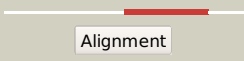
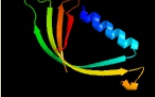
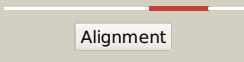

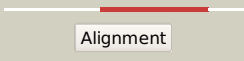

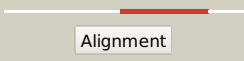

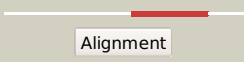

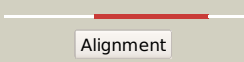

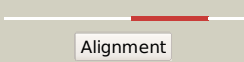

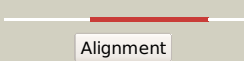

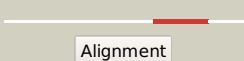
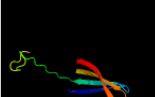
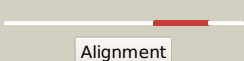
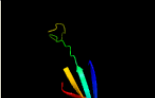
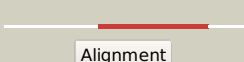






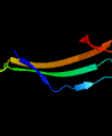





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1362c_(-)_1533954_1534616
Date	Wed Jul 31 22:05:46 BST 2019
Unique Job ID	9ff3c25ba95d75cc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5d9rA_</a>	 Alignment		97.4	17	<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		97.1	11	<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="#">c5cnlA_</a>	 Alignment		97.1	9	<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
4	<a href="#">c5u9oD_</a>	 Alignment		97.0	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
5	<a href="#">d2rfra1</a>	 Alignment		96.7	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
6	<a href="#">d3d9ra1</a>	 Alignment		96.5	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> ECA1476-like
7	<a href="#">d3b8la1</a>	 Alignment		96.5	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
8	<a href="#">d2ux0a1</a>	 Alignment		96.4	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
9	<a href="#">d3stda_</a>	 Alignment		96.4	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
10	<a href="#">d1ldpa_</a>	 Alignment		96.4	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
11	<a href="#">c3wz4F_</a>	 Alignment		96.3	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)

12	<a href="#">c4i4kB</a>	Alignment		96.2	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
13	<a href="#">d1hkxa</a>	Alignment		96.2	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
14	<a href="#">d3ef8a1</a>	Alignment		95.7	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
15	<a href="#">d3cu3a1</a>	Alignment		95.6	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
16	<a href="#">c3robC</a>	Alignment		95.5	8	<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
17	<a href="#">d2rgqa1</a>	Alignment		95.3	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
18	<a href="#">c5ig4A</a>	Alignment		95.1	8	<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
19	<a href="#">d2chca1</a>	Alignment		94.9	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
20	<a href="#">c4ovmE</a>	Alignment		94.9	17	<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
21	<a href="#">d2f86b1</a>	Alignment	not modelled	94.7	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
22	<a href="#">c3soyA</a>	Alignment	not modelled	94.5	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
23	<a href="#">d3ebya1</a>	Alignment	not modelled	94.4	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
24	<a href="#">c5ig5E</a>	Alignment	not modelled	94.1	16	<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="#">c3h51A</a>	Alignment	not modelled	93.9	26	<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
26	<a href="#">c6of9G</a>	Alignment	not modelled	93.8	18	<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
27	<a href="#">c3wz3A</a>	Alignment	not modelled	93.7	10	<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
						<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein with a ntf2-like

28	<a href="#">c3gqrA</a>	Alignment	not modelled	93.5	13	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
29	<a href="#">c4gb5A</a>	Alignment	not modelled	93.3	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 kfla4162 protein from kribbella flavida
30	<a href="#">d2b1xb1</a>	Alignment	not modelled	93.2	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
31	<a href="#">c4nhfF</a>	Alignment	not modelled	92.8	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
32	<a href="#">c3k7cC</a>	Alignment	not modelled	92.8	24	<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
33	<a href="#">c3hx8A</a>	Alignment	not modelled	92.4	22	<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
34	<a href="#">c3bb9D</a>	Alignment	not modelled	92.1	19	<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
35	<a href="#">c4lehA</a>	Alignment	not modelled	91.9	11	<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
36	<a href="#">c5i97C</a>	Alignment	not modelled	91.9	11	<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
37	<a href="#">c3f7sA</a>	Alignment	not modelled	91.7	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
38	<a href="#">c2gbxF</a>	Alignment	not modelled	91.3	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
39	<a href="#">c3ub1C</a>	Alignment	not modelled	91.2	14	<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
40	<a href="#">d2cc3a1</a>	Alignment	not modelled	91.0	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> VirB8-like
41	<a href="#">d3ejva1</a>	Alignment	not modelled	90.9	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
42	<a href="#">d3blza1</a>	Alignment	not modelled	87.0	20	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Sbal0622-like
43	<a href="#">d3e99a1</a>	Alignment	not modelled	87.0	8	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
44	<a href="#">c5ig0A</a>	Alignment	not modelled	86.7	18	<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="#">c2bhmE</a>	Alignment	not modelled	86.2	17	<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
46	<a href="#">d2bhma1</a>	Alignment	not modelled	84.7	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> VirB8-like
47	<a href="#">c4hzbE</a>	Alignment	not modelled	84.0	36	<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
48	<a href="#">c2qguA</a>	Alignment	not modelled	83.9	12	<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="#">c4meiA</a>	Alignment	not modelled	83.7	7	<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
50	<a href="#">c3gwrA</a>	Alignment	not modelled	83.5	10	<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
51	<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
52	<a href="#">d3cnxa1</a>	Alignment	not modelled	78.3	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SAV4671-like

53	<a href="#">d2r4ia1</a>	Alignment	not modelled	76.3	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> CHU142-like
54	<a href="#">c2rsxA</a>	Alignment	not modelled	75.2	32	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yoeb; <b>PDBTitle:</b> solution structure of iesa, an inhibitor protein of dl-endopeptidases2 from bacillus subtilis
55	<a href="#">d3b7ca1</a>	Alignment	not modelled	73.4	19	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
56	<a href="#">d3bb9a1</a>	Alignment	not modelled	68.3	20	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
57	<a href="#">c3kspA</a>	Alignment	not modelled	67.1	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 exigubacterium sibiricum 255-153 at 2.59 a resolution
58	<a href="#">c3fkaD</a>	Alignment	not modelled	66.4	33	<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="#">d1vqqa1</a>	Alignment	not modelled	56.7	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Penicillin binding protein 2a (PBP2A), N-terminal domain
60	<a href="#">c4fczB</a>	Alignment	not modelled	56.1	11	<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
61	<a href="#">c4o3vA</a>	Alignment	not modelled	54.6	9	<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
62	<a href="#">c3dukD</a>	Alignment	not modelled	53.5	26	<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
63	<a href="#">c3fsdA</a>	Alignment	not modelled	52.7	14	<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
64	<a href="#">d2owpa1</a>	Alignment	not modelled	46.8	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
65	<a href="#">c1mwuA</a>	Alignment	not modelled	46.2	15	<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.
66	<a href="#">c6f0kA</a>	Alignment	not modelled	39.7	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c family protein; <b>PDBTitle:</b> alternative complex iii
67	<a href="#">c3ke7A</a>	Alignment	not modelled	38.2	24	<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
68	<a href="#">d1ulib</a>	Alignment	not modelled	38.2	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
69	<a href="#">c6bjuD</a>	Alignment	not modelled	37.8	16	<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
70	<a href="#">c4ouqA</a>	Alignment	not modelled	33.9	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 (bf1468) from2 bacteroides fragilis ych46 at 1.55 a resolution
71	<a href="#">c4or1A</a>	Alignment	not modelled	33.4	29	<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
72	<a href="#">c3hzpA</a>	Alignment	not modelled	31.9	19	<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
73	<a href="#">c2ml6A</a>	Alignment	not modelled	28.0	35	<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
74	<a href="#">c5ve9C</a>	Alignment	not modelled	27.7	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
75	<a href="#">c1zzaA</a>	Alignment	not modelled	26.5	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> stannin; <b>PDBTitle:</b> solution nmr structure of the membrane protein stannin
						<b>PDB header:</b> de novo protein

76	<a href="#">c5up5A</a>	Alignment	not modelled	26.1	36	<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
77	<a href="#">c4ce4i</a>	Alignment	not modelled	25.8	10	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> mrlp9; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
78	<a href="#">c1zeqX</a>	Alignment	not modelled	24.7	10	<b>PDB header:</b> metal binding protein <b>Chain:</b> X: <b>PDB Molecule:</b> rcation efflux system protein cusf; <b>PDBTitle:</b> 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
79	<a href="#">d1v5ra1</a>	Alignment	not modelled	23.8	33	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> GAS2 domain-like <b>Family:</b> GAS2 domain
80	<a href="#">d1wqlb1</a>	Alignment	not modelled	21.5	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
81	<a href="#">c3efyB</a>	Alignment	not modelled	19.3	20	<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
82	<a href="#">d2gxfa1</a>	Alignment	not modelled	14.9	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> YybH-like
83	<a href="#">c2n6uA</a>	Alignment	not modelled	13.6	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
84	<a href="#">c5ts4A</a>	Alignment	not modelled	13.0	19	<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
85	<a href="#">c4r4gA</a>	Alignment	not modelled	12.8	23	<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
86	<a href="#">c2i55A</a>	Alignment	not modelled	11.8	15	<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
87	<a href="#">d2rcda1</a>	Alignment	not modelled	11.4	22	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
88	<a href="#">c3gzxB</a>	Alignment	not modelled	11.4	16	<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
89	<a href="#">c1xofB</a>	Alignment	not modelled	10.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> bbahett1; <b>PDBTitle:</b> heterooligomeric beta beta alpha miniprotein
90	<a href="#">c3qk9B</a>	Alignment	not modelled	10.0	13	<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
91	<a href="#">c2kncA</a>	Alignment	not modelled	9.2	11	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
92	<a href="#">d2cw9a1</a>	Alignment	not modelled	8.7	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> TIM44-like
93	<a href="#">d1o7nb</a>	Alignment	not modelled	8.4	4	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
94	<a href="#">d2bmob1</a>	Alignment	not modelled	6.8	8	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
95	<a href="#">c2k9yA</a>	Alignment	not modelled	6.7	11	<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
96	<a href="#">c2k9yB</a>	Alignment	not modelled	6.7	11	<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
97	<a href="#">c2w2rA</a>	Alignment	not modelled	6.5	25	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein; <b>PDBTitle:</b> structure of the vesicular stomatitis virus matrix protein
98	<a href="#">c1sn9B</a>	Alignment	not modelled	6.5	33	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> tetrameric beta-beta-alpha mini-protein; <b>PDBTitle:</b> an oligomeric domain-swapped beta-beta-alpha mini-protein
99	<a href="#">c1sn9A</a>	Alignment	not modelled	6.5	33	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> tetrameric beta-beta-alpha mini-protein; <b>PDBTitle:</b> an oligomeric domain-swapped beta-beta-alpha mini-protein