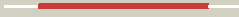






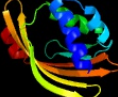
















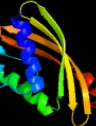







# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2740_(-)_3053243_3053692
Date	Wed Aug 7 12:50:39 BST 2019
Unique Job ID	bb041b5d5e589d46

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2bnga1</a>	 Alignment		100.0	98	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Limonene-1,2-epoxide hydrolase-like
2	<a href="#">d1nwwa_</a>	 Alignment		99.9	26	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Limonene-1,2-epoxide hydrolase-like
3	<a href="#">c3k0zB_</a>	 Alignment		99.9	18	<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) from <i>Bacillus cereus</i> ATCC 10987 at 1.91 Å resolution
4	<a href="#">d3dm8a1</a>	 Alignment		99.9	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rpa4348-like
5	<a href="#">c5aigA_</a>	 Alignment		99.9	31	<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-epoxide hydrolases from hot spring metagenomic libraries. tomsk-sample-3 valpromide complex
6	<a href="#">c4h3uB_</a>	 Alignment		99.9	18	<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 <i>Catenulipora acidiphila</i> DSM 44928
7	<a href="#">d3ebta1</a>	 Alignment		99.9	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase
8	<a href="#">c6d34B_</a>	 Alignment		99.9	14	<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
9	<a href="#">d2gexa1</a>	 Alignment		99.9	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase
10	<a href="#">d3ec9a1</a>	 Alignment		99.9	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
11	<a href="#">d2geya1</a>	 Alignment		99.9	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase

12	<a href="#">d3dmca1</a>	Alignment		99.9	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
13	<a href="#">c5aiiP</a>	Alignment		99.9	27	<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
14	<a href="#">c3f8hA</a>	Alignment		99.9	16	<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
15	<a href="#">d2f99a1</a>	Alignment		99.9	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase
16	<a href="#">c3fh1A</a>	Alignment		99.9	16	<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
17	<a href="#">c3fgyB</a>	Alignment		99.9	20	<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
18	<a href="#">c5evhA</a>	Alignment		99.9	21	<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
19	<a href="#">c3b4oB</a>	Alignment		99.9	18	<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
20	<a href="#">c3kkgA</a>	Alignment		99.9	13	<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
21	<a href="#">c3wmdA</a>	Alignment	not modelled	99.9	16	<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
22	<a href="#">d1sjwa</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase
23	<a href="#">d1tuha</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Hypothetical protein egc068 from a soil-derived mobile gene cassette
24	<a href="#">c1tuhA</a>	Alignment	not modelled	99.9	19	<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
25	<a href="#">c4lqqA</a>	Alignment	not modelled	99.9	16	<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
26	<a href="#">d1s5aa</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
27	<a href="#">c3f7xA</a>	Alignment	not modelled	99.9	18	<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
28	<a href="#">d1z1sa1</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like

29	<a href="#">c3g8zA_</a>	Alignment	not modelled	99.9	15	<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-like fold (np_639274.1) from xanthomonas campestris at 1.90 a resolution
30	<a href="#">c3f9sB_</a>	Alignment	not modelled	99.9	14	<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
31	<a href="#">c1z1sA_</a>	Alignment	not modelled	99.9	20	<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
32	<a href="#">c5x7IA_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> tsrd; <b>PDBTitle:</b> structure of tsrd from streptomyces laurentii
33	<a href="#">c4lmiA_</a>	Alignment	not modelled	99.9	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
34	<a href="#">c3i0yC_</a>	Alignment	not modelled	99.9	20	<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
35	<a href="#">c3ff0A_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> phenazine biosynthesis protein phzb2; <b>PDBTitle:</b> crystal structure of a phenazine biosynthesis-related protein (phzb2)2 from pseudomonas aeruginosa at 1.90 a resolution
36	<a href="#">c3hk4B_</a>	Alignment	not modelled	99.9	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
37	<a href="#">c3grdA_</a>	Alignment	not modelled	99.9	10	<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
38	<a href="#">c3f14A_</a>	Alignment	not modelled	99.9	11	<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
39	<a href="#">d1oh0a_</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ketosteroid isomerase-like
40	<a href="#">d2k54a1</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Atu0742-like
41	<a href="#">c3f40A_</a>	Alignment	not modelled	99.8	22	<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
42	<a href="#">c5cxoA_</a>	Alignment	not modelled	99.8	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
43	<a href="#">d3en8a1</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rpa4348-like
44	<a href="#">d1ohpa1</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ketosteroid isomerase-like
45	<a href="#">d2a15a1</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ketosteroid isomerase-like
46	<a href="#">c6a5hB_</a>	Alignment	not modelled	99.8	9	<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
47	<a href="#">c4kvhA_</a>	Alignment	not modelled	99.8	21	<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
48	<a href="#">c3msoA_</a>	Alignment	not modelled	99.8	16	<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
49	<a href="#">c3ff2A_</a>	Alignment	not modelled	99.8	21	<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
50	<a href="#">c3ehcA_</a>	Alignment	not modelled	99.8	17	<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
51	<a href="#">c3f8xD_</a>	Alignment	not modelled	99.8	12	<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

52	<a href="#">c3g0kA</a>	Alignment	not modelled	99.8	22	<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
53	<a href="#">c4u13B</a>	Alignment	not modelled	99.8	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
54	<a href="#">c5x9jB</a>	Alignment	not modelled	99.8	13	<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
55	<a href="#">c3h3hA</a>	Alignment	not modelled	99.8	17	<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
56	<a href="#">d3dxa01</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Atu0744-like
57	<a href="#">c5wqhE</a>	Alignment	not modelled	99.7	9	<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-terretinin d
58	<a href="#">c5x9kA</a>	Alignment	not modelled	99.7	8	<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
59	<a href="#">c3rgaA</a>	Alignment	not modelled	99.7	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
60	<a href="#">c3fjA</a>	Alignment	not modelled	99.6	16	<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
61	<a href="#">d1m98a2</a>	Alignment	not modelled	99.5	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Orange carotenoid protein, C-terminal domain
62	<a href="#">c3ke7A</a>	Alignment	not modelled	99.4	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 distasonis atcc 8503 at 1.45 a resolution
63	<a href="#">c6fejA</a>	Alignment	not modelled	99.4	14	<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
64	<a href="#">c3gwrA</a>	Alignment	not modelled	99.1	22	<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
65	<a href="#">c3g16A</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein with cystatin-like fold; <b>PDBTitle:</b> crystal structure of protein of unknown function with cystatin-like2 fold (yp_001022489.1) from methylobium petroleophilum pm1 at 1.45 a3 resolution
66	<a href="#">c3robC</a>	Alignment	not modelled	99.0	14	<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
67	<a href="#">c3h51A</a>	Alignment	not modelled	99.0	13	<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
68	<a href="#">d3bb9a1</a>	Alignment	not modelled	99.0	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
69	<a href="#">d3d9ra1</a>	Alignment	not modelled	98.9	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> ECA1476-like
70	<a href="#">c3hx8A</a>	Alignment	not modelled	98.9	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
71	<a href="#">c3bb9D</a>	Alignment	not modelled	98.9	17	<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
72	<a href="#">d3cxa1</a>	Alignment	not modelled	98.9	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SAV4671-like
73	<a href="#">d2rcda1</a>	Alignment	not modelled	98.9	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
74	<a href="#">c5ig0A</a>	Alignment	not modelled	98.8	10	<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
75	<a href="#">d2qxfa1</a>	Alignment	not modelled	98.8	22	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like

