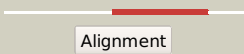
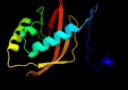


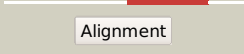

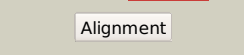

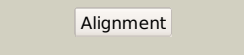

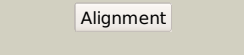

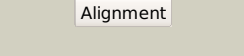

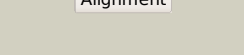

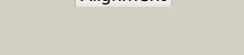

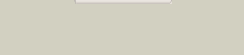














# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0361 (- )_438823_439650
Date	Tue Jul 23 14:50:43 BST 2019
Unique Job ID	e8512a12e9e2f321

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4y4vB_</a>	 Alignment		99.0	13	<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
2	<a href="#">c3h51A_</a>	 Alignment		98.8	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
3	<a href="#">d3cxa1</a>	 Alignment		98.8	21	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SAV4671-like
4	<a href="#">c3robC_</a>	 Alignment		98.8	12	<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
5	<a href="#">d2rcda1</a>	 Alignment		98.8	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
6	<a href="#">d3b7ca1</a>	 Alignment		98.7	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
7	<a href="#">c3hx8A_</a>	 Alignment		98.7	12	<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
8	<a href="#">d3blza1</a>	 Alignment		98.7	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Sbal0622-like
9	<a href="#">c6bjuD_</a>	 Alignment		98.7	12	<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
10	<a href="#">d3bb9a1</a>	 Alignment		98.7	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
11	<a href="#">c3f7sA_</a>	 Alignment		98.6	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized ntf2-like protein; <b>PDBTitle:</b> crystal structure of a ntf2-like protein of unknown function (pp_4556)2 from pseudomonas putida kt2440 at 2.11 a resolution

12	<a href="#">d2owpa1</a>	Alignment		98.6	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
13	<a href="#">d1vqqa1</a>	Alignment		98.6	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Penicillin binding protein 2a (PBP2A), N-terminal domain
14	<a href="#">c3soyaA</a>	Alignment		98.6	17	<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. It2
15	<a href="#">c3gwrA</a>	Alignment		98.6	11	<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
16	<a href="#">c3fkaD</a>	Alignment		98.5	18	<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
17	<a href="#">d3d9ra1</a>	Alignment		98.5	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> ECA1476-like
18	<a href="#">c3bb9D</a>	Alignment		98.5	15	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized orphan protein; <b>PDBTitle:</b> crystal structure of a putative ketosteroid isomerase (sfrj_1973) from2 shewanella frigidimarina ncimb 400 at 1.80 a resolution
19	<a href="#">d2r4ia1</a>	Alignment		98.5	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> CHU142-like
20	<a href="#">c4i4kB</a>	Alignment		98.5	11	<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
21	<a href="#">c3dukD</a>	Alignment	not modelled	98.5	15	<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
22	<a href="#">c3kspA</a>	Alignment	not modelled	98.5	14	<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
23	<a href="#">d2gxfa1</a>	Alignment	not modelled	98.5	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> YybH-like
24	<a href="#">c3gzaA</a>	Alignment	not modelled	98.4	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
25	<a href="#">c3ke7A</a>	Alignment	not modelled	98.4	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 (yp_001303366.1)2 from parabacteroides distasonis atcc 8503 at 1.45 a resolution
26	<a href="#">c5ig4A</a>	Alignment	not modelled	98.4	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
27	<a href="#">c5ig5E</a>	Alignment	not modelled	98.4	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

