

# Phyre2

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 Description RVBD0033\_(acpA)\_36607\_36870  
 Date Tue Jul 23 14:50:06 BST 2019  
 Unique Job ID 5450472b2314c7a6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2cgqA_</a>	Alignment		99.7	99	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein acpa; <b>PDBTitle:</b> a putative acyl carrier protein(rv0033) from mycobacterium2 tuberculosis
2	<a href="#">c2n98A_</a>	Alignment		99.6	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> solution structure of acyl carrier protein lipd from actinoplanes2 friulensis
3	<a href="#">c2mf4A_</a>	Alignment		99.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hybrid polyketide synthase-non ribosomal peptide <b>PDBTitle:</b> 1h, 13c, 15n chemical shift assignments of streptomyces virginiae vira2 acp5a
4	<a href="#">c6c4qA_</a>	Alignment		99.6	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase pks13; <b>PDBTitle:</b> 1.16 angstrom resolution crystal structure of acyl carrier protein2 domain (residues 1-100) of polyketide synthase pks13 from3 mycobacterium tuberculosis
5	<a href="#">d1klpa_</a>	Alignment		99.6	23	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
6	<a href="#">c2lteA_</a>	Alignment		99.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> specialized acyl carrier protein; <b>PDBTitle:</b> solution nmr structure of the specialized acyl carrier protein pa33342 (apo) from pseudomonas aeruginosa, northeast structural genomics3 consortium target pat415
7	<a href="#">c2liuA_</a>	Alignment		99.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cura; <b>PDBTitle:</b> nmr structure of holo-acpi domain from cura module from lyngbya2 majuscula
8	<a href="#">c4hkgB_</a>	Alignment		99.6	12	<b>PDB header:</b> phosphopantetheine binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphopantetheine attachment site family protein; <b>PDBTitle:</b> crystal structure of free-standing peptidyl carrier protein from2 uncharacterized acinetobacter baumannii secondary metabolic pathway
9	<a href="#">d1nq4a_</a>	Alignment		99.5	16	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
10	<a href="#">c4ca3A_</a>	Alignment		99.5	14	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> hybrid polyketide synthase-non ribosomal peptide <b>PDBTitle:</b> solution structure of streptomyces virginiae vira acp5b
11	<a href="#">c2afdA_</a>	Alignment		99.5	14	<b>PDB header:</b> ligand binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein asl1650; <b>PDBTitle:</b> solution structure of asl1650, an acyl carrier protein from anabaena2 sp. pcc 7120 with a variant phosphopantetheinylation-site sequence

12	<a href="#">c2dnwA_</a>	Alignment		99.5	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> solution structure of rsgi ruh-059, an acp domain of acyl2 carrier protein, mitochondrial [precursor] from human cdna
13	<a href="#">d1t8ka_</a>	Alignment		99.5	31	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
14	<a href="#">c6h0jA_</a>	Alignment		99.5	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> type i modular polyketide synthase; <b>PDBTitle:</b> a1-type acp domain from module 5 of mlsA1
15	<a href="#">c2qnwA_</a>	Alignment		99.5	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> toxoplasma gondii apicoplast-targeted acyl carrier protein
16	<a href="#">c2ehtA_</a>	Alignment		99.5	32	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> crystal structure of acyl carrier protein from aquifex aeolicus (form2 2)
17	<a href="#">c5hvcA_</a>	Alignment		99.5	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type i modular polyketide synthase; <b>PDBTitle:</b> solution structure of the apo state of the acyl carrier protein from2 the mlsA2 subunit of the mycolactone polyketide synthase
18	<a href="#">c2ju2A_</a>	Alignment		99.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> erythronolide synthase; <b>PDBTitle:</b> minimized mean solution structure of the acyl carrier2 protein domain from module 2 of 6-deoxyerythronolide b3 synthase (debs)
19	<a href="#">c2m5rA_</a>	Alignment		99.5	21	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> solution structure of holo-acyl carrier protein of leishmania major
20	<a href="#">c5mtiA_</a>	Alignment		99.5	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphopantetheine-binding protein; <b>PDBTitle:</b> bamb_5917 acyl-carrier protein
