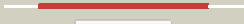



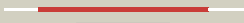














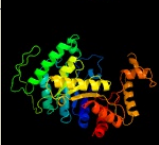






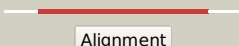

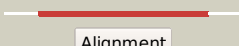

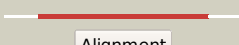

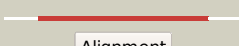







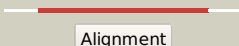


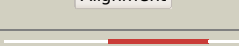
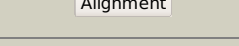
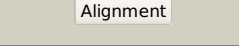

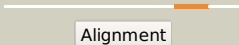


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2951c_(- )_3303113_3304258
Date	Thu Aug 8 16:20:11 BST 2019
Unique Job ID	050f854aeafdfcb9

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5tlcA_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dibenzothiophene desulfurization enzyme a; <b>PDBTitle:</b> crystal structure of bdsa from bacillus subtilis wu-s2b
2	<a href="#">d1ezwa_</a>	 Alignment		100.0	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
3	<a href="#">c1z69D_</a>	 Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> coenzyme f420-dependent n(5),n(10)- <b>PDBTitle:</b> crystal structure of methylenetetrahydromethanopterin2 reductase (mer) in complex with coenzyme f420
4	<a href="#">d1luca_</a>	 Alignment		100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Bacterial luciferase (alkanal monooxygenase)
5	<a href="#">c5w4zA_</a>	 Alignment		100.0	18	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin lyase; <b>PDBTitle:</b> crystal structure of riboflavin lyase (rcae) with modified fmn and2 substrate riboflavin
6	<a href="#">c3raoB_</a>	 Alignment		100.0	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative luciferase-like monooxygenase; <b>PDBTitle:</b> crystal structure of the luciferase-like monooxygenase from bacillus2 cereus atcc 10987.
7	<a href="#">c3sdoB_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitrotriacetate monooxygenase; <b>PDBTitle:</b> structure of a nitrotriacetate monooxygenase from burkholderia2 pseudomallei
8	<a href="#">d1f07a_</a>	 Alignment		100.0	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
9	<a href="#">d1rhca_</a>	 Alignment		100.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
10	<a href="#">d1tvla_</a>	 Alignment		100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Ssud-like monooxygenases
11	<a href="#">c1tvIA_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein ytnj; <b>PDBTitle:</b> structure of ytnj from bacillus subtilis

12	<a href="#">c5dqpA_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> edta monoxygenase; <b>PDBTitle:</b> edta monoxygenase (emoa) from chelativorans sp. bnc1
13	<a href="#">c2wgkA_</a>	 Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3,6-diketocamphane 1,6 monoxygenase; <b>PDBTitle:</b> type ii baeyer-villiger monoxygenase oxygenating2 constituent of 3,6-diketocamphane 1,6 monoxygenase from3 pseudomonas putida
14	<a href="#">d1lucb_</a>	 Alignment		100.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Bacterial luciferase (alkanal monoxygenase)
15	<a href="#">c3b9nB_</a>	 Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alkane monoxygenase; <b>PDBTitle:</b> crystal structure of long-chain alkane monoxygenase (lada)
16	<a href="#">c6ak1B_</a>	 Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dimethyl-sulfide monoxygenase; <b>PDBTitle:</b> crystal structure of dmoa from hyphomicrobium sulfonivorans
17	<a href="#">c2i7qA_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monoxygenase; <b>PDBTitle:</b> crystal structure of monoxygenase from agrobacterium tumefaciens
18	<a href="#">d1nqka_</a>	 Alignment		100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Ssud-like monoxygenases
19	<a href="#">c3c8nB_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable f420-dependent glucose-6-phosphate dehydrogenase <b>PDBTitle:</b> crystal structure of apo-fgd1 from mycobacterium tuberculosis
20	<a href="#">c6friD_</a>	 Alignment		100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> alkanal monoxygenase beta chain; <b>PDBTitle:</b> structure of luxb from photobacterium leiognathi
21	<a href="#">c5wanA_</a>	 Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrimidine monoxygenase ruta; <b>PDBTitle:</b> crystal structure of a flavoenzyme ruta in the pyrimidine catabolic2 pathway
22	<a href="#">c2b81D_</a>	 Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> luciferase-like monoxygenase; <b>PDBTitle:</b> crystal structure of the luciferase-like monoxygenase from bacillus2 cereus
23	<a href="#">d1nfpa_</a>	 Alignment	not modelled	100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Non-fluorescent flavoprotein (luxF, FP390)
24	<a href="#">d1fvpa_</a>	 Alignment	not modelled	99.3	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Non-fluorescent flavoprotein (luxF, FP390)
25	<a href="#">d1r3sa_</a>	 Alignment	not modelled	83.4	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MetE-like <b>Family:</b> Uroporphyrinogen decarboxylase, UROD
26	<a href="#">c1jpkA_</a>	 Alignment	not modelled	83.3	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase
27	<a href="#">c4exqA_</a>	 Alignment	not modelled	82.2	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> crystal structure of uroporphyrinogen decarboxylase (upd) from2 burkholderia thailandensis e264
28	<a href="#">c2ze3A_</a>	 Alignment	not modelled	81.5	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dfa0005; <b>PDBTitle:</b> crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus

29	<a href="#">c3fa4D</a>	Alignment	not modelled	79.8	19	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> 2,3-dimethylmalate lyase; <b>PDBTitle:</b> crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
30	<a href="#">c3lyeA</a>	Alignment	not modelled	79.3	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oxaloacetate acetyl hydrolase; <b>PDBTitle:</b> crystal structure of oxaloacetate acetylhydrolase
31	<a href="#">c1zlpA</a>	Alignment	not modelled	75.8	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> petal death protein; <b>PDBTitle:</b> petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
32	<a href="#">c3qy6A</a>	Alignment	not modelled	75.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase ywqe; <b>PDBTitle:</b> crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases
33	<a href="#">d1s2wa</a>	Alignment	not modelled	74.2	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like
34	<a href="#">c1bf2A</a>	Alignment	not modelled	73.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isoamylase; <b>PDBTitle:</b> structure of pseudomonas isoamylase
35	<a href="#">c3b8fF</a>	Alignment	not modelled	73.2	19	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> pa4872 oxaloacetate decarboxylase; <b>PDBTitle:</b> crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+
36	<a href="#">c2hjpA</a>	Alignment	not modelled	69.9	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphonopyruvate hydrolase; <b>PDBTitle:</b> crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
37	<a href="#">c3eooL</a>	Alignment	not modelled	69.6	17	<b>PDB header:</b> lyase <b>Chain:</b> L: <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
38	<a href="#">c4zr8B</a>	Alignment	not modelled	68.5	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> structure of uroporphyrinogen decarboxylase from acetobacter2 baumannii
39	<a href="#">d1m53a2</a>	Alignment	not modelled	67.6	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
40	<a href="#">c5gquA</a>	Alignment	not modelled	67.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-alpha-glucan branching enzyme glgb; <b>PDBTitle:</b> crystal structure of branching enzyme from cyanothecae sp. atcc 51142
41	<a href="#">c1ehaA</a>	Alignment	not modelled	67.4	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyltrehalose trehalohydrolase; <b>PDBTitle:</b> crystal structure of glycosyltrehalose trehalohydrolase from2 sulfolobus solfataricus
42	<a href="#">d1ua7a2</a>	Alignment	not modelled	67.2	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
43	<a href="#">c3faxA</a>	Alignment	not modelled	67.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> reticulocyte binding protein; <b>PDBTitle:</b> the crystal structure of gbs pullulanase sap in complex with2 maltotetraose
44	<a href="#">d1ujqa</a>	Alignment	not modelled	66.3	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like
45	<a href="#">c2by0A</a>	Alignment	not modelled	66.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> maltooligosyltrehalose trehalohydrolase; <b>PDBTitle:</b> is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
46	<a href="#">c6aavA</a>	Alignment	not modelled	65.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosyltransferase; <b>PDBTitle:</b> crystal structure of alpha-glucosyl transfer enzyme, xgta at 1.722 angstrom resolution
47	<a href="#">d1uoka2</a>	Alignment	not modelled	65.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
48	<a href="#">c2wjeA</a>	Alignment	not modelled	65.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase cpsb; <b>PDBTitle:</b> crystal structure of the tyrosine phosphatase cps4b from2 streptococcus pneumoniae tigr4.
49	<a href="#">c2qiWA</a>	Alignment	not modelled	65.3	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pep phosphonmutase; <b>PDBTitle:</b> crystal structure of a putative phosphoenolpyruvate phosphonmutase2 (ncg1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
50	<a href="#">d1lwHa2</a>	Alignment	not modelled	64.8	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
51	<a href="#">d1muma</a>	Alignment	not modelled	64.6	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like
52	<a href="#">c3k1dA</a>	Alignment	not modelled	64.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-alpha-glucan-branching enzyme; <b>PDBTitle:</b> crystal structure of glycogen branching enzyme synonym: 1,4-alpha-d-2 glucan:1,4-alpha-d-glucan 6-glucosyl-transferase from mycobacterium3 tuberculosis h37rv
53	<a href="#">c3m07A</a>	Alignment	not modelled	64.1	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative alpha amylase; <b>PDBTitle:</b> 1.4 angstrom resolution crystal structure of putative alpha amylase2 from salmonella typhimurium.
54	<a href="#">c2va0A</a>	Alignment	not modelled	63.4	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative alkaline amylopullulanase;

