#">c3hzaA_</a>	Alignment	not modelled	60.4	20	<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
60	<a href="#">c3kspA_</a>	Alignment	not modelled	59.0	9	<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
61	<a href="#">c3ke7A_</a>	Alignment	not modelled	57.4	14	<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
62	<a href="#">d1ulib_</a>	Alignment	not modelled	55.7	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
63	<a href="#">c3gzxB_</a>	Alignment	not modelled	50.6	19	<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
64	<a href="#">d2rcda1</a>	Alignment	not modelled	48.2	19	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
65	<a href="#">c6bjuD_</a>	Alignment	not modelled	45.9	18	<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
66	<a href="#">c3dukD_</a>	Alignment	not modelled	44.9	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
67	<a href="#">c3fsdA_</a>	Alignment	not modelled	43.4	13	<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
68	<a href="#">d1wqlb1</a>	Alignment	not modelled	42.7	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
69	<a href="#">d1vqqa1</a>	Alignment	not modelled	42.1	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Penicillin binding protein 2a (PBP2A), N-terminal domain
70	<a href="#">c1mwuA_</a>	Alignment	not modelled	38.8	13	<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.
71	<a href="#">c4r4gA_</a>	Alignment	not modelled	34.5	13	<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="#">c1zeqX_</a>	Alignment	not modelled	32.8	15	<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
73	<a href="#">c4o3vA_</a>	Alignment	not modelled	25.2	13	<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
74	<a href="#">d2owpa1</a>	Alignment	not modelled	25.2	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
75	<a href="#">c2l9uB_</a>	Alignment	not modelled	25.0	23	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-3; <b>PDBTitle:</b> spatial structure of dimeric erbb3 transmembrane domain
76	<a href="#">c5ve9C_</a>	Alignment	not modelled	24.6	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

77	<a href="#">d2bmob1</a>	Alignment	not modelled	24.5	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
78	<a href="#">c2l9uA</a>	Alignment	not modelled	23.5	23	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-3; <b>PDBTitle:</b> spatial structure of dimeric erbb3 transmembrane domain
79	<a href="#">c4ce4i</a>	Alignment	not modelled	23.0	14	<b>PDB header:</b> ribosome <b>Chain:</b> l: <b>PDB Molecule:</b> mrpl9; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
80	<a href="#">d1v5ra1</a>	Alignment	not modelled	22.9	38	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> GAS2 domain-like <b>Family:</b> GAS2 domain
81	<a href="#">c2ml6A</a>	Alignment	not modelled	17.7	47	<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
82	<a href="#">c5up5A</a>	Alignment	not modelled	15.8	29	<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
83	<a href="#">c4ouqA</a>	Alignment	not modelled	15.3	37	<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
84	<a href="#">c4or1A</a>	Alignment	not modelled	14.9	21	<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
85	<a href="#">d2gxfa1</a>	Alignment	not modelled	14.1	22	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> YybH-like
86	<a href="#">c3i0uA</a>	Alignment	not modelled	12.9	27	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphothreonine lyase ospf; <b>PDBTitle:</b> structure of the type iii effector/phosphothreonine lyase ospf from2 shigella flexneri
87	<a href="#">c2z8nB</a>	Alignment	not modelled	11.8	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 27.5 kda virulence protein; <b>PDBTitle:</b> structural basis for the catalytic mechanism of phosphothreonine lyase
88	<a href="#">c2l55A</a>	Alignment	not modelled	11.5	20	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> silb,silver efflux protein, mfp component of the three <b>PDBTitle:</b> solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
89	<a href="#">c5djQ</a>	Alignment	not modelled	11.3	29	<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.
90	<a href="#">c5djQ</a>	Alignment	not modelled	11.3	29	<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.
91	<a href="#">c5djQ</a>	Alignment	not modelled	11.3	29	<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.
92	<a href="#">c5djQ</a>	Alignment	not modelled	11.3	29	<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.
93	<a href="#">c2micA</a>	Alignment	not modelled	10.8	24	<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
94	<a href="#">c2micB</a>	Alignment	not modelled	10.8	24	<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
95	<a href="#">c5ts4A</a>	Alignment	not modelled	9.5	14	<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
96	<a href="#">c6f0kA</a>	Alignment	not modelled	8.7	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
97	<a href="#">d1o7nb</a>	Alignment	not modelled	8.2	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
98	<a href="#">d2cw9a1</a>	Alignment	not modelled	7.7	5	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> TIM44-like
99	<a href="#">c4y4vB</a>	Alignment	not modelled	6.8	8	<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