
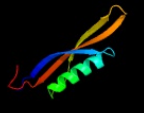






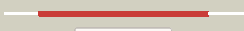




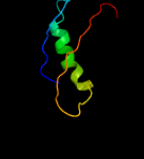



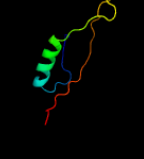

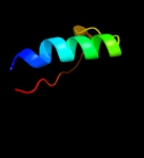




# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0379\_secE2\_455978\_456193  
 Date Tue Jul 23 14:50:45 BST 2019  
 Unique Job ID 19a2e4947be96934

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3onrl_</a>	 Alignment		100.0	97	<b>PDB header:</b> metal binding protein <b>Chain:</b> I: <b>PDB Molecule:</b> protein transport protein sece2; <b>PDBTitle:</b> crystal structure of the calcium chelating immunodominant antigen,2 calcium dodecin (rv0379),from mycobacterium tuberculosis with a novel3 calcium-binding site
2	<a href="#">c3oqtP_</a>	 Alignment		99.9	21	<b>PDB header:</b> flavoprotein <b>Chain:</b> P: <b>PDB Molecule:</b> rv1498a protein; <b>PDBTitle:</b> crystal structure of rv1498a protein from mycobacterium tuberculosis
3	<a href="#">c6r1eC_</a>	 Alignment		99.9	23	<b>PDB header:</b> flavoprotein <b>Chain:</b> C: <b>PDB Molecule:</b> dodecin; <b>PDBTitle:</b> structure of dodecin from streptomyces coelicolor
4	<a href="#">c2vxaL_</a>	 Alignment		99.9	23	<b>PDB header:</b> flavoprotein <b>Chain:</b> L: <b>PDB Molecule:</b> dodecin; <b>PDBTitle:</b> h.halophila dodecin in complex with riboflavin
5	<a href="#">d2ux9a1</a>	 Alignment		99.9	33	<b>Fold:</b> Dodecin subunit-like <b>Superfamily:</b> Dodecin-like <b>Family:</b> Dodecin-like
6	<a href="#">d2cc6a1</a>	 Alignment		99.5	31	<b>Fold:</b> Dodecin subunit-like <b>Superfamily:</b> Dodecin-like <b>Family:</b> Dodecin-like
7	<a href="#">c5lw8A_</a>	 Alignment		53.1	19	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein tonb; <b>PDBTitle:</b> nmr solution structure of helicobacter pylori tonb-ctd (residues 194-2 285)
8	<a href="#">d1ulqa2</a>	 Alignment		45.9	23	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
9	<a href="#">c6fipA_</a>	 Alignment		38.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein tonb; <b>PDBTitle:</b> solution nmr structure of pseudomonas aeruginosa tonb ctd
10	<a href="#">d1m3ka2</a>	 Alignment		30.5	23	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
11	<a href="#">c4ubwB_</a>	 Alignment		30.4	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase fada5; <b>PDBTitle:</b> apo structure of the 3-ketoacyl-coa thiolase fada5 from m.2 tuberculosis