21	<a href="#">c2fvfA_</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> structure of 10:0-acp (protein with docked fatty acid)
22	<a href="#">d1vkua_</a>	Alignment	not modelled	99.5	23	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
23	<a href="#">c2mr7A_</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> non-ribosomal peptide synthetase; <b>PDBTitle:</b> apo structure of the peptidyl carrier protein domain 7 of the2 teicoplanin producing non-ribosomal peptide synthetase
24	<a href="#">c4zjbG_</a>	Alignment	not modelled	99.5	35	<b>PDB header:</b> lyase/biosynthetic protein <b>Chain:</b> G: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> crystal structure of (3r)-hydroxyacyl-acyl carrier protein2 dehydratase(fabz) in complex with holo-acp from helicobacter pylori
25	<a href="#">d2af8a_</a>	Alignment	not modelled	99.5	21	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
26	<a href="#">c3ejbC_</a>	Alignment	not modelled	99.5	30	<b>PDB header:</b> oxidoreductase/lipid transport <b>Chain:</b> C: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> crystal structure of p450bioi in complex with tetradecanoic acid2 ligated acyl carrier protein
27	<a href="#">c5kp8B_</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> curb; <b>PDBTitle:</b> crystal structure of the curacin biosynthetic pathway hmg synthase in2 complex with acetyl donor-acp
28	<a href="#">c5u3hA_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> hmpw2 nonribosomal peptide synthetase; <b>PDBTitle:</b> solution structure of apo pcp1 from yersiniabactin synthetase
						<b>PDB header:</b> oxidoreductase

29	<a href="#">c5msvB</a>	Alignment	not modelled	99.5	15	<b>Chain:</b> B; <b>PDB Molecule:</b> thioester reductase domain-containing protein; <b>PDBTitle:</b> structure of the phosphopantetheine modified pcp-r didomain of 2 carboxylic acid reductase (car) in complex with nadp
30	<a href="#">c2l4bA</a>	Alignment	not modelled	99.5	28	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> solution structure of a putative acyl carrier protein from anaplasma2 phagocytophilum. seattle structural genomics center for infectious3 disease target anpha.01018.a
31	<a href="#">c5zk4D</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> disa protein; <b>PDBTitle:</b> the structure of dszs acyltransferase with carrier protein
32	<a href="#">c1x3oA</a>	Alignment	not modelled	99.5	32	<b>PDB header:</b> lipid transport <b>Chain:</b> A; <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> crystal structure of the acyl carrier protein from thermus2 thermophilus hb8
33	<a href="#">c2cnrA</a>	Alignment	not modelled	99.5	25	<b>PDB header:</b> lipid transport <b>Chain:</b> A; <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> structural studies on the interaction of scfas acp with2 acps
34	<a href="#">c2l9fA</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> cale8; <b>PDBTitle:</b> nmr solution structure of meacp
35	<a href="#">c2n50A</a>	Alignment	not modelled	99.5	29	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> novel structural components contribute to the high thermal stability2 of acyl carrier protein from enterococcus faecalis
36	<a href="#">c2cq8A</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> 10-formyltetrahydrofolate dehydrogenase; <b>PDBTitle:</b> solution structure of rsgi ruh-033, a pp-binding domain of 2 10-ftfhfdh from human cdna
37	<a href="#">c2kr5A</a>	Alignment	not modelled	99.5	11	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> aflatoxin biosynthesis polyketide synthase; <b>PDBTitle:</b> solution structure of an acyl carrier protein domain from fungal type2 i polyketide synthase
38	<a href="#">c2loIA</a>	Alignment	not modelled	99.4	28	<b>PDB header:</b> lipid transport <b>Chain:</b> A; <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> nmr structure of an acyl-carrier protein from rickettsia prowazekii,2 seattle structural genomics center for infectious disease (ssgcid)
39	<a href="#">c4dxeH</a>	Alignment	not modelled	99.4	36	<b>PDB header:</b> transferase <b>Chain:</b> H; <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> 2.52 angstrom resolution crystal structure of the acyl-carrier-protein2 synthase (acps)-acyl carrier protein (acp) protein-protein complex3 from staphylococcus aureus subsp. aureus col
40	<a href="#">c2kcia</a>	Alignment	not modelled	99.4	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative acyl carrier protein; <b>PDBTitle:</b> solution nmr structure of gmet_2339 from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr141
