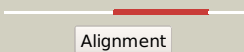

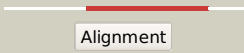



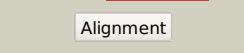



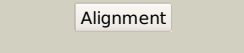

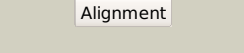



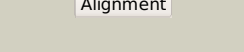

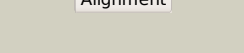

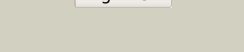






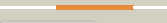



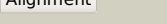
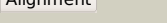




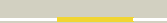

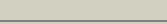





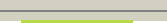


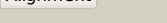
# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0175 (-) _206812_207453
Date	Tue Jul 23 14:50:22 BST 2019
Unique Job ID	1074088a20582e34

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5d9rA_</a>	 Alignment		97.0	8	<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		96.9	9	<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="#">d1hkxa_</a>	 Alignment		96.5	9	<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="#">c5i97C_</a>	 Alignment		96.4	7	<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
5	<a href="#">d3d9ra1</a>	 Alignment		95.8	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> ECA1476-like
6	<a href="#">c5u9oD_</a>	 Alignment		95.6	16	<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="#">d3cu3a1</a>	 Alignment		95.4	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
8	<a href="#">d2cc3a1</a>	 Alignment		95.4	7	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> VirB8-like
9	<a href="#">c4nhfF_</a>	 Alignment		95.3	8	<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
10	<a href="#">c4i4kB_</a>	 Alignment		95.3	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
11	<a href="#">d2f86b1</a>	 Alignment		95.2	9	<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

12	<a href="#">c5ig4A_</a>	Alignment		95.1	7	<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
13	<a href="#">d3stda_</a>	Alignment		95.0	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
14	<a href="#">c3a76B_</a>	Alignment		94.9	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
15	<a href="#">d3b8la1</a>	Alignment		94.8	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
16	<a href="#">c3h51A_</a>	Alignment		94.7	10	<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="#">c4ovmE_</a>	Alignment		94.7	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
18	<a href="#">c5cn1A_</a>	Alignment		94.5	11	<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
19	<a href="#">d3ef8a1</a>	Alignment		94.4	7	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
20	<a href="#">d1ldpa_</a>	Alignment		94.2	19	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
21	<a href="#">c3gza_</a>	Alignment	not modelled	94.1	8	<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
22	<a href="#">d2rgqa1</a>	Alignment	not modelled	93.2	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
23	<a href="#">c3wz4F_</a>	Alignment	not modelled	92.6	15	<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)
24	<a href="#">d2rfra1</a>	Alignment	not modelled	92.6	8	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
25	<a href="#">c3wz3A_</a>	Alignment	not modelled	92.5	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
26	<a href="#">d2bhma1</a>	Alignment	not modelled	90.9	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> VirB8-like
27	<a href="#">c5ig5E_</a>	Alignment	not modelled	90.9	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
28	<a href="#">c2bhmE_</a>	Alignment	not modelled	90.8	10	<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