12	<a href="#">d1fc3a_</a>	Alignment		26.5	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> Spo0A
13	<a href="#">d1qd1a1</a>	Alignment		26.4	26	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Formiminotransferase domain of formiminotransferase-cyclodeaminase. <b>Family:</b> Formiminotransferase domain of formiminotransferase-cyclodeaminase.
14	<a href="#">d1lq1a_</a>	Alignment		25.4	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> Spo0A
15	<a href="#">d1wdkc2</a>	Alignment		24.9	23	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
16	<a href="#">c1ulqD_</a>	Alignment		24.0	21	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> putative acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystal structure of tt0182 from thermus thermophilus hb8
17	<a href="#">c2jxpA_</a>	Alignment		22.9	11	<b>PDB header:</b> lipoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> putative lipoprotein b; <b>PDBTitle:</b> solution nmr structure of uncharacterized lipoprotein b2 from nitrosomonas europaea. northeast structural genomics3 target ner45a
18	<a href="#">c3svkB_</a>	Alignment		22.8	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystal structure of acetyl-coa acetyltransferase from mycobacterium2 avium
19	<a href="#">c3brtC_</a>	Alignment		22.8	17	<b>PDB header:</b> transferase/transcription <b>Chain:</b> C: <b>PDB Molecule:</b> inhibitor of nuclear factor kappa-b kinase subunit beta, <b>PDBTitle:</b> nemo/ikk association domain structure
20	<a href="#">c1wl5A_</a>	Alignment		22.4	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coenzyme a acetyltransferase 2; <b>PDBTitle:</b> human cytosolic acetoacetyl-coa thiolase
21	<a href="#">c2ibyD_</a>	Alignment	not modelled	21.2	21	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystallographic and kinetic studies of human mitochondrial2 acetoacetyl-coa thiolase (t2): the importance of potassium and3 chloride for its structure and function
22	<a href="#">d1kwia_</a>	Alignment	not modelled	21.0	32	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Cystatin/monellin <b>Family:</b> Cathelicidin motif
23	<a href="#">c3o6uB_</a>	Alignment	not modelled	20.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein cpe2226; <b>PDBTitle:</b> crystal structure of cpe2226 protein from clostridium perfringens.2 northeast structural genomics consortium target cpr195
24	<a href="#">d1afwa2</a>	Alignment	not modelled	20.6	16	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
25	<a href="#">c2k9kA_</a>	Alignment	not modelled	20.5	21	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> tonb2; <b>PDBTitle:</b> molecular characterization of the tonb2 protein from vibrio2 anguillarum
26	<a href="#">c4c2jA_</a>	Alignment	not modelled	20.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase, mitochondrial; <b>PDBTitle:</b> crystal structure of human mitochondrial 3-ketoacyl-coa2 thiolase in complex with coa
27	<a href="#">c4e1lC_</a>	Alignment	not modelled	19.3	25	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acetoacetyl-coa thiolase 2; <b>PDBTitle:</b> crystal structure of acetoacetyl-coa thiolase (thla2) from clostridium2 difficile
28	<a href="#">c2m2kA_</a>	Alignment	not modelled	18.4	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> hasb protein; <b>PDBTitle:</b> the structure of hasb ctd

29	<a href="#">c2d9zA_</a>	Alignment	not modelled	18.1	36	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase c, nu type; <b>PDBTitle:</b> solution structure of the ph domain of protein kinase c, nu2 type from human
30	<a href="#">c4h62O_</a>	Alignment	not modelled	18.1	21	<b>PDB header:</b> transcription <b>Chain:</b> Q: <b>PDB Molecule:</b> mediator of rna polymerase ii transcription subunit 17; <b>PDBTitle:</b> structure of the saccharomyces cerevisiae mediator subcomplex2 med17c/med11c/med22c
31	<a href="#">c6bn2A_</a>	Alignment	not modelled	18.1	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystal structure of acetyl-coa acetyltransferase from elizabethkingia2 anophelis nuhp1
32	<a href="#">c5oarC_</a>	Alignment	not modelled	16.8	28	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-hexosaminidase; <b>PDBTitle:</b> crystal structure of native beta-n-acetylhexosaminidase isolated from2 aspergillus oryzae
33	<a href="#">c4egvC_</a>	Alignment	not modelled	16.7	21	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystal structure of a monomeric scp2-thiolase like protein type 12 (stlp1) from mycobacterium smegmatis
34	<a href="#">d2dy1a3</a>	Alignment	not modelled	16.6	17	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Translational machinery components
35	<a href="#">c4q35B_</a>	Alignment	not modelled	16.4	12	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> lps-assembly lipoprotein lpte; <b>PDBTitle:</b> structure of a membrane protein
36	<a href="#">c1tt9B_</a>	Alignment	not modelled	15.4	26	<b>PDB header:</b> transferase, lyase <b>Chain:</b> B: <b>PDB Molecule:</b> formimidoyltransferase-cyclodeaminase <b>PDBTitle:</b> structure of the bifunctional and golgi associated2 formiminotransferase cyclodeaminase octamer
37	<a href="#">c3ss6B_</a>	Alignment	not modelled	15.2	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystal structure of the bacillus anthracis acetyl-coa2 acetyltransferase
38	<a href="#">c5vidI_</a>	Alignment	not modelled	15.1	40	<b>PDB header:</b> toxin <b>Chain:</b> I: <b>PDB Molecule:</b> bot.0671.2; <b>PDBTitle:</b> receptor binding domain of bont/b in complex with mini-protein binder2 bot.0671.2
39	<a href="#">c5vidG_</a>	Alignment	not modelled	15.1	40	<b>PDB header:</b> toxin <b>Chain:</b> G: <b>PDB Molecule:</b> bot.0671.2; <b>PDBTitle:</b> receptor binding domain of bont/b in complex with mini-protein binder2 bot.0671.2
40	<a href="#">d1tola2</a>	Alignment	not modelled	14.8	20	<b>Fold:</b> TolA/TonB C-terminal domain <b>Superfamily:</b> TolA/TonB C-terminal domain <b>Family:</b> TolA
41	<a href="#">c2iikA_</a>	Alignment	not modelled	14.3	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase, peroxisomal; <b>PDBTitle:</b> crystal structure of human peroxisomal acetyl-coa acyl transferase 12 (acaa1)
42	<a href="#">c4nzsA_</a>	Alignment	not modelled	13.8	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-ketothiolase bktb; <b>PDBTitle:</b> crystal structure of beta-ketothiolase bktb b from ralstonia eutropha2 h16
43	<a href="#">c5ab6E_</a>	Alignment	not modelled	13.6	29	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> scp2-thiolase like protein; <b>PDBTitle:</b> crystal structure of trypanosoma brucei scp2-thiolase like2 protein (tbslp) in complex with acetoacetyl-coa.
44	<a href="#">c4g7xB_</a>	Alignment	not modelled	12.7	11	<b>PDB header:</b> protein binding/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> tola protein; <b>PDBTitle:</b> crystal structure of a complex between the ctxphi piiii n-terminal2 domain and the vibrio cholerae tola c-terminal domain
45	<a href="#">c3gkuB_</a>	Alignment	not modelled	12.7	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable rna-binding protein; <b>PDBTitle:</b> crystal structure of a probable rna-binding protein from clostridium2 symbiosum atcc 14940
46	<a href="#">d2bv3a3</a>	Alignment	not modelled	12.5	11	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Translational machinery components
47	<a href="#">c4yccC_</a>	Alignment	not modelled	12.4	28	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of putative lipoprotein from peptoclostridium2 difficile 630 (fragment)
48	<a href="#">c3goaA_</a>	Alignment	not modelled	12.2	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase; <b>PDBTitle:</b> crystal structure of the salmonella typhimurium fada 3-ketoacyl-coa2 thiolase
49	<a href="#">c4n45B_</a>	Alignment	not modelled	12.1	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystal structure of reduced form of thiolase from clostridium2 acetobutylicum
50	<a href="#">d1vkza1</a>	Alignment	not modelled	12.1	28	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
51	<a href="#">c1qd1A_</a>	Alignment	not modelled	12.1	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> formiminotransferase-cyclodeaminase; <b>PDBTitle:</b> the crystal structure of the formiminotransferase domain of2 formiminotransferase-cyclodeaminase.
52	<a href="#">d2pjua1</a>	Alignment	not modelled	12.0	28	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> PrpR receptor domain-like <b>Family:</b> PrpR receptor domain-like
53	<a href="#">c2zkqe_</a>	Alignment	not modelled	12.0	22	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> E: <b>PDB Molecule:</b> rna expansion segment es6 part ii; <b>PDBTitle:</b> structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
54	<a href="#">d1dwna_</a>	Alianment	not modelled	11.8	29	<b>Fold:</b> RNA bacteriophage capsid protein <b>Superfamily:</b> RNA bacteriophage capsid protein

						<b>Family:</b> RNA bacteriophage capsid protein
55	<a href="#">d1nfpA_</a>	Alignment	not modelled	11.5	31	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Non-fluorescent flavoprotein (luxF, FP390)
56	<a href="#">c3hz4A_</a>	Alignment	not modelled	11.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from methanosarcina mazei
57	<a href="#">d2uube2</a>	Alignment	not modelled	10.8	16	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Ribosomal S5 protein, N-terminal domain
58	<a href="#">c2ow8f_</a>	Alignment	not modelled	10.6	23	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> <b>PDBTitle:</b> crystal structure of a 70s ribosome-trna complex reveals functional2 interactions and rearrangements. this file, 2ow8, contains the 30s3 ribosome subunit, two trna, and mrna molecules. 50s ribosome subunit4 is in the file 1vsa.
59	<a href="#">c6bjaA_</a>	Alignment	not modelled	10.6	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa acetyltransferase a; <b>PDBTitle:</b> crystal structure of acat5 thiolase from ascaris suum in complex with2 coenzyme a
60	<a href="#">d1pkpa2</a>	Alignment	not modelled	10.6	16	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Ribosomal S5 protein, N-terminal domain
61	<a href="#">c1afwB_</a>	Alignment	not modelled	10.5	14	<b>PDB header:</b> thiolase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-ketoacetyl-coa thiolase; <b>PDBTitle:</b> the 1.8 angstrom crystal structure of the dimeric2 peroxisomal thiolase of saccharomyces cerevisiae
62	<a href="#">c6q2zB_</a>	Alignment	not modelled	10.5	17	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> upf0339 family protein; <b>PDBTitle:</b> nmr solution structure of the hvo_2922 protein from haloferax volcanii
63	<a href="#">d2qale2</a>	Alignment	not modelled	10.4	15	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Ribosomal S5 protein, N-terminal domain
64	<a href="#">c1gshA_</a>	Alignment	not modelled	10.2	29	<b>PDB header:</b> glutathione biosynthesis ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione biosynthetic ligase; <b>PDBTitle:</b> structure of escherichia coli glutathione synthetase at ph 7.5
65	<a href="#">c2c7yB_</a>	Alignment	not modelled	10.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase 2; <b>PDBTitle:</b> plant enzyme
66	<a href="#">c2x9aB_</a>	Alignment	not modelled	10.0	26	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> membrane spanning protein, required for outer membrane <b>PDBTitle:</b> crystal structure of g3p from phage if1 in complex with its2 coreceptor, the c-terminal domain of tola
67	<a href="#">c6bjbB_</a>	Alignment	not modelled	9.7	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase a; <b>PDBTitle:</b> crystal structure of acat2-c91s thiolase from ascaris suum in complex2 with propionyl-coa and nitrate
68	<a href="#">c3brvC_</a>	Alignment	not modelled	9.6	17	<b>PDB header:</b> transferase/transcription <b>Chain:</b> C: <b>PDB Molecule:</b> inhibitor of nuclear factor kappa-b kinase subunit beta; <b>PDBTitle:</b> nemo/ikkb association domain structure
69	<a href="#">d1r4ca_</a>	Alignment	not modelled	9.5	19	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Cystatin/monellin <b>Family:</b> Cystatins
70	<a href="#">c6aqpA_</a>	Alignment	not modelled	9.4	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> aspergillus fumigatus cytosolic thiolase: acetylated enzyme in complex2 with coa and potassium ions
71	<a href="#">d3eeqa1</a>	Alignment	not modelled	9.3	7	<b>Fold:</b> CobE/GbiG C-terminal domain-like <b>Superfamily:</b> CobE/GbiG C-terminal domain-like <b>Family:</b> CobE/GbiG C-terminal domain-like
72	<a href="#">c4wysB_</a>	Alignment	not modelled	9.3	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> crystal structure of thiolase from escherichia coli
73	<a href="#">d1gsoa1</a>	Alignment	not modelled	9.3	16	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
74	<a href="#">c2wuaA_</a>	Alignment	not modelled	9.1	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetoacetyl coa thiolase; <b>PDBTitle:</b> structure of the peroxisomal 3-ketoacyl-coa thiolase from sunflower
75	<a href="#">d1ihra_</a>	Alignment	not modelled	9.1	21	<b>Fold:</b> ToIA/TonB C-terminal domain <b>Superfamily:</b> ToIA/TonB C-terminal domain <b>Family:</b> TonB
76	<a href="#">d1w26a2</a>	Alignment	not modelled	9.0	24	<b>Fold:</b> Ribosome binding domain-like <b>Superfamily:</b> Trigger factor ribosome-binding domain <b>Family:</b> Trigger factor ribosome-binding domain
77	<a href="#">c4x8wE_</a>	Alignment	not modelled	8.9	27	<b>PDB header:</b> gene regulation <b>Chain:</b> E: <b>PDB Molecule:</b> loquacious, isoform b; <b>PDBTitle:</b> dsrbd3 of loquacious
78	<a href="#">c2kzxA_</a>	Alignment	not modelled	8.8	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of a3dht5 from clostridium thermocellum,2 northeast structural genomics consortium target cmr116
79	<a href="#">d1e5ma2</a>	Alignment	not modelled	8.8	11	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
						<b>PDB header:</b> unknown function

80	<a href="#">c4eycA_</a>	Alignment	not modelled	8.7	17	<b>Chain:</b> A: <b>PDB Molecule:</b> cathelicidin antimicrobial peptide; <b>PDBTitle:</b> crystal structure of the cathelin-like domain of human cathelicidin2 ll-37 (hclcd)
81	<a href="#">d1p9ya_</a>	Alignment	not modelled	8.6	21	<b>Fold:</b> Ribosome binding domain-like <b>Superfamily:</b> Trigger factor ribosome-binding domain <b>Family:</b> Trigger factor ribosome-binding domain
82	<a href="#">c3hk4B_</a>	Alignment	not modelled	8.3	18	<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
83	<a href="#">d3by5a1</a>	Alignment	not modelled	8.2	19	<b>Fold:</b> CobE/GbiG C-terminal domain-like <b>Superfamily:</b> CobE/GbiG C-terminal domain-like <b>Family:</b> CobE/GbiG C-terminal domain-like
84	<a href="#">c3by5A_</a>	Alignment	not modelled	8.2	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> cobalamin biosynthesis protein; <b>PDBTitle:</b> crystal structure of cobalamin biosynthesis protein chig from2 agrobacterium tumefaciens str. c58
85	<a href="#">c1eg0B_</a>	Alignment	not modelled	8.2	13	<b>PDB header:</b> ribosome <b>PDB COMPND:</b>
86	<a href="#">c3bbnE_</a>	Alignment	not modelled	8.2	19	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> ribosomal protein s5; <b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
87	<a href="#">c5xyiC_</a>	Alignment	not modelled	8.1	24	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
88	<a href="#">d2w6ka1</a>	Alignment	not modelled	8.1	11	<b>Fold:</b> CobE/GbiG C-terminal domain-like <b>Superfamily:</b> CobE/GbiG C-terminal domain-like <b>Family:</b> CobE/GbiG C-terminal domain-like
89	<a href="#">d2coaa1</a>	Alignment	not modelled	8.1	36	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Pleckstrin-homology domain (PH domain)
90	<a href="#">c2d3tC_</a>	Alignment	not modelled	8.1	23	<b>PDB header:</b> lyase, oxidoreductase/transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-ketoacyl-coa thiolase; <b>PDBTitle:</b> fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v
91	<a href="#">d1eiwa_</a>	Alignment	not modelled	8.0	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Hypothetical protein MTH538 <b>Family:</b> Hypothetical protein MTH538
92	<a href="#">c2pjuD_</a>	Alignment	not modelled	8.0	29	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> propionate catabolism operon regulatory protein; <b>PDBTitle:</b> crystal structure of propionate catabolism operon regulatory protein2 prpr
93	<a href="#">c5z79F_</a>	Alignment	not modelled	7.9	21	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> hydroxymethylidihydropterin pyrophosphokinase- <b>PDBTitle:</b> crystal structure analysis of the hppk-dhps in complex with substrates
94	<a href="#">c5ixmH_</a>	Alignment	not modelled	7.9	8	<b>PDB header:</b> transport protein <b>Chain:</b> H: <b>PDB Molecule:</b> lps-assembly lipoprotein lpte; <b>PDBTitle:</b> the lps transporter lptde from yersinia pestis, core complex
95	<a href="#">c2vu2D_</a>	Alignment	not modelled	7.9	21	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyl-coa acetyltransferase; <b>PDBTitle:</b> biosynthetic thiolase from z. ramigera. complex with s-pantetheine-11-2 pivalate.
96	<a href="#">d1tqyb2</a>	Alignment	not modelled	7.8	26	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
97	<a href="#">c6et9D_</a>	Alignment	not modelled	7.7	25	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyl-coa acetyltransferase thiolase; <b>PDBTitle:</b> structure of the acetoacetyl-coa-thiolase/hmg-coa-synthase complex2 from methanothermococcus thermolithotrophicus at 2.75 a
98	<a href="#">c1p6gE_</a>	Alignment	not modelled	7.5	18	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 30s ribosomal protein s5; <b>PDBTitle:</b> real space refined coordinates of the 30s subunit fitted into the low2 resolution cryo-em map of the ef-g.gtp state of e. coli 70s ribosome
99	<a href="#">c5svhB_</a>	Alignment	not modelled	7.5	43	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> mll/c-myb chimera; <b>PDBTitle:</b> crystal structure of the kix domain of cbp in complex with a mll/c-myb2 chimera