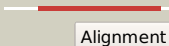
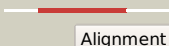







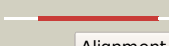









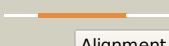
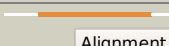
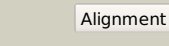
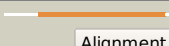




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0333 (-) _398254_398628
Date	Tue Jul 23 14:50:40 BST 2019
Unique Job ID	8c93a63262a7d549

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3f40A_</a>	Alignment		96.7	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized ntf2-like protein; <b>PDBTitle:</b> crystal structure of ntf2-like protein of unknown function2 (yp_677363.1) from cytophaga hutchinsonii atcc 33406 at 1.27 a3 resolution
2	<a href="#">c4kvhA_</a>	Alignment		96.6	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ketosteroid isomerase fold protein hmuk_0747; <b>PDBTitle:</b> crystal structure of ketosteroid isomerase fold protein hmuk_0747
3	<a href="#">d2k54a1</a>	Alignment		96.1	22	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Atu0742-like
4	<a href="#">c3ff2A_</a>	Alignment		95.9	29	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized cystatin fold protein (yp_497570.1) from <b>PDBTitle:</b> crystal structure of an uncharacterized cystatin fold protein2 (saro_2299) from novosphingobium aromaticivorans dsm at 1.90 a3 resolution
5	<a href="#">c4u13B_</a>	Alignment		95.7	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative polyketide cyclase sma1630; <b>PDBTitle:</b> crystal structure of putative polyketide cyclase (protein sma1630)2 from sinorhizobium meliloti at 2.3 a resolution
6	<a href="#">c5evhA_</a>	Alignment		95.4	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of known function protein from kribbella flavida dsm2 17836
7	<a href="#">c6fejA_</a>	Alignment		95.2	25	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> all4940 protein; <b>PDBTitle:</b> anaebaena apo-c-terminal domain homolog protein
8	<a href="#">d1m98a2</a>	Alignment		95.1	27	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Orange carotenoid protein, C-terminal domain
9	<a href="#">c3h3hA_</a>	Alignment		93.9	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized snoal-like protein; <b>PDBTitle:</b> crystal structure of a snoal-like protein of unknown function2 (bth_ii0226) from burkholderia thailandensis e264 at 1.60 a3 resolution
10	<a href="#">d1z1sa1</a>	Alignment		93.4	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
11	<a href="#">d3dm8a1</a>	Alignment		93.3	29	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rpa4348-like

12	<a href="#">d3dmca1</a>	 Alignment		93.1	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
13	<a href="#">d1oh0a_</a>	 Alignment		92.8	19	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ketosteroid isomerase-like
14	<a href="#">c4h3uB_</a>	 Alignment		92.4	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of hypothetical protein with ketosteroid isomerase-2 like protein fold from catenulispora acidiphila dsm 44928
15	<a href="#">c5aigA_</a>	 Alignment		92.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> limonene-1,2-epoxide hydrolase; <b>PDBTitle:</b> discovery and characterization of thermophilic limonene-1,2-epoxide2 hydrolases from hot spring metagenomic libraries. tomsk-sample-3 valpromide complex
16	<a href="#">d1ohpa1</a>	 Alignment		91.1	32	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ketosteroid isomerase-like
17	<a href="#">d2bnga1</a>	 Alignment		90.4	22	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Limonene-1,2-epoxide hydrolase-like
18	<a href="#">c3fgyB_</a>	 Alignment		90.3	24	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized ntf2-like protein; <b>PDBTitle:</b> crystal structure of a ntf2-like protein (bx_e_b1094) from burkholderia2 xenovorans lb400 at 1.59 a resolution
19	<a href="#">c3rgaA_</a>	 Alignment		89.9	25	<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
20	<a href="#">d3en8a1</a>	 Alignment		89.7	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rpa4348-like
21	<a href="#">c3f8xD_</a>	 Alignment	not modelled	89.5	20	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> putative delta-5-3-ketosteroid isomerase; <b>PDBTitle:</b> crystal structure of a putative delta-5-3-ketosteroid isomerase2 (eca2236) from pectobacterium atrosepticum scri1043 at 1.55 a3 resolution
22	<a href="#">c5ig0A_</a>	 Alignment	not modelled	88.7	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
23	<a href="#">c5aiiP_</a>	 Alignment	not modelled	88.5	33	<b>PDB header:</b> hydrolase <b>Chain:</b> P: <b>PDB Molecule:</b> limonene-1,2-epoxide hydrolase; <b>PDBTitle:</b> discovery and characterization of thermophilic limonene-1,2-epoxide2 hydrolases from hot spring metagenomic libraries.3 ch55-sample-peg complex
24	<a href="#">d2gexa1</a>	 Alignment	not modelled	88.5	20	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase
25	<a href="#">c3ke7A_</a>	 Alignment	not modelled	88.2	20	<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
26	<a href="#">c3msoA_</a>	 Alignment	not modelled	88.2	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> steroid delta-isomerase; <b>PDBTitle:</b> crystal structure of a steroid delta-isomerase (np_250810.1) from2 pseudomonas aeruginosa at 2.57 a resolution
27	<a href="#">c1z1sA_</a>	 Alignment	not modelled	87.0	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pa3332; <b>PDBTitle:</b> crystal structure of putative isomerase pa3332 from2 pseudomonas aeruginosa
28	<a href="#">c3wmdA_</a>	 Alignment	not modelled	86.3	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable monensin biosynthesis