						<b>Family:</b> YybH-like
76	<a href="#">d2r4ia1</a>	Alignment	not modelled	98.8	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> CHU142-like
77	<a href="#">c1m98A_</a>	Alignment	not modelled	98.8	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> orange carotenoid protein; <b>PDBTitle:</b> crystal structure of orange carotenoid protein
78	<a href="#">c3f7sA_</a>	Alignment	not modelled	98.8	16	<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
79	<a href="#">d2rfr1</a>	Alignment	not modelled	98.7	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
80	<a href="#">c4ovmE_</a>	Alignment	not modelled	98.7	12	<b>PDB header:</b> unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein sgcj; <b>PDBTitle:</b> crystal structure of sgcj protein from streptomyces carzinostaticus
81	<a href="#">d3cu3a1</a>	Alignment	not modelled	98.7	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
82	<a href="#">c3gqrA_</a>	Alignment	not modelled	98.6	13	<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
83	<a href="#">d2owpa1</a>	Alignment	not modelled	98.6	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
84	<a href="#">c3fsdA_</a>	Alignment	not modelled	98.6	11	<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
85	<a href="#">d3b7ca1</a>	Alignment	not modelled	98.6	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
86	<a href="#">d2rgqa1</a>	Alignment	not modelled	98.5	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
87	<a href="#">d2ux0a1</a>	Alignment	not modelled	98.5	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
88	<a href="#">c5ig4A_</a>	Alignment	not modelled	98.5	12	<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
89	<a href="#">c5ig5E_</a>	Alignment	not modelled	98.5	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
90	<a href="#">c6of9G_</a>	Alignment	not modelled	98.4	14	<b>PDB header:</b> unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> camkii hub; <b>PDBTitle:</b> structure of the chlamydomonas reinhardtii camkii hub homology domain
91	<a href="#">c3soyA_</a>	Alignment	not modelled	98.4	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
92	<a href="#">d1hkxa_</a>	Alignment	not modelled	98.4	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
93	<a href="#">d3b8la1</a>	Alignment	not modelled	98.4	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
94	<a href="#">c3kspA_</a>	Alignment	not modelled	98.4	5	<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
95	<a href="#">c4i4kB_</a>	Alignment	not modelled	98.3	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein sgcj; <b>PDBTitle:</b> streptomyces globosporus c-1027 9-membered enediyne conserved protein2 sgce6
96	<a href="#">d2chca1</a>	Alignment	not modelled	98.2	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
97	<a href="#">c6bjuD_</a>	Alignment	not modelled	98.2	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
98	<a href="#">d3er7a1</a>	Alignment	not modelled	98.2	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Exig0174-like
99	<a href="#">c3a76B_</a>	Alignment	not modelled	98.1	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> gamma-hexachlorocyclohexane dehydrochlorinase; <b>PDBTitle:</b> the crystal structure of lina <b>Fold:</b> Cystatin-like



100	<a href="#">d2f86b1</a>	Alignment	not modelled	98.1	13	<b>Superfamily:</b> NTF2-like <b>Family:</b> Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
101	<a href="#">c4lehA</a>	Alignment	not modelled	98.1	9	<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 (clocsi_03134)2 from clostridium scindens atcc 35704 at 2.90 a resolution
102	<a href="#">d3blza1</a>	Alignment	not modelled	98.0	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Sbal0622-like
103	<a href="#">d3ef8a1</a>	Alignment	not modelled	97.9	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
104	<a href="#">d3ebya1</a>	Alignment	not modelled	97.8	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
105	<a href="#">c5xe7A</a>	Alignment	not modelled	97.7	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigj; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis extracytoplasmic2 function sigma factor sigj
106	<a href="#">d3ejva1</a>	Alignment	not modelled	97.7	21	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
107	<a href="#">d3stda</a>	Alignment	not modelled	97.6	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
108	<a href="#">c3lygA</a>	Alignment	not modelled	97.6	15	<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 function2 (yp_270605.1) from colwellia psychrerythraea 34h at 1.61 a resolution
109	<a href="#">c3dukD</a>	Alignment	not modelled	97.6	10	<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
110	<a href="#">d3e99a1</a>	Alignment	not modelled	97.6	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
111	<a href="#">c5tpjA</a>	Alignment	not modelled	97.5	23	<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
112	<a href="#">d1idpa</a>	Alignment	not modelled	97.4	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
113	<a href="#">c3gzbc</a>	Alignment	not modelled	97.3	20	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> putative snoal-like polyketide cyclase; <b>PDBTitle:</b> crystal structure of putative snoal-like polyketide cyclase2 (yp_001182657.1) from shewanella putrefaciens cn-32 at 1.44 a3 resolution
114	<a href="#">c3gzxB</a>	Alignment	not modelled	97.1	19	<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
115	<a href="#">c3fkaD</a>	Alignment	not modelled	97.1	10	<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
116	<a href="#">c4gb5A</a>	Alignment	not modelled	96.9	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
117	<a href="#">d1ulib</a>	Alignment	not modelled	96.8	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
118	<a href="#">d2imja1</a>	Alignment	not modelled	96.4	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PFL3262-like
119	<a href="#">c4y4vB</a>	Alignment	not modelled	96.2	6	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical secreted protein; <b>PDBTitle:</b> structure of helicobacter pylori csd6 in the d-ala-bound state
120	<a href="#">d1wqlb1</a>	Alignment	not modelled	95.7	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit