Phyre^2

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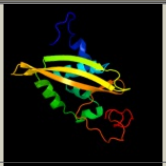
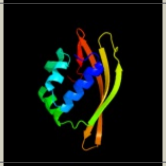
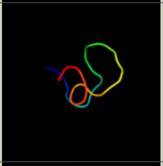
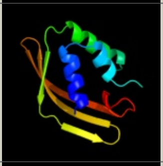
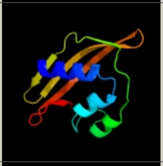
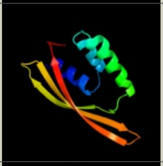
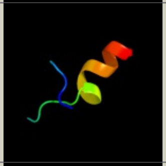
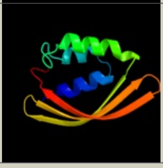
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2i9wA_	Alignment		100.0	36	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a sec-c motif containing protein (psyc_2064) from2 psychrobacter arcticus at 1.75 a resolution
2	c2jq5A_	Alignment		100.0	35	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**sec-c motif; **PDBTitle:** solution structure of rpa3114, a sec-c motif containing2 protein from rhodopseudomonas palustris; northeast3 structural genomics consortium target rpt5 / ontario4 center for structural proteomics target rp3097
3	d2i9wa1	Alignment		100.0	34	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SEC-C associated NTF2-like domain
4	c1ozbI_	Alignment		98.9	71	**PDB header:**protein transport **Chain:** I: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** crystal structure of secb complexed with seca c-terminus
5	d1ozbi_	Alignment		98.9	71	**Fold:**Sec-C motif **Superfamily:**Sec-C motif **Family:**Sec-C motif
6	c1ozbJ_	Alignment		98.9	71	**PDB header:**protein transport **Chain:** J: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** crystal structure of secb complexed with seca c-terminus
7	d1tm6a_	Alignment		98.9	80	**Fold:**Sec-C motif **Superfamily:**Sec-C motif **Family:**Sec-C motif
8	c1tm6A_	Alignment		98.9	80	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** nmr structure of the free zinc binding c-terminal domain of2 seca
9	d2i9wa3	Alignment		97.7	57	**Fold:**Sec-C motif **Superfamily:**Sec-C motif **Family:**Sec-C motif
10	c3gwrA_	Alignment		96.8	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**putative calcium/calmodulin-dependent protein kinase type **PDBTitle:** 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
11	d2r4ia1	Alignment		96.5	15	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**CHU142-like

12	c3kspA_	Alignment		96.4	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**calcium/calmodulin-dependent kinase ii association domain; **PDBTitle:** crystal structure of a putative ca/calmodulin-dependent kinase ii2 association domain (exig_1688) from exiguobacterium sibiricum 255-153 at 2.59 a resolution
13	d3cnxa1	Alignment		95.7	17	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SAV4671-like
14	c3ke7A_	Alignment		95.5	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative ketosteroid isomerase; **PDBTitle:** crystal structure of putative ketosteroid isomerase (yp_001303366.1)2 from parabacteroides distasonis atcc 8503 at 1.45 a resolution
15	d2f86b1	Alignment		94.9	16	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
16	c3f14A_	Alignment		94.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized ntf2-like protein; **PDBTitle:** crystal structure of ntf2-like protein of unknown function2 (yp_680363.1) from cytophaga hutchinsonii atcc 33406 at 1.45 a3 resolution
17	c3gzrA_	Alignment		94.3	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein with a ntf2-like fold; **PDBTitle:** crystal structure of an uncharacterized protein with a cystatin-like2 fold (cc_2572) from caulobacter vibrioides at 1.40 a resolution
18	d2ux0a1	Alignment		94.1	13	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
19	d2i9wa2	Alignment		94.0	48	**Fold:**Sec-C motif **Superfamily:**Sec-C motif **Family:**Sec-C motif
20	d2bnga1	Alignment		94.0	12	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Limonene-1,2-epoxide hydrolase-like
21	d3dm8a1	Alignment	not modelled	93.3	10	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Rpa4348-like
22	d2rcda1	Alignment	not modelled	93.0	16	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**BxeB1374-like
23	d2k54a1	Alignment	not modelled	92.8	19	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Atu0742-like
24	d3bb9a1	Alignment	not modelled	92.6	13	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SO0125-like
25	d2a15a1	Alignment	not modelled	91.9	13	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Ketosteroid isomerase-like