29	<a href="#">c3f7sA</a>	 Alignment	not modelled	90.7	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
30	<a href="#">d3b7ca1</a>	 Alignment	not modelled	90.4	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
31	<a href="#">c6of9G</a>	 Alignment	not modelled	90.2	14	<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
32	<a href="#">d3ebya1</a>	 Alignment	not modelled	89.1	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
33	<a href="#">c3robC</a>	 Alignment	not modelled	88.9	7	<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
34	<a href="#">c3gwrA</a>	 Alignment	not modelled	88.6	8	<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="#">c4gb5A</a>	 Alignment	not modelled	87.0	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="#">c4hzbE</a>	 Alignment	not modelled	86.9	18	<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
37	<a href="#">c4lehA</a>	 Alignment	not modelled	86.7	6	<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
38	<a href="#">c3soyA</a>	 Alignment	not modelled	85.4	7	<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
39	<a href="#">d2b1xb1</a>	 Alignment	not modelled	82.9	8	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
40	<a href="#">d2chca1</a>	 Alignment	not modelled	82.5	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
41	<a href="#">c3bb9D</a>	 Alignment	not modelled	79.6	14	<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
42	<a href="#">c6bjuD</a>	 Alignment	not modelled	75.1	7	<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
43	<a href="#">d3ejva1</a>	 Alignment	not modelled	73.4	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
44	<a href="#">c4meiA</a>	 Alignment	not modelled	72.7	10	<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
45	<a href="#">c5ig0A</a>	 Alignment	not modelled	70.0	21	<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
46	<a href="#">d3cnxa1</a>	 Alignment	not modelled	67.9	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SAV4671-like
47	<a href="#">d3bb9a1</a>	 Alignment	not modelled	67.7	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
48	<a href="#">c2rsxA</a>	 Alignment	not modelled	67.4	21	<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
49	<a href="#">d2owpa1</a>	 Alignment	not modelled	67.1	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
50	<a href="#">c4fczB</a>	 Alignment	not modelled	65.2	20	<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
51	<a href="#">c2gbxF</a>	 Alignment	not modelled	64.8	14	<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
52	<a href="#">c3k7cC</a>	 Alignment	not modelled	62.2	11	<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
53	<a href="#">c4o3vA</a>	 Alignment	not modelled	59.8	11	<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
54	<a href="#">d2r4ia1</a>	Alignment	not modelled	56.6	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> CHU142-like
55	<a href="#">c3ub1C</a>	Alignment	not modelled	54.5	8	<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
56	<a href="#">c3ke7A</a>	Alignment	not modelled	53.3	17	<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
57	<a href="#">d3blza1</a>	Alignment	not modelled	49.5	6	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Sbal0622-like
58	<a href="#">c3hx8A</a>	Alignment	not modelled	47.7	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 (np_103587.1) from2 mesorhizobium loti at 1.45 a resolution
59	<a href="#">d1vqqa1</a>	Alignment	not modelled	41.9	8	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Penicillin binding protein 2a (PBP2A), N-terminal domain
60	<a href="#">d3e99a1</a>	Alignment	not modelled	37.7	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
61	<a href="#">c6f0kA</a>	Alignment	not modelled	37.5	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c family protein; <b>PDBTitle:</b> alternative complex iii
62	<a href="#">c6hwhX</a>	Alignment	not modelled	37.2	19	<b>PDB header:</b> electron transport <b>Chain:</b> X: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 4; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
63	<a href="#">c3fkaD</a>	Alignment	not modelled	34.9	20	<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
64	<a href="#">c3fsdA</a>	Alignment	not modelled	34.5	20	<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
65	<a href="#">c2n6uA</a>	Alignment	not modelled	33.0	21	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> astexin2-dc4; <b>PDBTitle:</b> solution study of astexin2-dc4
66	<a href="#">c3kspA</a>	Alignment	not modelled	31.5	4	<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
67	<a href="#">c2qguA</a>	Alignment	not modelled	31.5	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
68	<a href="#">c3hzaA</a>	Alignment	not modelled	31.1	8	<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 natl2a at 1.40 a resolution
69	<a href="#">c4ouqA</a>	Alignment	not modelled	30.8	13	<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
70	<a href="#">c3dukD</a>	Alignment	not modelled	30.1	8	<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
71	<a href="#">d2rcda1</a>	Alignment	not modelled	29.0	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
72	<a href="#">c5up5A</a>	Alignment	not modelled	26.5	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
73	<a href="#">c3qzxB</a>	Alignment	not modelled	26.2	13	<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
74	<a href="#">c4r4gA</a>	Alignment	not modelled	26.0	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
75	<a href="#">c4or1A</a>	Alignment	not modelled	24.6	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 a duf4783 family protein (bacova_04304) from2 bacteroides ovatus atcc 8483 at 1.40 a resolution
76	<a href="#">c5uwaB</a>	Alignment	not modelled	20.6	12	<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