54	<a href="#">c3yavA</a>	Alignment	not modelled	63.4	43	<b>PDBTitle:</b> catalytic module of the multi-modular glycogen-degrading pneumococcal2 virulence factor spua <b>PDB header:</b> hydrolase
55	<a href="#">c3wy3A</a>	Alignment	not modelled	62.7	8	<b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> crystal structure of alpha-glucosidase mutant d202n in complex with2 glucose and glycerol
56	<a href="#">c2ze0A</a>	Alignment	not modelled	62.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> alpha-glucosidase gsj
57	<a href="#">d1jpdx1</a>	Alignment	not modelled	61.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
58	<a href="#">c5m99A</a>	Alignment	not modelled	61.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> functional characterization and crystal structure of thermostable2 amylase from thermotoga petrophila, reveals high thermostability and3 an archaic form of dimerization
59	<a href="#">c3ih1A</a>	Alignment	not modelled	61.9	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
60	<a href="#">c4r33A</a>	Alignment	not modelled	61.6	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> nosl; <b>PDBTitle:</b> x-ray structure of the tryptophan lyase nosl with tryptophan and s-2 adenosyl-l-homocysteine bound
61	<a href="#">d1g5aa2</a>	Alignment	not modelled	61.5	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
62	<a href="#">c4lsbA</a>	Alignment	not modelled	60.4	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lyase/mutase; <b>PDBTitle:</b> crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315
63	<a href="#">c1jgiA</a>	Alignment	not modelled	59.9	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> amylsucrase; <b>PDBTitle:</b> crystal structure of the active site mutant glu328gln of amylsucrase2 from neisseria polysaccharea in complex with the natural substrate3 sucrose
64	<a href="#">c4wxcC</a>	Alignment	not modelled	59.9	17	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> biotin and thiamin synthesis associated; <b>PDBTitle:</b> crystal structure of hydrg: a maturase of the [fefe]-hydrogenase
65	<a href="#">c1m7xC</a>	Alignment	not modelled	58.8	23	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 1,4-alpha-glucan branching enzyme; <b>PDBTitle:</b> the x-ray crystallographic structure of branching enzyme
66	<a href="#">c5brqA</a>	Alignment	not modelled	58.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 13; <b>PDBTitle:</b> crystal structure of bacillus licheniformis trehalose-6-phosphate2 hydrolase (treA)
67	<a href="#">c4j7rA</a>	Alignment	not modelled	58.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isoamylase; <b>PDBTitle:</b> crystal structure of chlamydomonas reinhardtii isoamylase 1 (isa1)
68	<a href="#">c3amlA</a>	Alignment	not modelled	58.4	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> os06g0726400 protein; <b>PDBTitle:</b> structure of the starch branching enzyme i (bei) from oryza sativa l
69	<a href="#">c1lwhA</a>	Alignment	not modelled	58.4	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-alpha-glucanotransferase; <b>PDBTitle:</b> crystal structure of t. maritima 4-alpha-glucanotransferase
70	<a href="#">d1wzla3</a>	Alignment	not modelled	58.3	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
71	<a href="#">d2guya2</a>	Alignment	not modelled	58.3	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
72	<a href="#">c2aaaA</a>	Alignment	not modelled	58.0	15	<b>PDB header:</b> glycosidase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> calcium binding in alpha-amylases: an x-ray diffraction study at 2.12 angstroms resolution of two enzymes from aspergillus
73	<a href="#">d1ea9c3</a>	Alignment	not modelled	58.0	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
74	<a href="#">c4mb1A</a>	Alignment	not modelled	57.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oligo-1,6-glucosidase 1; <b>PDBTitle:</b> the structure of mall mutant enzyme g202p from bacillus subtilus
75	<a href="#">d1ht6a2</a>	Alignment	not modelled	57.2	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
76	<a href="#">d1r30a</a>	Alignment	not modelled	57.1	6	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Radical SAM enzymes <b>Family:</b> Biotin synthase
77	<a href="#">c1r30A</a>	Alignment	not modelled	57.1	6	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> biotin synthase; <b>PDBTitle:</b> the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme
78	<a href="#">c3zoaB</a>	Alignment	not modelled	57.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> trehalose synthase/amylase tres; <b>PDBTitle:</b> the structure of trehalose synthase (tres) of mycobacterium2 smegmatis in complex with acarbose
79	<a href="#">c5x7uA</a>	Alignment	not modelled	57.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose synthase; <b>PDBTitle:</b> trehalose synthase from thermobaculum terrenum
						<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> neopullulanase;

80	<a href="#">c1jibA_</a>	Alignment	not modelled	56.8	19	<b>PDBTitle:</b> complex of alpha-amylase ii (tva ii) from thermoactinomyces2 vulgaris r-47 with maltotetraose based on a crystal soaked3 with maltohexaose.
81	<a href="#">c4mg4G_</a>	Alignment	not modelled	56.4	14	<b>PDB header:</b> unknown function <b>Chain:</b> G; <b>PDB Molecule:</b> phosphonomutase; <b>PDBTitle:</b> crystal structure of a putative phosphonomutase from burkholderia2 cenocepacia j2315
82	<a href="#">d1gvia3</a>	Alignment	not modelled	56.3	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
83	<a href="#">c5zxB_</a>	Alignment	not modelled	56.1	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> cyclic maltosyl-maltose hydrolase; <b>PDBTitle:</b> cyclic alpha-maltosyl-(1-->6)-maltose hydrolase from arthrobacter2 globiformis, ligand-free form
84	<a href="#">c2wcsA_</a>	Alignment	not modelled	55.7	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> alpha amylase, catalytic region; <b>PDBTitle:</b> crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
85	<a href="#">c1uokA_</a>	Alignment	not modelled	55.6	15	<b>PDB header:</b> glucosidase <b>Chain:</b> A; <b>PDB Molecule:</b> oligo-1,6-glucosidase; <b>PDBTitle:</b> crystal structure of b. cereus oligo-1,6-glucosidase
86	<a href="#">c3czkA_</a>	Alignment	not modelled	55.5	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> sucrose hydrolase; <b>PDBTitle:</b> crystal structure analysis of sucrose hydrolase(suh) e322q-sucrose2 complex
87	<a href="#">c2ejaB_</a>	Alignment	not modelled	55.5	11	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
88	<a href="#">d2aaaa2</a>	Alignment	not modelled	55.3	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
89	<a href="#">d2gja2</a>	Alignment	not modelled	55.2	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
90	<a href="#">c2ya1A_</a>	Alignment	not modelled	55.1	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative alkaline amylopullulanase; <b>PDBTitle:</b> product complex of a multi-modular glycogen-degrading pneumococcal2 virulence factor spua
91	<a href="#">c4aefB_</a>	Alignment	not modelled	54.6	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> neopullulanase (alpha-amylase ii); <b>PDBTitle:</b> the crystal structure of thermostable amylase from the pyrococcus
92	<a href="#">c4tvuA_</a>	Alignment	not modelled	54.3	12	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> trehalose synthase; <b>PDBTitle:</b> crystal structure of trehalose synthase from deinococcus radiodurans2 reveals a closed conformation for catalysis of the intramolecular3 isomerization
93	<a href="#">c6gyaA_</a>	Alignment	not modelled	54.2	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> a-amylase; <b>PDBTitle:</b> amylase in complex with branched ligand
94	<a href="#">c4gkIA_</a>	Alignment	not modelled	53.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> crystal structure of a noncanonic maltogenic alpha-amylase amyb from2 thermotoga neapolitana
95	<a href="#">d1qhoa4</a>	Alignment	not modelled	53.5	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
96	<a href="#">c5ykbB_</a>	Alignment	not modelled	53.4	12	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> trehalose synthase; <b>PDBTitle:</b> the n253f mutant structure of trehalose synthase from deinococcus2 radiodurans reveals an open active-site conformation
97	<a href="#">c2infB_</a>	Alignment	not modelled	53.0	15	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> crystal structure of uroporphyrinogen decarboxylase from bacillus2 subtilis
98	<a href="#">d1avaa2</a>	Alignment	not modelled	52.8	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
99	<a href="#">c2z1kA_</a>	Alignment	not modelled	52.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> (neo)pullulanase; <b>PDBTitle:</b> crystal structure of ttha1563 from thermus thermophilus hb8
100	<a href="#">c1m53A_</a>	Alignment	not modelled	52.3	11	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> isomaltulose synthase; <b>PDBTitle:</b> crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
101	<a href="#">c4aieA_</a>	Alignment	not modelled	50.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> glucan 1,6-alpha-glucosidase; <b>PDBTitle:</b> structure of glucan-1,6-alpha-glucosidase from lactobacillus2 acidophilus ncfm
102	<a href="#">c1bagA_</a>	Alignment	not modelled	50.5	8	<b>PDB header:</b> alpha-amylase <b>Chain:</b> A; <b>PDB Molecule:</b> alpha-1,4-glucan-4-glucanohydrolase; <b>PDBTitle:</b> alpha-amylase from bacillus subtilis complexed with2 maltopentaose
103	<a href="#">d1bf2a3</a>	Alignment	not modelled	50.2	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
104	<a href="#">c4e2oA_</a>	Alignment	not modelled	50.1	15	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> crystal structure of alpha-amylase from geobacillus thermoleovorans,2 gta, complexed with acarbose
105	<a href="#">d1j0ha3</a>	Alignment	not modelled	49.9	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
						<b>Fold:</b> TIM beta/alpha-barrel

106	<a href="#">d2bhua3</a>	Alignment	not modelled	49.8	12	<b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
107	<a href="#">d2d69a1</a>	Alignment	not modelled	49.8	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
108	<a href="#">d1j93a_</a>	Alignment	not modelled	49.5	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MetE-like <b>Family:</b> Uroporphyrinogen decarboxylase, UROD
109	<a href="#">c1qhoA_</a>	Alignment	not modelled	49.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
110	<a href="#">c2yb1A_</a>	Alignment	not modelled	49.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
111	<a href="#">c4rtbA_</a>	Alignment	not modelled	48.4	13	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> hydg protein; <b>PDBTitle:</b> x-ray structure of the fefe-hydrogenase maturase hydg from2 carboxydotherrmus hydrogenoformans
112	<a href="#">c3zt5D_</a>	Alignment	not modelled	48.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> putative glucanohydrolase pep1a; <b>PDBTitle:</b> glge isoform 1 from streptomyces coelicolor with maltose2 bound
113	<a href="#">d1ob0a2</a>	Alignment	not modelled	47.7	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
114	<a href="#">c5do8A_</a>	Alignment	not modelled	47.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> lmo0184 protein; <b>PDBTitle:</b> 1.8 angstrom crystal structure of listeria monocytogenes lmo01842 alpha-1,6-glucosidase
115	<a href="#">c2vncB_</a>	Alignment	not modelled	47.2	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> glycogen operon protein glgx; <b>PDBTitle:</b> crystal structure of glycogen debranching enzyme trex from2 sulfolobus solfataricus
116	<a href="#">c2zidA_</a>	Alignment	not modelled	47.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dextran glucosidase; <b>PDBTitle:</b> crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
117	<a href="#">d1eh9a3</a>	Alignment	not modelled	47.0	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
118	<a href="#">c2dh3A_</a>	Alignment	not modelled	46.9	12	<b>PDB header:</b> transport protein, signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> 4f2 cell-surface antigen heavy chain; <b>PDBTitle:</b> crystal structure of human ed-4f2hc
119	<a href="#">c3a47A_</a>	Alignment	not modelled	46.6	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> oligo-1,6-glucosidase; <b>PDBTitle:</b> crystal structure of isomaltase from saccharomyces cerevisiae
120	<a href="#">c4u33F_</a>	Alignment	not modelled	46.0	19	<b>PDB header:</b> transferase <b>Chain:</b> F; <b>PDB Molecule:</b> alpha-1,4-glucan:maltose-1-phosphate maltosyltransferase; <b>PDBTitle:</b> structure of mtb glge bound to maltose