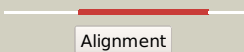
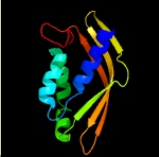
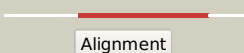

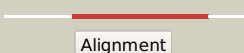
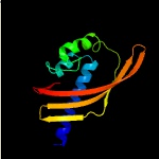
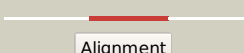
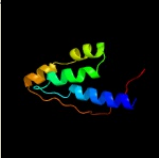



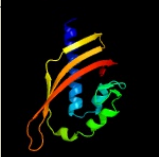
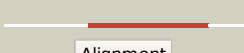

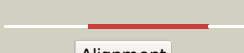










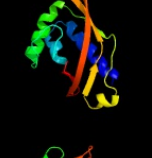

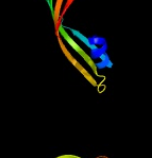
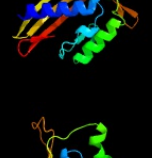

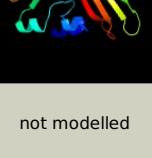


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0199 (-) _236550_237209
Date	Tue Jul 23 14:50:25 BST 2019
Unique Job ID	fe4c919ba2e0c402

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5cnlA_</a>	 Alignment		96.7	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 (Ipg0120) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1 at 2.65 a resolution
2	<a href="#">c3wz3A_</a>	 Alignment		96.6	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
3	<a href="#">d2ux0a1</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
4	<a href="#">c3wz4F_</a>	 Alignment		95.9	14	<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="#">c5d9rA_</a>	 Alignment		95.8	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
6	<a href="#">d1hkxa_</a>	 Alignment		95.0	16	<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
7	<a href="#">c4nhfF_</a>	 Alignment		94.8	12	<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
8	<a href="#">c5i97C_</a>	 Alignment		93.8	9	<b>PDB header:</b> protein transport <b>Chain:</b> C; <b>PDB Molecule:</b> conjugal transfer protein; <b>PDBTitle:</b> structural analysis and inhibition of traE from the pkm101 type iv2 secretion system
9	<a href="#">d3cu3a1</a>	 Alignment		92.4	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
10	<a href="#">d3d9ra1</a>	 Alignment		91.9	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> ECA1476-like
11	<a href="#">d2f86b1</a>	 Alignment		91.6	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

12	<a href="#">d2cc3a1</a>	Alignment		91.5	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> VirB8-like
13	<a href="#">c5ig4A_</a>	Alignment		91.1	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted protein; <b>PDBTitle:</b> crystal structure of n. vectensis camkii-a hub
14	<a href="#">c5ig5E_</a>	Alignment		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
15	<a href="#">c3h51A_</a>	Alignment		90.3	16	<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
16	<a href="#">c4i4kB_</a>	Alignment		89.9	6	<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
17	<a href="#">c3a76B_</a>	Alignment		89.7	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
18	<a href="#">c3gzrA_</a>	Alignment		89.1	11	<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="#">c3f7sA_</a>	Alignment		88.3	8	<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
20	<a href="#">c5u9oD_</a>	Alignment		87.9	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
21	<a href="#">c4ovmE_</a>	Alignment	not modelled	87.2	9	<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
22	<a href="#">c3robC_</a>	Alignment	not modelled	87.0	9	<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="#">d3b8la1</a>	Alignment	not modelled	86.6	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
24	<a href="#">d3stda_</a>	Alignment	not modelled	85.1	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
25	<a href="#">c6of9G_</a>	Alignment	not modelled	84.0	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
26	<a href="#">d2rfra1</a>	Alignment	not modelled	80.7	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
27	<a href="#">d2bhma1</a>	Alignment	not modelled	79.2	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> VirB8-like
28	<a href="#">c2bhmE_</a>	Alignment	not modelled	78.5	14	<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="#">c4bzhE_</a>	Alignment	not modelled	77.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> putative periplasmic protein;

29	<a href="#">c4nz6L</a>	Alignment	not modelled	77.2	10	<b>PDBTitle:</b> crystal structure of the type vi semet effector-immunity complex tae3-2 tai3 from ralstonia pickettii
30	<a href="#">d1ldpa</a>	Alignment	not modelled	77.2	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
31	<a href="#">d3ef8a1</a>	Alignment	not modelled	76.9	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
32	<a href="#">c3gwrA</a>	Alignment	not modelled	74.6	5	<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
33	<a href="#">c2rsxA</a>	Alignment	not modelled	70.0	5	<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
34	<a href="#">c4lehA</a>	Alignment	not modelled	68.7	14	<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 (closi_03134)2 from clostridium scindens atcc 35704 at 2.90 a resolution
35	<a href="#">d2rgqa1</a>	Alignment	not modelled	68.2	19	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
36	<a href="#">c3k7cC</a>	Alignment	not modelled	66.1	15	<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
37	<a href="#">d3ebya1</a>	Alignment	not modelled	65.7	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
38	<a href="#">c4o3vA</a>	Alignment	not modelled	65.4	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
39	<a href="#">d3ejva1</a>	Alignment	not modelled	64.6	24	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
40	<a href="#">d3b7ca1</a>	Alignment	not modelled	64.5	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
41	<a href="#">c4meiA</a>	Alignment	not modelled	63.0	13	<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="#">c3ub1C</a>	Alignment	not modelled	62.3	18	<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
43	<a href="#">d3blza1</a>	Alignment	not modelled	58.9	23	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Sba10622-like
44	<a href="#">d2b1xb1</a>	Alignment	not modelled	57.2	2	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
45	<a href="#">c3dukD</a>	Alignment	not modelled	57.0	33	<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
46	<a href="#">c3soyA</a>	Alignment	not modelled	54.8	4	<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
47	<a href="#">c3fkaD</a>	Alignment	not modelled	54.4	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
48	<a href="#">c3hx8A</a>	Alignment	not modelled	53.5	7	<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
49	<a href="#">c3bb9D</a>	Alignment	not modelled	52.0	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
50	<a href="#">c4fczB</a>	Alignment	not modelled	50.4	9	<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="#">d2chca1</a>	Alignment	not modelled	49.8	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
52	<a href="#">c5ig0A</a>	Alignment	not modelled	48.2	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
53	<a href="#">d2r4ia1</a>	Alignment	not modelled	46.8	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> CHU142-like

54	<a href="#">c2qguA</a>	Alignment	not modelled	46.4	15	<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 from 2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at 3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
55	<a href="#">d3bb9a1</a>	Alignment	not modelled	45.2	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
56	<a href="#">c4gb5A</a>	Alignment	not modelled	45.1	8	<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
57	<a href="#">c5uwaB</a>	Alignment	not modelled	44.2	14	<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
58	<a href="#">c4ouqA</a>	Alignment	not modelled	42.7	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) from 2 bacteroides fragilis ych46 at 1.55 a resolution
59	<a href="#">c3kspA</a>	Alignment	not modelled	33.8	3	<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
60	<a href="#">c4or1A</a>	Alignment	not modelled	33.7	8	<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) from 2 bacteroides ovatus atcc 8483 at 1.40 a resolution
61	<a href="#">d2owpa1</a>	Alignment	not modelled	28.1	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
62	<a href="#">c6bjuD</a>	Alignment	not modelled	27.4	0	<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
63	<a href="#">c3ke7A</a>	Alignment	not modelled	22.4	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 (yp_001303366.1)2 from parabacteroides distansonis atcc 8503 at 1.45 a resolution
64	<a href="#">c2n6uA</a>	Alignment	not modelled	22.0	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
65	<a href="#">c6f0kA</a>	Alignment	not modelled	21.9	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
66	<a href="#">c5up5A</a>	Alignment	not modelled	21.3	21	<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
67	<a href="#">c3hzpA</a>	Alignment	not modelled	18.8	10	<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
68	<a href="#">c4r4gA</a>	Alignment	not modelled	18.4	4	<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
69	<a href="#">c5ts4A</a>	Alignment	not modelled	17.1	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
70	<a href="#">c3fsdA</a>	Alignment	not modelled	15.1	12	<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
71	<a href="#">d3e99a1</a>	Alignment	not modelled	12.8	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
72	<a href="#">d3cnxa1</a>	Alignment	not modelled	12.2	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SAV4671-like
73	<a href="#">c2k1kB</a>	Alignment	not modelled	11.6	32	<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
74	<a href="#">c2k1IB</a>	Alignment	not modelled	11.6	32	<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
75	<a href="#">c2k1kA</a>	Alignment	not modelled	11.6	32	<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
76	<a href="#">c2k1IA</a>	Alignment	not modelled	11.6	32	<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
77	<a href="#">d2rcda1</a>	Alignment	not modelled	10.0	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like

78	<a href="#">c3r2cJ_</a>	Alignment	not modelled	9.3	17	<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
79	<a href="#">c2kncA_</a>	Alignment	not modelled	9.1	18	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
80	<a href="#">c2lyyB_</a>	Alignment	not modelled	8.8	17	<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
81	<a href="#">c3efyB_</a>	Alignment	not modelled	8.1	23	<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="#">c5ve9C_</a>	Alignment	not modelled	7.6	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
83	<a href="#">c1xofB_</a>	Alignment	not modelled	7.5	20	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> bbahett1; <b>PDBTitle:</b> heterooligomeric beta beta alpha miniprotein
84	<a href="#">c4w8jA_</a>	Alignment	not modelled	7.2	7	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> pesticidal crystal protein cry1ac; <b>PDBTitle:</b> structure of the full-length insecticidal protein cry1ac reveals2 intriguing details of toxin packaging into in vivo formed crystals
85	<a href="#">c5xlmB_</a>	Alignment	not modelled	7.2	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase pknI; <b>PDBTitle:</b> monomer form of m.tuberculosis pknI sensor domain
86	<a href="#">c1zeqX_</a>	Alignment	not modelled	7.1	0	<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
87	<a href="#">c4ce4i_</a>	Alignment	not modelled	6.4	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
88	<a href="#">c3rgaA_</a>	Alignment	not modelled	6.3	18	<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
89	<a href="#">c6k4vA_</a>	Alignment	not modelled	6.2	25	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> smart chimeric peptide g6; <b>PDBTitle:</b> the solution structure of the smart chimeric peptide g6
90	<a href="#">c3j6vl_</a>	Alignment	not modelled	6.1	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
91	<a href="#">c2fyuE_</a>	Alignment	not modelled	5.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit, <b>PDBTitle:</b> crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
92	<a href="#">c5tfyl_</a>	Alignment	not modelled	5.8	23	<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.
93	<a href="#">d1v5ra1</a>	Alignment	not modelled	5.5	25	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> GAS2 domain-like <b>Family:</b> GAS2 domain
94	<a href="#">c6k4wA_</a>	Alignment	not modelled	5.5	25	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> scp-a6; <b>PDBTitle:</b> smart chimeric peptide scp-a6
95	<a href="#">c2gbxF_</a>	Alignment	not modelled	5.2	10	<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
96	<a href="#">d1t33a1</a>	Alignment	not modelled	5.1	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain