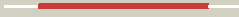























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1439c_(-) _1616967_1617392
Date	Wed Jul 31 22:05:55 BST 2019
Unique Job ID	48675a5549167000

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2bnga1</a>	 Alignment		98.4	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Limonene-1,2-epoxide hydrolase-like
2	<a href="#">c5aigA_</a>	 Alignment		98.3	18	<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
3	<a href="#">d1nwwa_</a>	 Alignment		98.3	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Limonene-1,2-epoxide hydrolase-like
4	<a href="#">d2geya1</a>	 Alignment		98.2	22	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Snoal-like polyketide cyclase
5	<a href="#">c3k0zB_</a>	 Alignment		98.1	14	<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
6	<a href="#">c3f9sB_</a>	 Alignment		98.1	12	<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
7	<a href="#">c5x7IA_</a>	 Alignment		98.0	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> tsrd; <b>PDBTitle:</b> structure of tsrd from streptomyces laurentii
8	<a href="#">c3ehcA_</a>	 Alignment		98.0	13	<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
9	<a href="#">c3h3hA_</a>	 Alignment		97.7	23	<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="#">c5evhA_</a>	 Alignment		97.6	13	<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
11	<a href="#">d1s5aa_</a>	 Alignment		97.6	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like

12	<a href="#">d1oh0a_</a>	Alignment		97.6	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ketosteroid isomerase-like
13	<a href="#">d2gexa1</a>	Alignment		97.5	21	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase
14	<a href="#">c3kkgA_</a>	Alignment		97.4	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative snoa-like polyketide cyclase; <b>PDBTitle:</b> crystal structure of putative snoa-like polyketide cyclase2 (yp_509242.1) from jannaschia sp. ccs1 at 1.40 a resolution
15	<a href="#">d3dm8a1</a>	Alignment		97.4	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rpa4348-like
16	<a href="#">c3msoA_</a>	Alignment		97.2	21	<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
17	<a href="#">c4h3uB_</a>	Alignment		97.2	19	<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
18	<a href="#">d1ohpa1</a>	Alignment		97.1	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ketosteroid isomerase-like
19	<a href="#">c3f8hA_</a>	Alignment		97.1	17	<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
20	<a href="#">c3i0yC_</a>	Alignment		97.1	14	<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
21	<a href="#">c4lqqA_</a>	Alignment	not modelled	97.0	18	<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
22	<a href="#">c3f14A_</a>	Alignment	not modelled	96.9	10	<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
23	<a href="#">d2f99a1</a>	Alignment	not modelled	96.8	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase
24	<a href="#">c3wmdA_</a>	Alignment	not modelled	96.7	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable monensin biosynthesis isomerase; <b>PDBTitle:</b> crystal structure of epoxide hydrolase monbi
25	<a href="#">d1sjwa_</a>	Alignment	not modelled	96.7	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase
26	<a href="#">d3dmca1</a>	Alignment	not modelled	96.6	21	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
27	<a href="#">c3fh1A_</a>	Alignment	not modelled	96.6	20	<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 (mll8193)2 from mesorhizobium loti at 1.60 a resolution
28	<a href="#">c5aiiP_</a>	Alignment	not modelled	96.6	21	<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
29	<a href="#">d3ebta1</a>	Alignment	not modelled	96.4	16 <b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase
30	<a href="#">c3g8zA</a>	Alignment	not modelled	96.4	14 <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
31	<a href="#">c3ff2A</a>	Alignment	not modelled	96.2	17 <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
32	<a href="#">d3ec9a1</a>	Alignment	not modelled	96.2	18 <b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
33	<a href="#">c6d34B</a>	Alignment	not modelled	96.1	15 <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
34	<a href="#">c3f40A</a>	Alignment	not modelled	96.1	15 <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
35	<a href="#">d2k54a1</a>	Alignment	not modelled	96.1	17 <b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Atu0742-like
36	<a href="#">c4lmiA</a>	Alignment	not modelled	95.9	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 putative ketosteroid isomerase from kribbella2 flavida dsm 17836
37	<a href="#">c3g0kA</a>	Alignment	not modelled	95.7	21 <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
38	<a href="#">c3f7xA</a>	Alignment	not modelled	95.7	13 <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
39	<a href="#">c1z1sA</a>	Alignment	not modelled	95.4	15 <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
40	<a href="#">c5cxoA</a>	Alignment	not modelled	95.4	16 <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
41	<a href="#">d1z1sa1</a>	Alignment	not modelled	95.3	16 <b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
42	<a href="#">c3grdA</a>	Alignment	not modelled	95.2	15 <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
43	<a href="#">c3hk4B</a>	Alignment	not modelled	94.6	17 <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
44	<a href="#">d3en8a1</a>	Alignment	not modelled	93.8	17 <b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rpa4348-like
45	<a href="#">c3fgyB</a>	Alignment	not modelled	93.8	18 <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
46	<a href="#">c3ff0A</a>	Alignment	not modelled	93.8	14 <b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> phenazine biosynthesis protein phzb 2; <b>PDBTitle:</b> crystal structure of a phenazine biosynthesis-related protein (phzb2)2 from pseudomonas aeruginosa at 1.90 a resolution
47	<a href="#">c3fijA</a>	Alignment	not modelled	93.2	12 <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
48	<a href="#">c3b4oB</a>	Alignment	not modelled	93.2	12 <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
49	<a href="#">c4u13B</a>	Alignment	not modelled	92.6	17 <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
50	<a href="#">d1tuha</a>	Alignment	not modelled	92.4	17 <b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Hypothetical protein egc068 from a soil-derived mobile gene cassette
51	<a href="#">c1tuhA</a>	Alignment	not modelled	92.4	17 <b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein egc068; <b>PDBTitle:</b> structure of bal32a from a soil-derived mobile gene cassette

52	<a href="#">d3dxa1</a>	Alignment	not modelled	91.5	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Atu0744-like
53	<a href="#">c3f8xD</a>	Alignment	not modelled	91.4	22	<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
54	<a href="#">c4kvhA</a>	Alignment	not modelled	91.1	22	<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
55	<a href="#">d2a15a1</a>	Alignment	not modelled	89.7	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ketosteroid isomerase-like
56	<a href="#">c3ke7A</a>	Alignment	not modelled	83.8	13	<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="#">c3rgaA</a>	Alignment	not modelled	76.7	16	<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
58	<a href="#">c6a5hB</a>	Alignment	not modelled	73.7	14	<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
59	<a href="#">d3bb9a1</a>	Alignment	not modelled	72.4	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
60	<a href="#">c6fejA</a>	Alignment	not modelled	63.7	12	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> all4940 protein; <b>PDBTitle:</b> anabaena apo-c-terminal domain homolog protein
61	<a href="#">c5x9kA</a>	Alignment	not modelled	62.0	16	<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
62	<a href="#">d1m98a2</a>	Alignment	not modelled	55.6	23	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Orange carotenoid protein, C-terminal domain
63	<a href="#">c5x9jB</a>	Alignment	not modelled	54.3	9	<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
64	<a href="#">d2gxfa1</a>	Alignment	not modelled	51.8	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> YybH-like
65	<a href="#">c3bb9D</a>	Alignment	not modelled	42.3	15	<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
66	<a href="#">c3hx8A</a>	Alignment	not modelled	40.3	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
67	<a href="#">c4ovmE</a>	Alignment	not modelled	24.3	15	<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
68	<a href="#">c5ig4A</a>	Alignment	not modelled	21.7	15	<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
69	<a href="#">d3d9ra1</a>	Alignment	not modelled	21.2	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> ECA1476-like
70	<a href="#">c3f7sA</a>	Alignment	not modelled	19.0	11	<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
71	<a href="#">c3h51A</a>	Alignment	not modelled	17.5	22	<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
72	<a href="#">c1s4zC</a>	Alignment	not modelled	16.4	70	<b>PDB header:</b> gene regulation <b>Chain:</b> C: <b>PDB Molecule:</b> chromatin assembly factor 1 subunit a; <b>PDBTitle:</b> hp1 chromo shadow domain in complex with pxvl motif of caf-2 1
73	<a href="#">d3cu3a1</a>	Alignment	not modelled	15.1	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
74	<a href="#">c3gqrA</a>	Alignment	not modelled	12.7	20	<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="#">c5ig0A</a>	Alignment	not modelled	11.7	17	<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
76	<a href="#">c3robC</a>	Alignment	not modelled	9.8	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized conserved protein;

76	<a href="#">c3r0bc</a>	Alignment	not modelled	9.8	11	<b>PDBTitle:</b> the crystal structure of a conserved protein from planctomyces2 limnophilus dsm 3776 <b>PDB header:</b> membrane protein
77	<a href="#">c2h3oA</a>	Alignment	not modelled	9.7	57	<b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> structure of merf, a membrane protein with two trans-2 membrane helices
78	<a href="#">c2n2yA</a>	Alignment	not modelled	9.2	50	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> meiosis-expressed gene 1 protein; <b>PDBTitle:</b> solution structure of the meiosis-expressed gene 1 (meig1)
79	<a href="#">d2cqaa1</a>	Alignment	not modelled	8.9	67	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> TIP49 domain
80	<a href="#">c1sy9B</a>	Alignment	not modelled	8.0	57	<b>PDB header:</b> calcium-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> cyclic-nucleotide-gated olfactory channel; <b>PDBTitle:</b> structure of calmodulin complexed with a fragment of the2 olfactory cng channel
81	<a href="#">c5wqhE</a>	Alignment	not modelled	7.9	15	<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
82	<a href="#">d2ux0a1</a>	Alignment	not modelled	7.3	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
83	<a href="#">c3gwrA</a>	Alignment	not modelled	7.0	25	<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
84	<a href="#">d1pbaa</a>	Alignment	not modelled	6.8	41	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Protease propeptides/inhibitors <b>Family:</b> Pancreatic carboxypeptidase, activation domain
85	<a href="#">c5z62M</a>	Alignment	not modelled	6.8	31	<b>PDB header:</b> electron transport <b>Chain:</b> M: <b>PDB Molecule:</b> cytochrome c oxidase subunit 8a, mitochondrial; <b>PDBTitle:</b> structure of human cytochrome c oxidase
86	<a href="#">c5xj2C</a>	Alignment	not modelled	6.5	29	<b>PDB header:</b> transferase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized rna methyltransferase sp_1029; <b>PDBTitle:</b> structure of sprlmcid with u747 rna
87	<a href="#">c3dacB</a>	Alignment	not modelled	5.3	63	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cellular tumor antigen p53; <b>PDBTitle:</b> structure of the human mdmx protein bound to the p53 tumor suppressor2 transactivation domain
88	<a href="#">c3dacP</a>	Alignment	not modelled	5.3	63	<b>PDB header:</b> cell cycle <b>Chain:</b> P: <b>PDB Molecule:</b> cellular tumor antigen p53; <b>PDBTitle:</b> structure of the human mdmx protein bound to the p53 tumor suppressor2 transactivation domain
89	<a href="#">d2r4ia1</a>	Alignment	not modelled	5.2	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> CHU142-like
90	<a href="#">c6of9G</a>	Alignment	not modelled	5.2	11	<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
91	<a href="#">c1wazA</a>	Alignment	not modelled	5.0	57	<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="#">c2k87A</a>	Alignment	not modelled	5.0	55	<b>PDB header:</b> viral protein, rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> non-structural protein 3 of replicase polyprotein 1a; <b>PDBTitle:</b> nmr structure of a putative rna binding protein (sars1) from sars2 coronavirus