Phyre2

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Description	P33349
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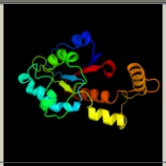
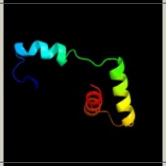
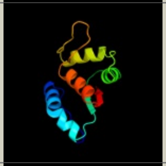
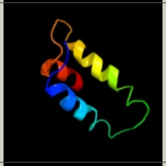
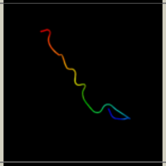
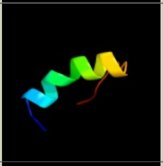
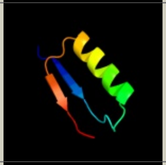
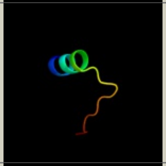
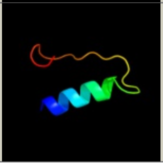
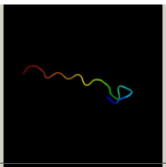
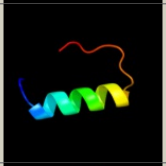
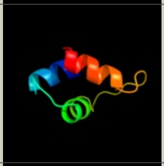
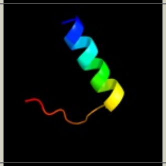
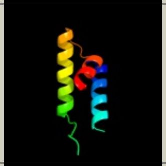
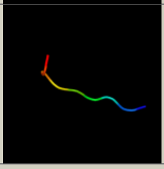
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2g5gx1	Alignment		97.6	12	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**ChaN-like
2	c3ol4B_	Alignment		77.8	10	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
3	c2qgmA_	Alignment		71.4	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**succinoglycan biosynthesis protein; **PDBTitle:** crystal structure of succinoglycan biosynthesis protein at2 the resolution 1.7 a. northeast structural genomics3 consortium target bcr136.
4	d2qgma1	Alignment		71.4	17	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**EreA-like
5	d2ebfx2	Alignment		56.7	11	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**PMT domain-like
6	c3f9vA_	Alignment		54.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**minichromosome maintenance protein mcm; **PDBTitle:** crystal structure of a near full-length archaeal mcm: functional2 insights for an aaa+ hexameric helicase
7	c1txkA_	Alignment		53.8	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glucans biosynthesis protein g; **PDBTitle:** crystal structure of escherichia coli opgg
8	c2ei9A_	Alignment		51.2	17	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**non-ltr retrotransposon r1bmks orf2 protein; **PDBTitle:** crystal structure of r1bm endonuclease domain
9	c3qfnA_	Alignment		50.9	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
10	d1hjra_	Alignment		48.6	29	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**RuvC resolvase
11	c2radB_	Alignment		47.5	14	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**succinoglycan biosynthesis protein; **PDBTitle:** crystal structure of the succinoglycan biosynthesis2 protein. northeast structural genomics consortium target3 bcr135

12	d1txka1	Alignment		46.4	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
13	d1ffva1	Alignment		43.8	14	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
14	d1wdua_	Alignment		38.1	8	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
15	d1v97a1	Alignment		35.7	23	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
16	d1n62a1	Alignment		34.7	14	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
17	d1kcfa2	Alignment		33.9	26	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Mitochondrial resolvase ydc2 catalytic domain
18	d1t3qa1	Alignment		32.8	21	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
19	c3f8tA_	Alignment		29.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted atpase involved in replication control, **PDBTitle:** crystal structure analysis of a full-length mcm homolog2 from methanopyrus kandleri
20	c3czcA_	Alignment		29.3	44	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
21	d1vkra_	Alignment	not modelled	28.7	20	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
22	c1vkrA_	Alignment	not modelled	28.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannitol-specific pts system enzyme iiabc components; **PDBTitle:** structure of iib domain of the mannitol-specific permease enzyme ii
23	c3b4sA_	Alignment	not modelled	28.5	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein luxt; **PDBTitle:** crystal structure of a luxt domain from vibrio2 parahaemolyticus rimd 2210633
24	d1zxia1	Alignment	not modelled	28.0	14	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
25	c1t3qD_	Alignment	not modelled	27.9	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**quinoline 2-oxidoreductase small subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
26	d1rm6c1	Alignment	not modelled	26.6	23	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
27	c1n60D_	Alignment	not modelled	26.2	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**carbon monoxide dehydrogenase small chain; **PDBTitle:** crystal structure of the cu,mo-co dehydrogenase (codh); cyanide-2 inactivated form
28	d1g8pa	Alignment	not modelled	25.6	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate

28	d1g8pa_	Alignment	not modelled	23.6	15	hydrolases **Family:**Extended AAA-ATPase domain
29	d5easa1	Alignment	not modelled	23.7	42	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Terpenoid cyclase N-terminal domain
30	c2kuyA_	Alignment	not modelled	23.4	42	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**prebacteriocin glycocin f; **PDBTitle:** structure of glycocin f
31	d3b55a1	Alignment	not modelled	23.2	10	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**EreA-like
32	c3eubJ_	Alignment	not modelled	22.4	23	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of desulfo-xanthine oxidase with xanthine
33	c1tvmA_	Alignment	not modelled	22.0	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, galactitol-specific iib component; **PDBTitle:** nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system
34	d1n1ba1	Alignment	not modelled	21.9	42	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Terpenoid cyclase N-terminal domain
35	c3hrdH_	Alignment	not modelled	20.1	18	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**nicotinate dehydrogenase small fes subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
36	c1ffuA_	Alignment	not modelled	19.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cuts, iron-sulfur protein of carbon monoxide **PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
37	c3g5rA_	Alignment	not modelled	19.6	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylenetetrahydrofolate--trna-(uracil-5-)- **PDBTitle:** crystal structure of thermus thermophilus trmfo in complex with2 tetrahydrofolate
38	c3nbxX_	Alignment	not modelled	19.3	18	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**atpase rava; **PDBTitle:** crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
39	d2yvta1	Alignment	not modelled	18.7	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
40	d1di0a_	Alignment	not modelled	17.8	9	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
41	c2obxH_	Alignment	not modelled	17.7	13	**PDB header:**transferase **Chain:** H: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase 1; **PDBTitle:** lumazine synthase ribh2 from mesorhizobium loti (gene mll7281, swiss-2 prot entry q986n2) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
42	c1rm6F_	Alignment	not modelled	17.7	26	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**4-hydroxybenzoyl-coa reductase gamma subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
43	c1kcfB_	Alignment	not modelled	17.7	31	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical 30.2 kd protein c25g10.02 in **PDBTitle:** crystal structure of the yeast mitochondrial holliday2 junction resolvase, ydc2
44	c3b9jI_	Alignment	not modelled	17.7	23	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**xanthine oxidase; **PDBTitle:** structure of xanthine oxidase with 2-hydroxy-6-methylpurine
45	d1ejba_	Alignment	not modelled	17.4	9	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
46	d1rvv1_	Alignment	not modelled	17.0	9	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
47	d1vqqa1	Alignment	not modelled	16.9	36	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Penicillin binding protein 2a (PBP2A), N-terminal domain
48	d1c41a_	Alignment	not modelled	16.1	11	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
49	c2j63B_	Alignment	not modelled	16.1	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ap-endonuclease; **PDBTitle:** crystal structure of ap endonuclease lmap from leishmania2 major
50	d1m5wa_	Alignment	not modelled	15.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
51	d2q4qa1	Alignment	not modelled	15.9	23	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
52	d1hd7a_	Alignment	not modelled	15.9	4	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
						PDB header:dna binding protein

53	c2yvaB_	Alignment	not modelled	15.8	14	**Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa; **PDBTitle:** crystal structure of escherichia coli diaa
54	c3trjC_	Alignment	not modelled	15.8	13	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** structure of a phosphoheptose isomerase from francisella tularensis
55	c3oqvA_	Alignment	not modelled	15.7	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**albc; **PDBTitle:** albc, a cyclodipeptide synthase from streptomyces noursei
56	c2x7mA_	Alignment	not modelled	15.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from methanopyrus2 kandleri at 1.5 a resolution
57	d1b24a2	Alignment	not modelled	15.6	18	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Group I mobile intron endonuclease
58	c2hjpA_	Alignment	not modelled	14.9	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonopyruvate hydrolase; **PDBTitle:** crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
59	d1qh8b_	Alignment	not modelled	14.9	15	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
60	d1iowa1	Alignment	not modelled	14.8	10	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
61	d2dfaa1	Alignment	not modelled	14.7	17	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
62	d1zq1a2	Alignment	not modelled	14.6	11	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
63	d1q74a_	Alignment	not modelled	14.2	20	**Fold:**LmbE-like **Superfamily:**LmbE-like **Family:**LmbE-like
64	c3g4dB_	Alignment	not modelled	14.2	33	**PDB header:**lyase **Chain:** B: **PDB Molecule:**(+)-delta-cadinene synthase isozyme xc1; **PDBTitle:** crystal structure of (+)-delta-cadinene synthase from gossypium2 arboreum and evolutionary divergence of metal binding motifs for3 catalysis
65	c2j5cB_	Alignment	not modelled	14.1	33	**PDB header:**lyase **Chain:** B: **PDB Molecule:**1,8-cineole synthase; **PDBTitle:** rational conversion of substrate and product specificity2 in a monoterpene synthase. structural insights into the3 molecular basis of rapid evolution.
66	d1hc7a1	Alignment	not modelled	13.9	9	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
67	c3g6sA_	Alignment	not modelled	13.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative endonuclease/exonuclease/phosphatase **PDBTitle:** crystal structure of the2 endonuclease/exonuclease/phosphatase (bvu_0621) from3 bacteroides vulgatus. northeast structural genomics4 consortium target bvr56d
68	c2xhzC_	Alignment	not modelled	13.7	12	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**arabinose 5-phosphate isomerase; **PDBTitle:** probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
69	c3mk3L_	Alignment	not modelled	13.7	6	**PDB header:**transferase **Chain:** L: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase; **PDBTitle:** crystal structure of lumazine synthase from salmonella typhimurium lt2
70	d1uana_	Alignment	not modelled	13.6	26	**Fold:**LmbE-like **Superfamily:**LmbE-like **Family:**LmbE-like
71	d1vyba_	Alignment	not modelled	13.6	32	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
72	c2x9qA_	Alignment	not modelled	13.5	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cyclodipeptide synthetase; **PDBTitle:** structure of the mycobacterium tuberculosis protein, rv2275,2 demonstrates that cyclodipeptide synthetases are related3 to type i trna-synthetases.
73	d1wsaa_	Alignment	not modelled	13.2	40	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
74	d1kz1a_	Alignment	not modelled	13.1	10	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
75	d1nj8a1	Alignment	not modelled	13.0	10	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
76	c1n20A_	Alignment	not modelled	13.0	42	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**(+)-bornyl diphosphate synthase; **PDBTitle:** (+)-bornyl diphosphate synthase: complex with mg and 3-aza-2 2,3-dihydrogeranyl diphosphate
77	d1nqua_	Alignment	not modelled	13.0	6	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase

78	d1iwpb_	Alignment	not modelled	12.8	17	**Fold:**Anticodon-binding domain-like **Superfamily:**B12-dependent dehydatase associated subunit **Family:**Diol dehydratase, beta subunit
79	d2cula1	Alignment	not modelled	12.7	11	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GidA-like
80	d2d6fa2	Alignment	not modelled	12.5	13	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
81	d1uh5a_	Alignment	not modelled	12.3	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
82	c1hx9A_	Alignment	not modelled	12.3	42	**PDB header:**lyase **Chain:** A: **PDB Molecule:**5-epi-aristolochene synthase; **PDBTitle:** crystal structure of teas w273s form 1
83	c2ongA_	Alignment	not modelled	12.0	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4s-limonene synthase; **PDBTitle:** crystal structure of of limonene synthase with 2-2 fluorogeranyl diphosphate (fgpp).
84	d1nj1a1	Alignment	not modelled	12.0	12	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
85	c3r89A_	Alignment	not modelled	11.9	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**orotidine 5'-phosphate decarboxylase; **PDBTitle:** crystal structure of orotidine 5-phosphate decarboxylase from2 anaerococcus prevotii dsm 20548
86	c2jc5A_	Alignment	not modelled	11.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exodeoxyribonuclease; **PDBTitle:** apurinic apyrimidinic (ap) endonuclease (nape) from2 neisseria meningitidis
87	d2pd4a1	Alignment	not modelled	11.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
88	d2gc6a1	Alignment	not modelled	11.7	6	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**Folylpolyglutamate synthetase, C-terminal domain
89	c3lo3E_	Alignment	not modelled	11.4	35	**PDB header:**structure genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved functionally unknown2 protein from colwellia psychrerythraea 34h.
90	c2bibA_	Alignment	not modelled	11.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**teichoic acid phosphorylcholine esterase/ choline binding **PDBTitle:** crystal structure of the complete modular teichioic acid2 phosphorylcholine esterase pce (cbpe) from streptococcus3 pneumoniae
91	c3lx6B_	Alignment	not modelled	11.4	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cytosine-specific methyltransferase; **PDBTitle:** structure of probable cytosine-specific methyltransferase from2 shigella flexneri
92	d3bzka5	Alignment	not modelled	11.3	6	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
93	c2ixdB_	Alignment	not modelled	11.3	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmbe-related protein; **PDBTitle:** crystal structure of the putative deacetylase bc1534 from2 bacilus cereus
94	c1zlpA_	Alignment	not modelled	11.2	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**petal death protein; **PDBTitle:** petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
95	c3tebA_	Alignment	not modelled	11.2	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease/exonuclease/phosphatase; **PDBTitle:** endonuclease/exonuclease/phosphatase family protein from leptotrichia2 buccalis c-1013-b
96	c3iv4A_	Alignment	not modelled	11.2	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** a putative oxidoreductase with a thioredoxin fold
97	c3n0fA_	Alignment	not modelled	11.2	42	**PDB header:**lyase **Chain:** A: **PDB Molecule:**isoprene synthase; **PDBTitle:** crystal structure of isoprene synthase from grey poplar leaves2 (populus x canescens)
98	d1v6ta_	Alignment	not modelled	10.8	17	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
99	d1eexb_	Alignment	not modelled	10.7	11	**Fold:**Anticodon-binding domain-like **Superfamily:**B12-dependent dehydatase associated subunit **Family:**Diol dehydratase, beta subunit