28	<a href="#">c3wmbA_</a>	Alignment	not modelled	88.3	33	isomerase; <b>PDBTitle:</b> crystal structure of epoxide hydrolase monbi
29	<a href="#">c3k0zB_</a>	Alignment	not modelled	86.3	13	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> putative polyketide cyclase; <b>PDBTitle:</b> crystal structure of putative polyketide cyclase (np_977253.1) from2 bacillus cereus atcc 10987 at 1.91 a resolution
30	<a href="#">d3ebta1</a>	Alignment	not modelled	85.7	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Snoal-like polyketide cyclase
31	<a href="#">d2rcda1</a>	Alignment	not modelled	85.3	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
32	<a href="#">c5cxoA_</a>	Alignment	not modelled	85.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> epoxide hydrolase; <b>PDBTitle:</b> intriguing role of epoxide hydrolase/cyclase-like enzyme salbiii in2 pyran ring formation in polyether salinomycin
33	<a href="#">c3fljA_</a>	Alignment	not modelled	84.5	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein conserved in bacteria with a <b>PDBTitle:</b> crystal structure of uncharacterized protein conserved in bacteria2 with a cystatin-like fold (yp_168589.1) from silicibacter pomeroyi3 dss-3 at 2.00 a resolution
34	<a href="#">d1nwwa_</a>	Alignment	not modelled	84.2	22	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Limonene-1,2-epoxide hydrolase-like
35	<a href="#">c3robC_</a>	Alignment	not modelled	82.8	19	<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
36	<a href="#">d2a15a1</a>	Alignment	not modelled	82.0	25	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ketosteroid isomerase-like
37	<a href="#">c3f14A_</a>	Alignment	not modelled	82.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized ntf2-like protein; <b>PDBTitle:</b> crystal structure of ntf2-like protein of unknown function2 (yp_680363.1) from cytophaga hutchinsonii atcc 33406 at 1.45 a3 resolution
38	<a href="#">c3fh1A_</a>	Alignment	not modelled	81.9	12	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized ntf2-like protein; <b>PDBTitle:</b> crystal structure of a ntf2-like protein of unknown function (ml18193)2 from mesorhizobium loti at 1.60 a resolution
39	<a href="#">c3i0yC_</a>	Alignment	not modelled	81.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> C; <b>PDB Molecule:</b> putative polyketide cyclase; <b>PDBTitle:</b> crystal structure of a putative polyketide cyclase (xcc0381) from2 xanthomonas campestris pv. campestris at 1.50 a resolution
40	<a href="#">c3g0kA_</a>	Alignment	not modelled	80.9	15	<b>PDB header:</b> ca-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative membrane protein; <b>PDBTitle:</b> crystal structure of a protein of unknown function with a cystatin-2 like fold (saro_2880) from novosphingobium aromaticivorans dsm at3 1.30 a resolution
41	<a href="#">d2owpa1</a>	Alignment	not modelled	80.4	25	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
42	<a href="#">c3bb9D_</a>	Alignment	not modelled	78.8	7	<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
43	<a href="#">d1s5aa_</a>	Alignment	not modelled	78.5	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
44	<a href="#">c6d34B_</a>	Alignment	not modelled	76.0	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B; <b>PDB Molecule:</b> terc; <b>PDBTitle:</b> apo crystal structure of terc, a terfestatin biosynthesis enzyme
45	<a href="#">d2geya1</a>	Alignment	not modelled	74.8	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Snoal-like polyketide cyclase
46	<a href="#">d3d9ra1</a>	Alignment	not modelled	74.7	30	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> ECA1476-like
47	<a href="#">c3ehcA_</a>	Alignment	not modelled	74.3	20	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> snoal-like polyketide cyclase; <b>PDBTitle:</b> crystal structure of a snoal-like polyketide cyclase (atu3018) from2 agrobacterium tumefaciens str. c58 at 2.12 a resolution
48	<a href="#">d3dxa01</a>	Alignment	not modelled	73.7	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Atu0744-like
49	<a href="#">d3b7ca1</a>	Alignment	not modelled	73.4	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
50	<a href="#">c4lmiA_</a>	Alignment	not modelled	72.5	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of putative ketosteroid isomerase from kribbella2 flavida dsm 17836
51	<a href="#">c5x7lA_</a>	Alignment	not modelled	71.6	11	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> tsrd; <b>PDBTitle:</b> structure of tsrd from streptomyces laurentii
52	<a href="#">d3bb9a1</a>	Alignment	not modelled	69.8	6	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
						<b>PDB header:</b> unknown function

53	<a href="#">c1m98A_</a>	Alignment	not modelled	68.2	27	<b>Chain:</b> A: <b>PDB Molecule:</b> orange carotenoid protein; <b>PDBTitle:</b> crystal structure of orange carotenoid protein
54	<a href="#">d1tuha_</a>	Alignment	not modelled	66.2	22	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Hypothetical protein egc068 from a soil-derived mobile gene cassette
55	<a href="#">c1tuhA_</a>	Alignment	not modelled	66.2	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein egc068; <b>PDBTitle:</b> structure of bai32a from a soil-derived mobile gene cassette
56	<a href="#">d2f99a1</a>	Alignment	not modelled	64.3	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Snoal-like polyketide cyclase
57	<a href="#">d2gxfa1</a>	Alignment	not modelled	64.1	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> YybH-like
58	<a href="#">c4lqqa_</a>	Alignment	not modelled	63.9	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative polyketide cyclase; <b>PDBTitle:</b> crystal structure of a putative polyketide cyclase (cv_0247) from2 chromobacterium violaceum atcc 12472 at 2.72 a resolution
59	<a href="#">c3fsdA_</a>	Alignment	not modelled	63.8	19	<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
60	<a href="#">c4ovmE_</a>	Alignment	not modelled	62.1	16	<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
61	<a href="#">c3g8za_</a>	Alignment	not modelled	60.3	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein of unknown function with cystatin-like fold; <b>PDBTitle:</b> crystal structure of protein of unknown function with cystatin-like2 fold (np_639274.1) from xanthomonas campestris at 1.90 a resolution
62	<a href="#">d1sjwa_</a>	Alignment	not modelled	60.1	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Snoal-like polyketide cyclase
63	<a href="#">c5wqhE_</a>	Alignment	not modelled	59.7	19	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> isomerase trt14; <b>PDBTitle:</b> structure of fungal meroterpenoid isomerase trt14 complexed with2 substrate analog and endo-terretonin d
64	<a href="#">c3f8ha_</a>	Alignment	not modelled	59.0	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative polyketide cyclase; <b>PDBTitle:</b> crystal structure of a putative polyketide cyclase (tm1040_3560) from2 silicibacter sp. tm1040 at 2.00 a resolution
65	<a href="#">c3f7sa_</a>	Alignment	not modelled	57.5	21	<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
66	<a href="#">c3h51A_</a>	Alignment	not modelled	57.0	12	<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
67	<a href="#">c3f7xA_</a>	Alignment	not modelled	56.9	21	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative polyketide cyclase; <b>PDBTitle:</b> crystal structure of a putative polyketide cyclase (pp0894) from2 pseudomonas putida kt2440 at 1.24 a resolution
68	<a href="#">c5x9jB_</a>	Alignment	not modelled	56.2	11	<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
69	<a href="#">c5x9kA_</a>	Alignment	not modelled	55.7	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> austinol synthesis protein h; <b>PDBTitle:</b> strucutre of aush from aspergillus nidulans
70	<a href="#">c6a5hB_</a>	Alignment	not modelled	55.1	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> 101015d; <b>PDBTitle:</b> the structure of [4+2] and [6+4] cyclase in the biosynthetic pathway2 of unidentified natural product
71	<a href="#">c3gwrA_</a>	Alignment	not modelled	55.1	21	<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
72	<a href="#">d3ec9a1</a>	Alignment	not modelled	55.0	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
73	<a href="#">c3f9sB_</a>	Alignment	not modelled	53.6	6	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative polyketide cyclase; <b>PDBTitle:</b> crystal structure of a putative polyketide cyclase (lferr_0659) from2 acidithiobacillus ferrooxidans atcc at 1.76 a resolution
74	<a href="#">c3gzrA_</a>	Alignment	not modelled	48.5	15	<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
75	<a href="#">c6bjuD_</a>	Alignment	not modelled	46.5	23	<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
						<b>Fold:</b> Cystatin-like

76	<a href="#">d2r4ia1</a>	Alignment	not modelled	43.8	18	<b>Superfamily:</b> NTF2-like <b>Family:</b> CHU142-like
77	<a href="#">c4i4kB_</a>	Alignment	not modelled	38.9	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
78	<a href="#">d2ux0a1</a>	Alignment	not modelled	38.6	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
79	<a href="#">c6of9G_</a>	Alignment	not modelled	37.2	12	<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
80	<a href="#">c3hx8A_</a>	Alignment	not modelled	35.5	16	<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
81	<a href="#">c3kkgA_</a>	Alignment	not modelled	35.3	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative snoal-like polyketide cyclase; <b>PDBTitle:</b> crystal structure of putative snoal-like polyketide cyclase2 (yp_509242.1) from jannaschia sp. ccs1 at 1.40 a resolution
82	<a href="#">c3grdA_</a>	Alignment	not modelled	33.1	3	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized ntf2-superfamily protein; <b>PDBTitle:</b> crystal structure of ntf2-superfamily protein with unknown function2 (np_977240.1) from bacillus cereus atcc 10987 at 1.25 a resolution
83	<a href="#">c3hk4B_</a>	Alignment	not modelled	31.2	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> mlr7391 protein; <b>PDBTitle:</b> crystal structure of a putative snoal-like polyketide cyclase2 [carbohydrate phosphatase] (mlr7391) from mesorhizobium loti at 1.963 a resolution
84	<a href="#">d3cnxa1</a>	Alignment	not modelled	30.2	21	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SAV4671-like
85	<a href="#">c3soyA_</a>	Alignment	not modelled	27.0	12	<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
86	<a href="#">c5ig4A_</a>	Alignment	not modelled	25.3	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
87	<a href="#">c3b4oB_</a>	Alignment	not modelled	23.2	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> phenazine biosynthesis protein a/b; <b>PDBTitle:</b> crystal structure of phenazine biosynthesis protein phza/b2 from burkholderia cepacia r18194, apo form
88	<a href="#">d2chca1</a>	Alignment	not modelled	19.2	21	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
89	<a href="#">c3kspA_</a>	Alignment	not modelled	18.2	19	<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
90	<a href="#">c5ig5E_</a>	Alignment	not modelled	17.7	13	<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
91	<a href="#">d1hkxa_</a>	Alignment	not modelled	17.7	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
92	<a href="#">d2rfr1</a>	Alignment	not modelled	15.3	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
93	<a href="#">d1ds6b_</a>	Alignment	not modelled	15.2	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> RhoGDI-like
94	<a href="#">d1doab_</a>	Alignment	not modelled	13.7	19	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> RhoGDI-like
95	<a href="#">d3b8la1</a>	Alignment	not modelled	13.6	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
96	<a href="#">d1hh4e_</a>	Alignment	not modelled	12.6	19	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> RhoGDI-like
97	<a href="#">d2f86b1</a>	Alignment	not modelled	11.7	18	<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
98	<a href="#">c4lehA_</a>	Alignment	not modelled	11.3	10	<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
99	<a href="#">d3cu3a1</a>	Alignment	not modelled	11.1	20	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like