26	c3grdA_	Alignment	not modelled	91.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized ntf2-superfamily protein; **PDBTitle:** crystal structure of ntf2-superfamily protein with unknown2 function (np_977240.1) from bacillus cereus atcc 10987 at3 1.25 a resolution
27	d2geya1	Alignment	not modelled	91.5	19	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SnoaL-like polyketide cyclase
28	d3ec9a1	Alignment	not modelled	91.3	13	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**PhzA/PhzB-like

29	c3k0zB_	Alignment	not modelled	91.0	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative polyketide cyclase; **PDBTitle:** crystal structure of putative polyketide cyclase (np_977253.1) from2 bacillus cereus atcc 10987 at 1.91 a resolution
30	c3k7cC_	Alignment	not modelled	90.7	9	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**putative ntf2-like transpeptidase; **PDBTitle:** crystal structure of putative ntf2-like transpeptidase (np_281412.1)2 from campylobacter jejuni at 2.00 a resolution
31	c3fgyB_	Alignment	not modelled	90.4	19	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized ntf2-like protein; **PDBTitle:** crystal structure of a ntf2-like protein (bxe_b1094) from burkholderia2 xenovorans lb400 at 1.59 a resolution
32	d3b7ca1	Alignment	not modelled	90.3	13	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SO0125-like
33	c3g8zA_	Alignment	not modelled	89.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein of unknown function with cystatin-like fold; **PDBTitle:** crystal structure of protein of unknown function with cystatin-like2 fold (np_639274.1) from xanthomonas campestris at 1.90 a resolution
34	c1tuhA_	Alignment	not modelled	89.2	22	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein egc068; **PDBTitle:** structure of bal32a from a soil-derived mobile gene cassette
35	d1tuha_	Alignment	not modelled	89.2	22	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Hypothetical protein egc068 from a soil-derived mobile gene cassette
36	c3f7sA_	Alignment	not modelled	88.3	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized ntf2-like protein; **PDBTitle:** crystal structure of a ntf2-like protein of unknown function (pp_4556)2 from pseudomonas putida kt2440 at 2.11 a resolution
37	d1nwwa_	Alignment	not modelled	86.9	17	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Limonene-1,2-epoxide hydrolase-like
38	d3d9ra1	Alignment	not modelled	86.8	20	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**ECA1476-like
39	d2gxfa1	Alignment	not modelled	85.9	16	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**YybH-like
40	d1hkxa_	Alignment	not modelled	84.4	12	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
41	c3robC_	Alignment	not modelled	83.6	16	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved protein from planctomyces2 limnophilus dsm 3776
42	c3fsdA_	Alignment	not modelled	82.1	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ntf2-like protein of unknown function in nutrient uptake; **PDBTitle:** 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	d2gexa1	Alignment	not modelled	81.8	13	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SnoaL-like polyketide cyclase
44	d1s5aa_	Alignment	not modelled	80.6	14	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**PhzA/PhzB-like
45	d3ebta1	Alignment	not modelled	78.3	16	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SnoaL-like polyketide cyclase
46	d1ohpa1	Alignment	not modelled	77.7	19	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Ketosteroid isomerase-like
47	c3h51A_	Alignment	not modelled	77.5	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**putative calcium/calmodulin dependent protein kinase ii **PDBTitle:** crystal structure of putative calcium/calmodulin dependent protein2 kinase ii association domain (np_636218.1) from xanthomonas3 campestris at 1.70 a resolution
48	c3f7xA_	Alignment	not modelled	76.8	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative polyketide cyclase; **PDBTitle:** crystal structure of a putative polyketide cyclase (pp0894) from2 pseudomonas putida kt2440 at 1.24 a resolution
49	d1sjwa_	Alignment	not modelled	76.1	15	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SnoaL-like polyketide cyclase
50	c1z1sA_	Alignment	not modelled	73.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa3332; **PDBTitle:** crystal structure of putative isomerase pa3332 from2 pseudomonas aeruginosa
51	d1z1sa1	Alignment	not modelled	73.1	17	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**PhzA/PhzB-like
52	d1oh0a_	Alignment	not modelled	72.5	15	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Ketosteroid isomerase-like
53	d3dmca1	Alignment	not modelled	71.0	9	**Fold:**Cystatin-like **Superfamily:**NTF2-like

						Family: PhzA/PhzB-like
54	c3fh1A_	Alignment	not modelled	66.2	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized ntf2-like protein; **PDBTitle:** crystal structure of a ntf2-like protein of unknown function (mll8193)2 from mesorhizobium loti at 1.60 a resolution
55	c3hx8A_	Alignment	not modelled	64.3	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative ketosteroid isomerase; **PDBTitle:** crystal structure of putative ketosteroid isomerase2 (np_103587.1) from mesorhizobium loti at 1.45 a resolution
56	c3h3hA_	Alignment	not modelled	59.7	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized snoal-like protein; **PDBTitle:** crystal structure of a snoal-like protein of unknown function2 (bth_ii0226) from burkholderia thailandensis e264 at 1.60 a3 resolution
57	c3ff2A_	Alignment	not modelled	57.5	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized cystatin fold protein (yp_497570.1) from **PDBTitle:** crystal structure of an uncharacterized cystatin fold protein2 (saro_2299) from novosphingobium aromaticivorans dsm at 1.90 a3 resolution
58	c3ehcA_	Alignment	not modelled	55.8	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**snoal-like polyketide cyclase; **PDBTitle:** crystal structure of a snoal-like polyketide cyclase (atu3018) from2 agrobacterium tumefaciens str. c58 at 2.12 a resolution
59	c3hk4B_	Alignment	not modelled	54.2	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**mlr7391 protein; **PDBTitle:** crystal structure of a putative snoal-like polyketide cyclase2 [carbohydrate phosphatase] (mlr7391) from mesorhizobium loti at 1.963 a resolution
60	c3bb9D_	Alignment	not modelled	52.8	16	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**putative orphan protein; **PDBTitle:** crystal structure of a putative ketosteroid isomerase (sfri_1973) from2 shewanella frigidimarina ncimb 400 at 1.80 a resolution
61	d1vqqa1	Alignment	not modelled	50.0	12	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Penicillin binding protein 2a (PBP2A), N-terminal domain
62	c3f9sB_	Alignment	not modelled	49.9	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative polyketide cyclase; **PDBTitle:** crystal structure of a putative polyketide cyclase (lferr_0659) from2 acidithiobacillus ferrooxidans atcc at 1.76 a resolution
63	d2owpa1	Alignment	not modelled	47.6	12	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**BxeB1374-like
64	c3ff0A_	Alignment	not modelled	44.2	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**phenazine biosynthesis protein phzb 2; **PDBTitle:** crystal structure of a phenazine biosynthesis-related protein (phzb2)2 from pseudomonas aeruginosa at 1.90 a resolution
65	c3f8hA_	Alignment	not modelled	43.8	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative polyketide cyclase; **PDBTitle:** crystal structure of a putative polyketide cyclase (tm1040_3560) from2 silicibacter sp. tm1040 at 2.00 a resolution
66	c3soyA_	Alignment	not modelled	43.2	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**ntf2-like superfamily protein; **PDBTitle:** nuclear transport factor 2 (ntf2-like) superfamily protein from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
67	d2bmla1	Alignment	not modelled	41.5	53	**Fold:**beta-hairpin stack **Superfamily:**Cell wall binding repeat **Family:**Cell wall binding repeat
68	d2a1ka1	Alignment	not modelled	39.0	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Phage ssDNA-binding proteins
69	c3f40A_	Alignment	not modelled	38.4	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized ntf2-like protein; **PDBTitle:** crystal structure of ntf2-like protein of unknown function2 (yp_677363.1) from cytophaga hutchinsonii atcc 33406 at3 1.27 a resolution
70	d3blza1	Alignment	not modelled	37.2	12	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Sbal0622-like
71	c3msoA_	Alignment	not modelled	36.6	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**steroid delta-isomerase; **PDBTitle:** crystal structure of a steroid delta-isomerase (np_250810.1) from2 pseudomonas aeruginosa at 2.57 a resolution
72	d3b8la1	Alignment	not modelled	36.3	10	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**BaiE/LinA-like
73	d1gpca_	Alignment	not modelled	35.9	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Phage ssDNA-binding proteins
74	c2ra9A_	Alignment	not modelled	35.3	35	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein duf1285; **PDBTitle:** crystal structure of a duf1285 family protein (sbal_2486) from2 shewanella baltica os155 at 1.40 a resolution
75	c3hzpA_	Alignment	not modelled	35.3	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ntf2-like protein of unknown function; **PDBTitle:** crystal structure of ntf2-like protein of unknown function mn2a_05052 from prochlorococcus marinus (yp_291699.1) from prochlorococcus sp.3 natl2a at 1.40 a resolution
76	c3kkgA_	Alignment	not modelled	33.6	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative snoal-like polyketide cyclase; **PDBTitle:** crystal structure of putative snoal-like polyketide cyclase2 (yp_509242.1) from jannaschia sp. ccs1 at 1.40 a resolution

77	c3g0kA_	Alignment	not modelled	33.3	17	**PDB header:**ca-binding protein **Chain:** A: **PDB Molecule:**putative membrane protein; **PDBTitle:** 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
78	d2f99a1	Alignment	not modelled	32.5	16	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SnoaL-like polyketide cyclase
79	c3cooB_	Alignment	not modelled	32.2	20	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**spondin-1; **PDBTitle:** the crystal structure of reelin-n domain of f-spondin
80	d1wgea1	Alignment	not modelled	26.8	71	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
81	d1nuia2	Alignment	not modelled	25.8	56	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
82	d1o9ga_	Alignment	not modelled	25.7	100	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase AviRa
83	c3r1fO_	Alignment	not modelled	24.7	22	**PDB header:**transcription **Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr; **PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
84	d1njha_	Alignment	not modelled	24.2	15	**Fold:**Hypothetical protein YojF **Superfamily:**Hypothetical protein YojF **Family:**Hypothetical protein YojF
85	d1ywsa1	Alignment	not modelled	24.0	71	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
86	c3i0yC_	Alignment	not modelled	23.8	21	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**putative polyketide cyclase; **PDBTitle:** crystal structure of a putative polyketide cyclase (xcc0381) from2 xanthomonas campestris pv. campestris at 1.50 a resolution
87	d2baaa_	Alignment	not modelled	23.7	27	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Family 19 glycosidase
88	d1mo6a2	Alignment	not modelled	22.6	20	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
89	d1ubea2	Alignment	not modelled	21.8	25	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
90	d3dxoa1	Alignment	not modelled	21.6	14	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Atu0744-like
91	d1h8ga_	Alignment	not modelled	20.8	33	**Fold:**beta-hairpin stack **Superfamily:**Cell wall binding repeat **Family:**Cell wall binding repeat
92	d1u94a2	Alignment	not modelled	19.3	25	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
93	d2rgqa1	Alignment	not modelled	19.0	11	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Rv3472-like
94	c1ox3A_	Alignment	not modelled	18.7	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**fibritin; **PDBTitle:** crystal structure of mini-fibritin
95	c1mwuA_	Alignment	not modelled	18.6	12	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**penicillin-binding protein 2a; **PDBTitle:** structure of methicillin acyl-penicillin binding protein 2a2 from methicillin resistant staphylococcus aureus strain3 27r at 2.60 a resolution.
96	c3hiaB_	Alignment	not modelled	18.4	24	**PDB header:**choline-binding protein **Chain:** B: **PDB Molecule:**choline binding protein; **PDBTitle:** crystal structure of the choline binding domain of spr1274 in2 streptococcus pneumoniae
97	d3cu3a1	Alignment	not modelled	17.6	16	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**BaiE/LinA-like
98	d1xp8a2	Alignment	not modelled	17.3	25	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
99	c1z5sD_	Alignment	not modelled	17.1	20	**PDB header:**ligase **Chain:** D: **PDB Molecule:**ran-binding protein 2; **PDBTitle:** crystal structure of a complex between ubc9, sumo-1,2 rangap1 and nup358/ranbp2