77	<a href="#">c4ce4i</a>	Alignment	not modelled	20.0	6	<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
78	<a href="#">d1ulib</a>	Alignment	not modelled	18.8	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
79	<a href="#">c2lyyB</a>	Alignment	not modelled	18.5	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr structure of the protein nb7890a from shewanella sp
80	<a href="#">c5ve9C</a>	Alignment	not modelled	17.6	25	<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
81	<a href="#">c5ts4A</a>	Alignment	not modelled	17.5	24	<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
82	<a href="#">c2k9yB</a>	Alignment	not modelled	17.5	19	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> ephrin type-a receptor 2; <b>PDBTitle:</b> epha2 dimeric structure in the lipidic bicelle at ph 5.0
83	<a href="#">c2k9yA</a>	Alignment	not modelled	17.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ephrin type-a receptor 2; <b>PDBTitle:</b> epha2 dimeric structure in the lipidic bicelle at ph 5.0
84	<a href="#">d1v5ra1</a>	Alignment	not modelled	16.0	25	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> GAS2 domain-like <b>Family:</b> GAS2 domain
85	<a href="#">d1wqlb1</a>	Alignment	not modelled	15.6	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
86	<a href="#">c5o4uK</a>	Alignment	not modelled	14.7	12	<b>PDB header:</b> cell adhesion <b>Chain:</b> K; <b>PDB Molecule:</b> flagellin; <b>PDBTitle:</b> the flagellin of pyrococcus furiosus
87	<a href="#">c3r2cj</a>	Alignment	not modelled	14.5	30	<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
88	<a href="#">c5z1lL</a>	Alignment	not modelled	12.0	15	<b>PDB header:</b> protein fibril <b>Chain:</b> L; <b>PDB Molecule:</b> flagellin; <b>PDBTitle:</b> cryo-em structure of methanococcus maripaludis archaeellum
89	<a href="#">c2ks1B</a>	Alignment	not modelled	11.1	40	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> epidermal growth factor receptor; <b>PDBTitle:</b> heterodimeric association of transmembrane domains of erbB1 and erbB2 receptors enabling kinase activation
90	<a href="#">c5c0sA</a>	Alignment	not modelled	10.9	21	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> A; <b>PDB Molecule:</b> hemagglutinin, envelope glycoprotein, fibrin fusion <b>PDBTitle:</b> crystal structure of a generation 4 influenza hemagglutinin stabilized2 stem in complex with the broadly neutralizing antibody cr6261
91	<a href="#">c1wazA</a>	Alignment	not modelled	10.4	20	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> nmr structure determination of the bacterial mercury transporter,2 merf, in micelles
92	<a href="#">c5xyiU</a>	Alignment	not modelled	10.3	0	<b>PDB header:</b> ribosome <b>Chain:</b> U; <b>PDB Molecule:</b> ribosomal protein s10p/s20e, putative; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
93	<a href="#">c2mewA</a>	Alignment	not modelled	10.0	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
94	<a href="#">c2k1kA</a>	Alignment	not modelled	9.8	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
95	<a href="#">c2k1kB</a>	Alignment	not modelled	9.8	18	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
96	<a href="#">c2k1lB</a>	Alignment	not modelled	9.8	18	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
97	<a href="#">c2k1lA</a>	Alignment	not modelled	9.8	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
98	<a href="#">c5x9jB</a>	Alignment	not modelled	8.5	8	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> prhc; <b>PDBTitle:</b> strucutre of prhc from penicillium brasilianum nbrc 6234
99	<a href="#">c5tfyj</a>	Alignment	not modelled	7.8	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> J; <b>PDB Molecule:</b> flagellin; <b>PDBTitle:</b> the archaeal flagellum of methanospirillum hungatei strain jf1.