41	<a href="#">c2kwIA</a>	Alignment	not modelled	99.4	28	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> solution structure of acyl carrier protein from borrelia burgdorferi
42	<a href="#">c2roqA</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> enterobactin synthetase component f; <b>PDBTitle:</b> solution structure of the thiolation-thioesterase di-domain2 of enterobactin synthetase component f
43	<a href="#">c2fq2A</a>	Alignment	not modelled	99.4	31	<b>PDB header:</b> lipid transport <b>Chain:</b> A; <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> solution structure of minor conformation of holo-acyl2 carrier protein from malaria parasite plasmodium falciparum
44	<a href="#">c2jgpA</a>	Alignment	not modelled	99.4	12	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> tyrocidine synthetase 3; <b>PDBTitle:</b> structure of the tycc5-6 pcp-c bidomain of the tyrocidine2 synthetase tycc
45	<a href="#">c6gcsQ</a>	Alignment	not modelled	99.4	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q; <b>PDB Molecule:</b> acpm2 subunit; <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
46	<a href="#">c6gcsQ</a>	Alignment	not modelled	99.4	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O; <b>PDB Molecule:</b> acpm1 subunit; <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
47	<a href="#">c4pxhF</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> F; <b>PDB Molecule:</b> peptide synthetase; <b>PDBTitle:</b> structure of p450sky (cyp163b3), a cytochrome p450 from skyllamycin2 biosynthesis in complex with a peptidyl carrier protein domain
48	<a href="#">d1f80d</a>	Alignment	not modelled	99.4	32	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
49	<a href="#">c2jq4A</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> structural genomics <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein atu2571; <b>PDBTitle:</b> complete resonance assignments and solution structure calculation of 2 atc2521 (nesg id: att6) from agrobacterium tumefaciens
50	<a href="#">d2jq4a1</a>	Alignment	not modelled	99.4	16	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
51	<a href="#">c2l3vA</a>	Alignment	not modelled	99.4	29	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> nmr structure of acyl carrier protein from brucella melitensis
52	<a href="#">d1or5a</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
53	<a href="#">c5ejdK</a>	Alignment	not modelled	99.4	7	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> K; <b>PDB Molecule:</b> tqaa;

						<b>PDBTitle:</b> the crystal structure of holo t3ct
54	<a href="#">c4zxiA</a>	Alignment	not modelled	99.4	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> enterobactin synthase component f; <b>PDBTitle:</b> crystal structure of holo-entf a nonribosomal peptide synthetase in2 the thioester-forming conformation
55	<a href="#">d2gdwa1</a>	Alignment	not modelled	99.3	16	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Peptidyl carrier domain
56	<a href="#">c4bphA</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--poly(phosphoribitol) ligase subunit 2; <b>PDBTitle:</b> high resolution crystal structure of bacillus subtilis dltc
57	<a href="#">c2l22A</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> mupirocin didomain acyl carrier protein; <b>PDBTitle:</b> mupirocin didomain acp
58	<a href="#">c3ce7A</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> specific mitochondrial acyl carrier protein; <b>PDBTitle:</b> crystal structure of toxoplasma specific mitochondrial acyl carrier2 protein, 59.m03510
59	<a href="#">c5y08A</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-2,2'-bipyrrole-5-methanol synthase pigh; <b>PDBTitle:</b> solution structure of the apo doublet acyl carrier protein from2 prodigiosin biosynthesis
60	<a href="#">c4i4dA</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptide synthetase nrps type ii-pcp; <b>PDBTitle:</b> structure of blmi, a type-ii acyl-carrier-protein from streptomyces2 verticillus involved in bleomycin biosynthesis
61	<a href="#">c2n6yA</a>	Alignment	not modelled	99.3	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> hmwp2 nonribosomal peptide synthetase; <b>PDBTitle:</b> solution structure of holo arcp from yersiniabactin synthetase
