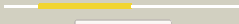

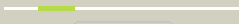
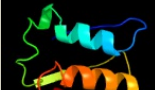



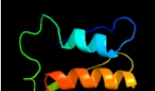
















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0628c_(- )_718764_719915
Date	Fri Jul 26 01:50:19 BST 2019
Unique Job ID	34c496d88c402ed7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1zfjA_</a>	 Alignment		79.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine monophosphate dehydrogenase; <b>PDBTitle:</b> inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
2	<a href="#">d1rq2a2</a>	 Alignment		62.7	16	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> Tubulin C-terminal domain-like <b>Family:</b> Tubulin, C-terminal domain
3	<a href="#">d2vapa2</a>	 Alignment		58.9	21	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> Tubulin C-terminal domain-like <b>Family:</b> Tubulin, C-terminal domain
4	<a href="#">d1w5fa2</a>	 Alignment		55.4	17	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> Tubulin C-terminal domain-like <b>Family:</b> Tubulin, C-terminal domain
5	<a href="#">c2zauB_</a>	 Alignment		54.8	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> selenide, water dikinase; <b>PDBTitle:</b> crystal structure of an n-terminally truncated2 selenophosphate synthetase from aquifex aeolicus
6	<a href="#">d1dbfa_</a>	 Alignment		51.0	13	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> YjgF-like <b>Family:</b> Chorismate mutase
7	<a href="#">d1vk3a2</a>	 Alignment		41.6	13	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
8	<a href="#">d1ufya_</a>	 Alignment		38.3	13	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> YjgF-like <b>Family:</b> Chorismate mutase
9	<a href="#">d1ofua2</a>	 Alignment		38.2	16	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> Tubulin C-terminal domain-like <b>Family:</b> Tubulin, C-terminal domain
10	<a href="#">c4z87B_</a>	 Alignment		36.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> structure of the imp dehydrogenase from ashbya gossypii bound to gdp
11	<a href="#">c1xhoB_</a>	 Alignment		34.7	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> chorismate mutase; <b>PDBTitle:</b> chorismate mutase from clostridium thermocellum cth-682

12	<a href="#">d1xhoa_</a>	Alignment		34.7	8	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> YjgF-like <b>Family:</b> Chorismate mutase
13	<a href="#">c4r3uD_</a>	Alignment		34.1	2	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-hydroxyisobutyryl-coa mutase small subunit; <b>PDBTitle:</b> crystal structure of 2-hydroxyisobutyryl-coa mutase
14	<a href="#">c4ldaF_</a>	Alignment		33.9	6	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> tadz; <b>PDBTitle:</b> crystal structure of a chey-like protein (tadz) from pseudomonas2 aeruginosa pao1 at 2.70 a resolution
15	<a href="#">c2xdqA_</a>	Alignment		32.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit n; <b>PDBTitle:</b> dark operative protochlorophyllide oxidoreductase (chlnc-hlb)2 complex
16	<a href="#">c2ayxA_</a>	Alignment		31.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor kinase protein rcsc; <b>PDBTitle:</b> solution structure of the e.coli rcsc c-terminus (residues2 700-949) containing linker region and phosphoreceiver3 domain
17	<a href="#">c1vliA_</a>	Alignment		27.3	20	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> spore coat polysaccharide biosynthesis protein spse; <b>PDBTitle:</b> crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
18	<a href="#">d2zaua1</a>	Alignment		26.7	18	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
19	<a href="#">c5uicA_</a>	Alignment		26.1	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> two-component response regulator; <b>PDBTitle:</b> structure of the francisella response regulator receiver domain, qseb
20	<a href="#">d1qh8a_</a>	Alignment		25.0	16	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
21	<a href="#">c1ny5A_</a>	Alignment	not modelled	24.9	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
22	<a href="#">c3rqiA_</a>	Alignment	not modelled	24.0	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator protein; <b>PDBTitle:</b> crystal structure of a response regulator protein from burkholderia2 pseudomallei with a phosphorylated aspartic acid, calcium ion and3 citrate
23	<a href="#">d1b74a1</a>	Alignment	not modelled	23.6	8	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/glutamate racemase <b>Family:</b> Aspartate/glutamate racemase
24	<a href="#">d1m1na_</a>	Alignment	not modelled	23.1	11	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
25	<a href="#">d1qe5a_</a>	Alignment	not modelled	22.0	29	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
26	<a href="#">c4k40B_</a>	Alignment	not modelled	22.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gdsl-like lipase/acylhydrolase family protein; <b>PDBTitle:</b> peptidoglycan o-acetylerase in action, 0 min
27	<a href="#">d1g2oa_</a>	Alignment	not modelled	22.0	33	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
28	<a href="#">c2yxba_</a>	Alignment	not modelled	21.9	6	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme b12-dependent mutase; <b>PDBTitle:</b> crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix

29	<a href="#">c6ekhY</a>	Alignment	not modelled	21.3	22	<b>PDB header:</b> metal binding protein <b>Chain:</b> Y: <b>PDB Molecule:</b> chemotaxis protein chey; <b>PDBTitle:</b> crystal structure of activated chey from methanococcus maripaludis
30	<a href="#">c5wlpA</a>	Alignment	not modelled	21.0	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> autophagy-related protein 32; <b>PDBTitle:</b> solution structure of the pseudo-receiver domain of atg32
31	<a href="#">d1ys7a2</a>	Alignment	not modelled	20.8	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
32	<a href="#">d3c9ua1</a>	Alignment	not modelled	20.4	14	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
33	<a href="#">c3bolB</a>	Alignment	not modelled	19.2	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 5-methyltetrahydrofolate s-homocysteine <b>PDBTitle:</b> cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
34	<a href="#">c5ep0A</a>	Alignment	not modelled	18.8	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative repressor protein luxo; <b>PDBTitle:</b> quorum-sensing signal integrator luxo - receiver+catalytic domains
35	<a href="#">c5n6yD</a>	Alignment	not modelled	18.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nitrogenase vanadium-iron protein alpha chain; <b>PDBTitle:</b> azotobacter vinelandii vanadium nitrogenase
36	<a href="#">c3stgA</a>	Alignment	not modelled	18.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase; <b>PDBTitle:</b> crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis
37	<a href="#">c5lwkB</a>	Alignment	not modelled	17.9	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> maer response regulator bound to beryllium trifluoride
38	<a href="#">c4qpiC</a>	Alignment	not modelled	17.9	8	<b>PDB header:</b> signaling protein/dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> cell cycle response regulator ctra; <b>PDBTitle:</b> 2.7 angstrom structure of a phosphotransferase in complex with a2 receiver domain
39	<a href="#">c4rndB</a>	Alignment	not modelled	17.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> v-type proton atpase subunit f; <b>PDBTitle:</b> crystal structure of the subunit df-assembly of the eukaryotic v-2 atpase.
40	<a href="#">c3dzdA</a>	Alignment	not modelled	17.4	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4 in the inactive2 state
41	<a href="#">c6ifhA</a>	Alignment	not modelled	17.3	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sporulation initiation phosphotransferase f; <b>PDBTitle:</b> unphosphorylated spo0f from paenisporosarcina sp. tg-14
42	<a href="#">c3hv2B</a>	Alignment	not modelled	17.2	20	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator/hd domain protein; <b>PDBTitle:</b> crystal structure of signal receiver domain of hd domain-containing2 protein from pseudomonas fluorescens pf-5
43	<a href="#">d1qh8b</a>	Alignment	not modelled	17.1	11	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
44	<a href="#">c3g8rA</a>	Alignment	not modelled	16.8	9	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable spore coat polysaccharide biosynthesis protein e; <b>PDBTitle:</b> crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
45	<a href="#">c3cu5B</a>	Alignment	not modelled	16.2	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> two component transcriptional regulator, arac family; <b>PDBTitle:</b> crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg
46	<a href="#">c1y80A</a>	Alignment	not modelled	15.9	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> predicted cobalamin binding protein; <b>PDBTitle:</b> structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
47	<a href="#">c4q7eA</a>	Alignment	not modelled	15.8	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator of a two component regulatory system; <b>PDBTitle:</b> non-phosphorylated hemr receiver domain from leptospira biflexa
48	<a href="#">c1w59B</a>	Alignment	not modelled	15.8	21	<b>PDB header:</b> cell division <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsz homolog 1; <b>PDBTitle:</b> ftsz dimer, empty (m. jannaschii)
49	<a href="#">d1vlia2</a>	Alignment	not modelled	15.5	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> NeuB-like
50	<a href="#">c5i4cA</a>	Alignment	not modelled	15.4	8	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein rcsb; <b>PDBTitle:</b> crystal structure of non-phosphorylated receiver domain of the stress2 response regulator rcsb from escherichia coli
51	<a href="#">c2rjnA</a>	Alignment	not modelled	15.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver:metal-dependent <b>PDBTitle:</b> crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
52	<a href="#">c2ynmC</a>	Alignment	not modelled	15.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit n; <b>PDBTitle:</b> structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4

						protochlorophyllide a
53	<a href="#">d1mvoa_</a>	Alignment	not modelled	14.9	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
54	<a href="#">c3outC_</a>	Alignment	not modelled	14.5	14	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of glutamate racemase from francisella tularensis2 subsp. tularensis schu s4 in complex with d-glutamate.
55	<a href="#">d1ny5a1</a>	Alignment	not modelled	14.2	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
56	<a href="#">c3sz8D_</a>	Alignment	not modelled	14.2	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase 2; <b>PDBTitle:</b> crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
57	<a href="#">d1m1nb_</a>	Alignment	not modelled	14.0	4	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
58	<a href="#">d1krwa_</a>	Alignment	not modelled	14.0	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
59	<a href="#">c4e7pA_</a>	Alignment	not modelled	14.0	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of receiver domain of putative narI family response2 regulator spr1814 from streptococcus pneumoniae in the presence of3 the phosphoryl analog beryll fluoride
60	<a href="#">d1peya_</a>	Alignment	not modelled	14.0	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
61	<a href="#">c3pdiB_</a>	Alignment	not modelled	13.8	18	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> nitrogenase mofe cofactor biosynthesis protein nifn; <b>PDBTitle:</b> precursor bound nifen
62	<a href="#">d1kgsa2</a>	Alignment	not modelled	13.8	8	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
63	<a href="#">c2vxyA_</a>	Alignment	not modelled	13.5	16	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> the structure of ftsz from bacillus subtilis at 1.7a2 resolution
64	<a href="#">d1jbea_</a>	Alignment	not modelled	13.4	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
65	<a href="#">c3b2nA_</a>	Alignment	not modelled	13.3	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein q99uf4; <b>PDBTitle:</b> crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
66	<a href="#">c1xuzA_</a>	Alignment	not modelled	12.7	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> polysialic acid capsule biosynthesis protein siac; <b>PDBTitle:</b> crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
67	<a href="#">c5m7nA_</a>	Alignment	not modelled	12.7	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen assimilation regulatory protein; <b>PDBTitle:</b> crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystal direct automated mounting and cryo-cooling3 technology
68	<a href="#">c3u0oA_</a>	Alignment	not modelled	12.5	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> selenide, water dikinase; <b>PDBTitle:</b> the crystal structure of selenophosphate synthetase from e. coli
69	<a href="#">c3crnA_</a>	Alignment	not modelled	12.2	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver domain protein, chey-like; <b>PDBTitle:</b> crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
70	<a href="#">d1clia1</a>	Alignment	not modelled	12.1	12	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
71	<a href="#">c4s05B_</a>	Alignment	not modelled	12.0	20	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding transcriptional regulator basr; <b>PDBTitle:</b> crystal structure of klebsiella pneumoniae pmra in complex with pmra2 box dna
72	<a href="#">d2zoda1</a>	Alignment	not modelled	11.9	19	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
73	<a href="#">d2g50a3</a>	Alignment	not modelled	11.8	19	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> Pyruvate kinase, C-terminal domain
74	<a href="#">d1dbwa_</a>	Alignment	not modelled	11.7	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
75	<a href="#">c3x43F_</a>	Alignment	not modelled	11.6	10	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> o-ureido-l-serine synthase; <b>PDBTitle:</b> crystal structure of o-ureido-l-serine synthase
76	<a href="#">d2zdra2</a>	Alignment	not modelled	11.5	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> NeuB-like
77	<a href="#">c3w9sB_</a>	Alignment	not modelled	11.5	18	<b>PDB header:</b> signaling protein/antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> ompr family response regulator in two-component regulatory <b>PDBTitle:</b> crystal structure analysis of the n-terminal receiver

						domain of2 response regulator pmra
78	<a href="#">c1b74A_</a>	Alignment	not modelled	11.4	8	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> glutamate racemase from aquifex pyrophilus
79	<a href="#">c3cz5B_</a>	Alignment	not modelled	11.4	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> two-component response regulator, luxr family; <b>PDBTitle:</b> crystal structure of two-component response regulator, luxr family,2 from aurantimonas sp. si85-9a1
80	<a href="#">c4e6fB_</a>	Alignment	not modelled	11.4	19	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf4468 family protein (bacova_04320) from2 bacteroides ovatus atcc 8483 at 1.49 a resolution
81	<a href="#">c5mg5P_</a>	Alignment	not modelled	11.1	15	<b>PDB header:</b> transferase <b>Chain:</b> P: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa synthase; <b>PDBTitle:</b> a multi-component acyltransferase phlabc from pseudomonas protegens2 soaked with the monoacetylphloroglucinol (magg)
82	<a href="#">d2e7ya1</a>	Alignment	not modelled	11.1	4	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> RNase Z-like
83	<a href="#">c5ijwA_</a>	Alignment	not modelled	11.1	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> glutamate racemase (muri) from mycobacterium smegmatis with bound d-2 glutamate, 1.8 angstrom resolution, x-ray diffraction
84	<a href="#">c3jteA_</a>	Alignment	not modelled	10.8	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of response regulator receiver domain protein from2 clostridium thermocellum
85	<a href="#">d1pkla3</a>	Alignment	not modelled	10.6	12	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> Pyruvate kinase, C-terminal domain
86	<a href="#">d1xpmA1</a>	Alignment	not modelled	10.6	13	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
87	<a href="#">c1w5fA_</a>	Alignment	not modelled	10.5	17	<b>PDB header:</b> cell division <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> ftsz, t7 mutated, domain swapped (t. maritima)
88	<a href="#">c2xdqB_</a>	Alignment	not modelled	10.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit b; <b>PDBTitle:</b> dark operative protochlorophyllide oxidoreductase (chl-chlb)2 complex
89	<a href="#">c3aerC_</a>	Alignment	not modelled	10.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit n; <b>PDBTitle:</b> structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
90	<a href="#">c2yihA_</a>	Alignment	not modelled	10.3	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cel44c; <b>PDBTitle:</b> structure of a paenibacillus polymyxa xyloglucanase from gh2 family 44 with xyloglucan
91	<a href="#">d1liua3</a>	Alignment	not modelled	10.2	17	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> Pyruvate kinase, C-terminal domain
92	<a href="#">c6dzkY_</a>	Alignment	not modelled	10.2	21	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> ribosome hibernation promoting factor; <b>PDBTitle:</b> cryo-em structure of mycobacterium smegmatis c(minus) 30s ribosomal2 subunit with mpy
93	<a href="#">c6grgD_</a>	Alignment	not modelled	9.8	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> microcin b17-processing protein mcbd; <b>PDBTitle:</b> e. coli microcin synthetase mcbcd complex with promccb17, adp and2 phosphate bound
94	<a href="#">c1ys7B_</a>	Alignment	not modelled	9.5	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein prra; <b>PDBTitle:</b> crystal structure of the response regulator protein prra complexed2 with mg2+
95	<a href="#">d2uube2</a>	Alignment	not modelled	9.4	37	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Ribosomal S5 protein, N-terminal domain
96	<a href="#">c4fylB_</a>	Alignment	not modelled	9.4	8	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> ribosome hibernation protein yhbh; <b>PDBTitle:</b> high-resolution x-ray structure of hpf from vibrio cholerae
97	<a href="#">d1yb2a1</a>	Alignment	not modelled	9.1	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like
98	<a href="#">c1yb2A_</a>	Alignment	not modelled	9.1	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ta0852; <b>PDBTitle:</b> structure of a putative methyltransferase from thermoplasma2 acidophilum.
99	<a href="#">c5ohxB_</a>	Alignment	not modelled	9.0	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cystathionine beta-synthase; <b>PDBTitle:</b> structure of active cystathionine b-synthase from apis mellifera