28	<a href="#">d2f86b1</a>	Alignment	not modelled	98.3	14	<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
29	<a href="#">d1hkxa</a>	Alignment	not modelled	98.3	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
30	<a href="#">d3cu3a1</a>	Alignment	not modelled	98.3	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
31	<a href="#">c6of9G</a>	Alignment	not modelled	98.2	19	<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
32	<a href="#">d2ux0a1</a>	Alignment	not modelled	98.2	15	<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
33	<a href="#">c1mwuA</a>	Alignment	not modelled	98.2	12	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 2a; <b>PDBTitle:</b> structure of methicillin acyl-penicillin binding protein 2a from 2 methicillin resistant staphylococcus aureus strain 27r at 2.60 a3 resolution.
34	<a href="#">c4ovmE</a>	Alignment	not modelled	98.2	14	<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
35	<a href="#">c3k7cC</a>	Alignment	not modelled	98.2	11	<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
36	<a href="#">c5ig0A</a>	Alignment	not modelled	98.2	14	<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
37	<a href="#">d2rffa1</a>	Alignment	not modelled	98.1	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
38	<a href="#">d2rgqa1</a>	Alignment	not modelled	98.0	5	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
39	<a href="#">d3b8la1</a>	Alignment	not modelled	97.9	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
40	<a href="#">d2chca1</a>	Alignment	not modelled	97.7	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
41	<a href="#">c4gb5A</a>	Alignment	not modelled	97.7	10	<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
42	<a href="#">c3fsdA</a>	Alignment	not modelled	97.6	17	<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
43	<a href="#">c4lehA</a>	Alignment	not modelled	97.6	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 (closci_03134)2 from clostridium scindens atcc 35704 at 2.90 a resolution
44	<a href="#">d3ejva1</a>	Alignment	not modelled	97.6	21	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
45	<a href="#">c3a76B</a>	Alignment	not modelled	97.6	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> gamma-hexachlorocyclohexane dehydrochlorinase; <b>PDBTitle:</b> the crystal structure of lina
46	<a href="#">d2k54a1</a>	Alignment	not modelled	97.6	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Atu0742-like
47	<a href="#">d1oh0a</a>	Alignment	not modelled	97.5	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ketosteroid isomerase-like
48	<a href="#">c5cxoA</a>	Alignment	not modelled	97.3	12	<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 in 2 pyran ring formation in polyether salinomycin
49	<a href="#">c3k0zB</a>	Alignment	not modelled	97.3	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) from 2 bacillus cereus atcc 10987 at 1.91 a resolution
50	<a href="#">d1idpa</a>	Alignment	not modelled	97.2	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
51	<a href="#">c6d34B</a>	Alignment	not modelled	97.2	10	<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
52	<a href="#">d3ec9a1</a>	Alignment	not modelled	97.2	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
53	<a href="#">d3ebye1</a>	Alignment	not modelled	97.1	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like

						<b>Family:</b> Ring hydroxylating beta subunit
54	<a href="#">c4kvhA_</a>	Alignment	not modelled	97.1	9	<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="#">d3stda_</a>	Alignment	not modelled	97.1	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
56	<a href="#">c3fh1A_</a>	Alignment	not modelled	97.1	14	<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
57	<a href="#">d3ef8a1</a>	Alignment	not modelled	97.1	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
58	<a href="#">c5u9oD_</a>	Alignment	not modelled	97.1	17	<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
59	<a href="#">d1tuha_</a>	Alignment	not modelled	97.1	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Hypothetical protein egc068 from a soil-derived mobile gene cassette
60	<a href="#">c1tuhA_</a>	Alignment	not modelled	97.1	12	<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
61	<a href="#">d3en8a1</a>	Alignment	not modelled	97.0	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rpa4348-like
62	<a href="#">c5d9rA_</a>	Alignment	not modelled	97.0	15	<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
63	<a href="#">c4ce4i_</a>	Alignment	not modelled	96.9	11	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> mprl9; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
64	<a href="#">c4hzbE_</a>	Alignment	not modelled	96.8	31	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> putative periplasmic protein; <b>PDBTitle:</b> crystal structure of the type vi semet effector-immunity complex tae3-2 tai3 from ralstonia pickettii
65	<a href="#">d3e99a1</a>	Alignment	not modelled	96.8	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
66	<a href="#">d3dmca1</a>	Alignment	not modelled	96.8	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
67	<a href="#">c5uwaB_</a>	Alignment	not modelled	96.7	8	<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
68	<a href="#">c2gbxF_</a>	Alignment	not modelled	96.7	12	<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
69	<a href="#">d1ohpa1</a>	Alignment	not modelled	96.7	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ketosteroid isomerase-like
70	<a href="#">c2qguA_</a>	Alignment	not modelled	96.7	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable signal peptide protein; <b>PDBTitle:</b> three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
71	<a href="#">c4u13B_</a>	Alignment	not modelled	96.6	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
72	<a href="#">d2cw9a1</a>	Alignment	not modelled	96.5	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> TIM44-like
73	<a href="#">c3ff2A_</a>	Alignment	not modelled	96.4	11	<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
74	<a href="#">c3f14A_</a>	Alignment	not modelled	96.4	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
75	<a href="#">c3fgyB_</a>	Alignment	not modelled	96.3	11	<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
76	<a href="#">c3f8hA_</a>	Alignment	not modelled	96.2	15	<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
77	<a href="#">d1nwwa_</a>	Alignment	not modelled	96.2	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Limonene-1,2-epoxide hydrolase-like

78	<a href="#">d3dm8a1</a>	Alignment	not modelled	96.2	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rpa4348-like
79	<a href="#">c5evhA</a>	Alignment	not modelled	96.1	11	<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
80	<a href="#">dlz1sa1</a>	Alignment	not modelled	96.1	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
81	<a href="#">c4lmiA</a>	Alignment	not modelled	96.0	11	<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
82	<a href="#">d3ebta1</a>	Alignment	not modelled	96.0	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Snoal-like polyketide cyclase
83	<a href="#">c3wmdA</a>	Alignment	not modelled	96.0	15	<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
84	<a href="#">c4fczB</a>	Alignment	not modelled	95.9	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> toluene-tolerance protein; <b>PDBTitle:</b> crystal structure of toluene-tolerance protein from pseudomonas putida2 (strain kt2440), northeast structural genomics consortium (nesg)3 target ppr99
85	<a href="#">d2f99a1</a>	Alignment	not modelled	95.9	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Snoal-like polyketide cyclase
86	<a href="#">c1z1sA</a>	Alignment	not modelled	95.7	9	<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
87	<a href="#">c5x7lA</a>	Alignment	not modelled	95.7	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> tsrd; <b>PDBTitle:</b> structure of tsrd from streptomyces laurentii
88	<a href="#">c3h3hA</a>	Alignment	not modelled	95.7	10	<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_i0226) from burkholderia thailandensis e264 at 1.60 a3 resolution
89	<a href="#">d2bnga1</a>	Alignment	not modelled	95.7	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Limonene-1,2-epoxide hydrolase-like
90	<a href="#">c3ehcA</a>	Alignment	not modelled	95.4	5	<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
91	<a href="#">c3msoA</a>	Alignment	not modelled	95.3	13	<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
92	<a href="#">d2b1xb1</a>	Alignment	not modelled	95.1	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
93	<a href="#">d1s5aa</a>	Alignment	not modelled	95.1	7	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
94	<a href="#">c3hk4B</a>	Alignment	not modelled	94.9	8	<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
95	<a href="#">c3f8xD</a>	Alignment	not modelled	94.8	13	<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
96	<a href="#">c5aigA</a>	Alignment	not modelled	94.7	14	<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
97	<a href="#">c6fejA</a>	Alignment	not modelled	94.5	13	<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
98	<a href="#">d2a15a1</a>	Alignment	not modelled	94.5	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ketosteroid isomerase-like
99	<a href="#">c4h3uB</a>	Alignment	not modelled	94.5	13	<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
100	<a href="#">c4v1ai</a>	Alignment	not modelled	94.3	15	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 22 of 2
101	<a href="#">c3f40A</a>	Alignment	not modelled	94.2	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_677363.1) from cytophaga hutchinsonii atcc 33406 at 1.27 a3 resolution
						<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative polyketide cyclase;

102	<a href="#">c3f9sB_</a>	Alignment	not modelled	94.2	10	<b>PDBTitle:</b> crystal structure of a putative polyketide cyclase (lferr_0659) from2 acidithiobacillus ferrooxidans atcc at 1.76 a resolution
103	<a href="#">d2geya1</a>	Alignment	not modelled	94.1	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase
104	<a href="#">d1ulib_</a>	Alignment	not modelled	94.0	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
105	<a href="#">c6a5hB_</a>	Alignment	not modelled	94.0	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
106	<a href="#">c5aiiP_</a>	Alignment	not modelled	94.0	15	<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
107	<a href="#">d2gexa1</a>	Alignment	not modelled	93.9	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase
108	<a href="#">c3grdA_</a>	Alignment	not modelled	93.6	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
109	<a href="#">c2jq5A_</a>	Alignment	not modelled	92.7	12	<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> sec-c motif; <b>PDBTitle:</b> solution structure of rpa3114, a sec-c motif containing protein from2 rhodospseudomonas palustris; northeast structural genomics consortium3 target rpt5 / ontario center for structural proteomics target rp3097
110	<a href="#">c3qzxB_</a>	Alignment	not modelled	92.3	14	<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
111	<a href="#">d3dxa1</a>	Alignment	not modelled	92.1	8	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Atu0744-like
112	<a href="#">c2i9wA_</a>	Alignment	not modelled	92.1	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a sec-c motif containing protein (psyc_2064) from2 psychrobacter arcticus at 1.75 a resolution
113	<a href="#">d2fxta1</a>	Alignment	not modelled	91.8	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> TIM44-like
114	<a href="#">c2rsxA_</a>	Alignment	not modelled	90.6	12	<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
115	<a href="#">c3rgaA_</a>	Alignment	not modelled	90.3	15	<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
116	<a href="#">c3i0yC_</a>	Alignment	not modelled	90.1	12	<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
117	<a href="#">c3g8zA_</a>	Alignment	not modelled	89.9	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-like2 fold (np_639274.1) from xanthomonas campestris at 1.90 a resolution
118	<a href="#">c3qk9B_</a>	Alignment	not modelled	89.6	16	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> mitochondrial import inner membrane translocase subunit <b>PDBTitle:</b> yeast tim44 c-terminal domain complexed with cymal-3
119	<a href="#">d1zo2a1</a>	Alignment	not modelled	89.4	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> NTF2-like
120	<a href="#">d1m98a2</a>	Alignment	not modelled	88.8	7	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Orange carotenoid protein, C-terminal domain