62	<a href="#">c4r0mA</a>	Alignment	not modelled	99.3	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> mcycg protein; <b>PDBTitle:</b> structure of mcyc a-pcp complexed with phenylalanyl-adenylate
63	<a href="#">c2vsqA</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> surfactin synthetase subunit 3; <b>PDBTitle:</b> structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module
64	<a href="#">c3lmoA</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> specialized acyl carrier protein; <b>PDBTitle:</b> crystal structure of specialized acyl carrier protein (rpa2022) from2 rhodospseudomonas palustris, northeast structural genomics consortium3 target rpr324
65	<a href="#">c5es8A</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> linear gramicidin synthetase subunit a; <b>PDBTitle:</b> crystal structure of the initiation module of lgra in the thiolation2 state
66	<a href="#">c2fq1A</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isochorismatase; <b>PDBTitle:</b> crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains
67	<a href="#">c4dg9A</a>	Alignment	not modelled	99.2	12	<b>PDB header:</b> ligase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> pa1221; <b>PDBTitle:</b> structure of holo-pa1221, an nrps protein containing adenylation and2 pcp domains bound to vinylsulfonamide inhibitor
68	<a href="#">c5ja2A</a>	Alignment	not modelled	99.2	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> enterobactin synthase component f; <b>PDBTitle:</b> entf, a terminal nonribosomal peptide synthetase module bound to the2 non-native mbth-like protein pa2412
69	<a href="#">c5mssA</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioester reductase domain-containing protein; <b>PDBTitle:</b> structure of the a-pcp didomain of carboxylic acid reductase (car)2 from segniliparus rugosus in complex with amp
70	<a href="#">c4h2sD</a>	Alignment	not modelled	99.2	23	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> aminoacyl carrier protein 1; <b>PDBTitle:</b> crystal structure of bradyrhizobium japonicum glycine-[carrier2 protein] ligase complexed with cognate carrier protein and amp
71	<a href="#">c4zxiA</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyrocidine synthetase 3; <b>PDBTitle:</b> crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine
72	<a href="#">d2pnga1</a>	Alignment	not modelled	99.2	23	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
73	<a href="#">d1dv5a</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> apo-D-alanyl carrier protein
74	<a href="#">c3rg2H</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> ligase <b>Chain:</b> H: <b>PDB Molecule:</b> enterobactin synthase component e (ente), 2,3-dihydro-2,3- <b>PDBTitle:</b> structure of a two-domain nrps fusion protein containing the ente2 adenylation domain and entb aryl-carrier protein from enterobactin3 biosynthesis
75	<a href="#">c5czdB</a>	Alignment	not modelled	99.1	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-carrier-protein; <b>PDBTitle:</b> the complex structure of vink with vinl
76	<a href="#">c2n5iA</a>	Alignment	not modelled	99.0	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl carrier protein plti; <b>PDBTitle:</b> plti-pyrrolyl
77	<a href="#">c6bugA</a>	Alignment	not modelled	98.9	23	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanyl carrier protein; <b>PDBTitle:</b> crystal structure of a membrane protein, crystal form i

78	<a href="#">c2my5A</a>	Alignment	not modelled	98.9	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl carrier protein; <b>PDBTitle:</b> solution structure of kstb-ppc in kosinostatin biosynthesis
79	<a href="#">c6cxtA</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase fold protein; <b>PDBTitle:</b> crystal structure of fad-dependent dehydrogenase
80	<a href="#">c5u89A</a>	Alignment	not modelled	98.1	19	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> amino acid adenylation domain protein; <b>PDBTitle:</b> crystal structure of a cross-module fragment from the dimodular nrps2 dhbf
81	<a href="#">c2lkiA</a>	Alignment	not modelled	97.7	27	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of holo acyl carrier protein ne2163 from2 nitrosomonas europaea. northeast structural genomics consortium3 target net1.
82	<a href="#">c2amwA</a>	Alignment	not modelled	97.6	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ne2163; <b>PDBTitle:</b> solution nmr structure of protein ne2163 from nitrosomonas europaea.2 northeast structural genomics consortium target net1.
83	<a href="#">c4v1am</a>	Alignment	not modelled	96.3	13	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 22 of 2
84	<a href="#">c3s8mA</a>	Alignment	not modelled	93.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-acyl carrier protein reductase; <b>PDBTitle:</b> the crystal structure of fabv
85	<a href="#">c2vkzC</a>	Alignment	not modelled	92.0	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> fatty acid synthase subunit alpha; <b>PDBTitle:</b> structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
86	<a href="#">c4h2uC</a>	Alignment	not modelled	86.7	33	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> aminoacyl carrier protein 1; <b>PDBTitle:</b> crystal structure of bradyrhizobium japonicum glycine:[carrier2 protein] ligase complexed with cognate carrier protein and atp
87	<a href="#">c6eqoB</a>	Alignment	not modelled	86.0	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coenzyme a synthetase; <b>PDBTitle:</b> tri-functional propionyl-coa synthase of erythrobacter sp. nap1 with2 bound nADP+ and phosphomethylphosphonic acid adenylate ester
88	<a href="#">c2uv8C</a>	Alignment	not modelled	82.7	11	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> fatty acid synthase subunit alpha (fas2); <b>PDBTitle:</b> crystal structure of yeast fatty acid synthase with stalled2 acyl carrier protein at 3.1 angstrom resolution
89	<a href="#">c6c4vA</a>	Alignment	not modelled	81.3	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase pks13; <b>PDBTitle:</b> 1.9 angstrom resolution crystal structure of acyl carrier protein2 domain (residues 1350-1461) of polyketide synthase pks13 from3 mycobacterium tuberculosis
90	<a href="#">c3hmjB</a>	Alignment	not modelled	79.6	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase subunit alpha; <b>PDBTitle:</b> saccharomyces cerevisiae fas type i
91	<a href="#">c2uv9B</a>	Alignment	not modelled	76.8	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase alpha subunits; <b>PDBTitle:</b> crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the alpha subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
92	<a href="#">c1vw48</a>	Alignment	not modelled	73.4	15	<b>PDB header:</b> ribosome <b>Chain:</b> 8: <b>PDB Molecule:</b> 54s ribosomal protein l13, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
93	<a href="#">c4b3yB</a>	Alignment	not modelled	66.1	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase; <b>PDBTitle:</b> cryo-em structure of the mycobacterial fatty acid synthase
94	<a href="#">c4ggoA</a>	Alignment	not modelled	57.0	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trans-2-enoyl-coa reductase; <b>PDBTitle:</b> crystal structure of trans-2-enoyl-coa reductase from treponema2 denticola
95	<a href="#">c5t81A</a>	Alignment	not modelled	53.4	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> epob; <b>PDBTitle:</b> rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from strangium cellulosum
96	<a href="#">c6cgoB</a>	Alignment	not modelled	51.4	22	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> condensation domain protein; <b>PDBTitle:</b> molecular basis for condensation domain-mediated chain release from2 the enacyloxin polyketide synthase
97	<a href="#">d2gyc31</a>	Alignment	not modelled	42.1	20	<b>Fold:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Superfamily:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Family:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain
98	<a href="#">c4h2tC</a>	Alignment	not modelled	40.8	33	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> aminoacyl carrier protein 1; <b>PDBTitle:</b> crystal structure of bradyrhizobium japonicum glycine:[carrier2 protein] ligase complexed with cognate carrier protein and an3 analogue of glycyl adenylate
99	<a href="#">c1rqtB</a>	Alignment	not modelled	38.4	20	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> nmr structure of dimeric n-terminal domain of ribosomal2 protein l7 from e.coli
100	<a href="#">d1rqtA</a>	Alignment	not modelled	38.4	20	<b>Fold:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Superfamily:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Family:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>PDB header:</b> ribosome

101	<a href="#">c1rqtA_</a>	Alignment	not modelled	38.4	20	<b>Chain:</b> A; <b>PDB Molecule:</b> 50S ribosomal protein L7/12; <b>PDBTitle:</b> nmr structure of dimeric n-terminal domain of ribosomal2 protein l7 from e.coli
102	<a href="#">c4rdmB_</a>	Alignment	not modelled	36.4	9	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B; <b>PDB Molecule:</b> restriction endonuclease r.ngovii; <b>PDBTitle:</b> crystal structure of r.ngoavii restriction endonuclease b3 domain with2 cognate dna
103	<a href="#">d1dd4d_</a>	Alignment	not modelled	30.9	29	<b>Fold:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Superfamily:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Family:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain
104	<a href="#">d2rk5a1</a>	Alignment	not modelled	24.8	17	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
105	<a href="#">c5gxtA_</a>	Alignment	not modelled	24.5	24	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> maltose-binding periplasmic protein,pigg; <b>PDBTitle:</b> crystal structure of pigg
106	<a href="#">d2pls1</a>	Alignment	not modelled	24.1	14	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
107	<a href="#">d2plia1</a>	Alignment	not modelled	23.6	17	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
108	<a href="#">c5yadA_</a>	Alignment	not modelled	22.7	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> meiosis regulator and mrna stability factor 1; <b>PDBTitle:</b> crystal structure of marf1 lotus domain from mus musculus
109	<a href="#">d1q1va_</a>	Alignment	not modelled	21.9	11	<b>Fold:</b> Another 3-helical bundle <b>Superfamily:</b> DEK C-terminal domain <b>Family:</b> DEK C-terminal domain
110	<a href="#">d1dd3a1</a>	Alignment	not modelled	21.1	22	<b>Fold:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Superfamily:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Family:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain