


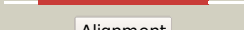













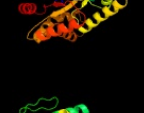






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3093c_(-)_3461757_3462761
Date	Thu Aug 8 16:20:27 BST 2019
Unique Job ID	ea09202e6038df74

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1z69D_</a>	 Alignment		100.0	20	<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
2	<a href="#">d1ezwa_</a>	 Alignment		100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
3	<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
4	<a href="#">d1f07a_</a>	 Alignment		100.0	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
5	<a href="#">c1tvIA_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein ytnj; <b>PDBTitle:</b> structure of ytnj from bacillus subtilis
6	<a href="#">d1tvIA_</a>	 Alignment		100.0	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Ssud-like monooxygenases
7	<a href="#">c3sdoB_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitrilotriacetate monooxygenase; <b>PDBTitle:</b> structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
8	<a href="#">c5w4zA_</a>	 Alignment		100.0	17	<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
9	<a href="#">c3b9nB_</a>	 Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alkane monooxygenase; <b>PDBTitle:</b> crystal structure of long-chain alkane monooxygenase (lada)
10	<a href="#">d1nqka_</a>	 Alignment		100.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Ssud-like monooxygenases
11	<a href="#">c6ak1B_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dimethyl-sulfide monooxygenase; <b>PDBTitle:</b> crystal structure of dmoa from hyphomicrobium sulfonivorans

12	<a href="#">d1luca_</a>	Alignment		100.0	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Bacterial luciferase (alkanal monooxygenase)
13	<a href="#">c5dqpA_</a>	Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> edta monooxygenase; <b>PDBTitle:</b> edta monooxygenase (emoa) from chelativorans sp. bnc1
14	<a href="#">d1rhca_</a>	Alignment		100.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
15	<a href="#">d1lucb_</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)
16	<a href="#">c3c8nB_</a>	Alignment		100.0	15	<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
17	<a href="#">c3raoB_</a>	Alignment		100.0	14	<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.
18	<a href="#">c2wgkA_</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3,6-diketocamphane 1,6 monooxygenase; <b>PDBTitle:</b> type ii baeyer-villiger monooxygenase oxygenating2 constituent of 3,6-diketocamphane 1,6 monooxygenase from3 pseudomonas putida
19	<a href="#">c2i7gA_</a>	Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monooxygenase; <b>PDBTitle:</b> crystal structure of monooxygenase from agrobacterium tumefaciens
20	<a href="#">c5wanA_</a>	Alignment		100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrimidine monooxygenase ruta; <b>PDBTitle:</b> crystal structure of a flavoenzyme ruta in the pyrimidine catabolic2 pathway
21	<a href="#">c6friD_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> alkanal monooxygenase beta chain; <b>PDBTitle:</b> structure of luxb from photobacterium leiognathi
22	<a href="#">c2b81D_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> luciferase-like monooxygenase; <b>PDBTitle:</b> crystal structure of the luciferase-like monooxygenase from bacillus2 cereus
23	<a href="#">d1nfpa_</a>	Alignment	not modelled	99.9	18	<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	99.0	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Non-fluorescent flavoprotein (luxF, FP390)
25	<a href="#">c3qy6A_</a>	Alignment	not modelled	86.6	16	<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
26	<a href="#">d1jpdx1</a>	Alignment	not modelled	85.2	28	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
27	<a href="#">c5tchG_</a>	Alignment	not modelled	83.9	17	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
28	<a href="#">d1jpmal</a>	Alignment	not modelled	78.8	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like

29	<a href="#">c1bf2A_</a>	Alignment	not modelled	76.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isoamylase; <b>PDBTitle:</b> structure of pseudomonas isoamylase
30	<a href="#">c2ekcA_</a>	Alignment	not modelled	75.6	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> structural study of project id aq_1548 from aquifex aeolicus vf5
31	<a href="#">d1m53a2</a>	Alignment	not modelled	73.0	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
32	<a href="#">d1ua7a2</a>	Alignment	not modelled	72.4	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
33	<a href="#">d1uoka2</a>	Alignment	not modelled	72.0	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
34	<a href="#">d1tzza1</a>	Alignment	not modelled	71.5	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
35	<a href="#">c1ehaA_</a>	Alignment	not modelled	70.5	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
36	<a href="#">d1lwha2</a>	Alignment	not modelled	70.4	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
37	<a href="#">c2ze0A_</a>	Alignment	not modelled	68.2	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> alpha-glucosidase gsj
38	<a href="#">c6aavA_</a>	Alignment	not modelled	68.0	23	<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
39	<a href="#">c3m07A_</a>	Alignment	not modelled	68.0	27	<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.
40	<a href="#">c2by0A_</a>	Alignment	not modelled	68.0	23	<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
41	<a href="#">c2ya0A_</a>	Alignment	not modelled	67.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative alkaline amylopullulanase; <b>PDBTitle:</b> catalytic module of the multi-modular glycogen-degrading pneumococcal2 virulence factor spua
42	<a href="#">c4mb1A_</a>	Alignment	not modelled	67.6	27	<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
43	<a href="#">d2fiqa1</a>	Alignment	not modelled	67.5	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> GatZ-like
44	<a href="#">c5m99A_</a>	Alignment	not modelled	66.5	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
45	<a href="#">d1ht6a2</a>	Alignment	not modelled	66.2	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
46	<a href="#">c1jgiA_</a>	Alignment	not modelled	66.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> amylosucrase; <b>PDBTitle:</b> crystal structure of the active site mutant glu328gln of amylosucrase2 from neisseria polysaccharea in complex with the natural substrate3 sucrose
47	<a href="#">c3faxA_</a>	Alignment	not modelled	65.8	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
48	<a href="#">c5brqA_</a>	Alignment	not modelled	65.6	15	<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)
49	<a href="#">d1g5aa2</a>	Alignment	not modelled	65.5	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
50	<a href="#">d2guya2</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
51	<a href="#">c3wy3A_</a>	Alignment	not modelled	64.7	19	<b>PDB header:</b> hydrolase <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
52	<a href="#">c2wjeA_</a>	Alignment	not modelled	64.5	15	<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 steptococcus pneumoniae tigr4.
53	<a href="#">c5zxbB_</a>	Alignment	not modelled	64.5	19	<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
54	<a href="#">d1wzla3</a>	Alignment	not modelled	64.4	23	<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

55	<a href="#">d1ea9c3</a>	Alignment	not modelled	64.4	23	<b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
56	<a href="#">c1lwhA_</a>	Alignment	not modelled	64.3	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
57	<a href="#">c4u33F_</a>	Alignment	not modelled	64.1	35	<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
58	<a href="#">c3qfeB_</a>	Alignment	not modelled	63.7	7	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative dihydrodipicolinate synthase family protein; <b>PDBTitle:</b> crystal structures of a putative dihydrodipicolinate synthase family2 protein from coccidioides immitis
59	<a href="#">c3ucqA_</a>	Alignment	not modelled	63.7	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> amylsucrase; <b>PDBTitle:</b> crystal structure of amylsucrase from deinococcus geothermalis
60	<a href="#">c3zoaB_</a>	Alignment	not modelled	63.5	23	<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
61	<a href="#">c3d0cB_</a>	Alignment	not modelled	63.2	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
62	<a href="#">c2aaaA_</a>	Alignment	not modelled	63.1	19	<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
63	<a href="#">c1uokA_</a>	Alignment	not modelled	62.6	19	<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
64	<a href="#">c4tvuA_</a>	Alignment	not modelled	62.6	25	<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
65	<a href="#">d1ob0a2</a>	Alignment	not modelled	62.1	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
66	<a href="#">c3czkA_</a>	Alignment	not modelled	62.1	23	<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
67	<a href="#">d1gvia3</a>	Alignment	not modelled	62.0	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
68	<a href="#">c4j7rA_</a>	Alignment	not modelled	62.0	19	<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)
69	<a href="#">d2gjpa2</a>	Alignment	not modelled	61.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
70	<a href="#">d2aaaa2</a>	Alignment	not modelled	61.5	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
71	<a href="#">c1m53A_</a>	Alignment	not modelled	61.3	19	<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
72	<a href="#">d1j0ha3</a>	Alignment	not modelled	60.9	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
73	<a href="#">c1qhoA_</a>	Alignment	not modelled	60.7	19	<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
74	<a href="#">d1bf2a3</a>	Alignment	not modelled	60.5	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
75	<a href="#">d1qhoa4</a>	Alignment	not modelled	60.4	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
76	<a href="#">c5x7uA_</a>	Alignment	not modelled	60.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose synthase; <b>PDBTitle:</b> trehalose synthase from thermobaculum terrenum
77	<a href="#">c3zt5D_</a>	Alignment	not modelled	60.1	38	<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
78	<a href="#">c2z1kA_</a>	Alignment	not modelled	59.9	27	<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
79	<a href="#">c5ykbB_</a>	Alignment	not modelled	59.7	25	<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
80	<a href="#">d2bhua3</a>	Alignment	not modelled	59.4	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
						<b>PDB header:</b> hydrolase

81	<a href="#">c4aefB</a>	Alignment	not modelled	59.4	12	<b>Chain:</b> B: <b>PDB Molecule:</b> neopullulanase (alpha-amylase ii); <b>PDBTitle:</b> the crystal structure of thermostable amylase from the pyrococcus
82	<a href="#">c1jibA</a>	Alignment	not modelled	59.3	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> neopullulanase; <b>PDBTitle:</b> complex of alpha-amylase ii (tva ii) from thermoactinomyces2 vulgaris r-47 with maltotetraose based on a crystal soaked3 with maltohexaose.
83	<a href="#">d1avaa2</a>	Alignment	not modelled	59.3	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
84	<a href="#">c4gkIA</a>	Alignment	not modelled	59.2	15	<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
85	<a href="#">d1eh9a3</a>	Alignment	not modelled	58.7	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
86	<a href="#">c3k8kB</a>	Alignment	not modelled	58.6	17	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-amylase, susg; <b>PDBTitle:</b> crystal structure of susg
87	<a href="#">d1o5ka</a>	Alignment	not modelled	58.5	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
88	<a href="#">c2wcsA</a>	Alignment	not modelled	58.4	15	<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)
89	<a href="#">c3a47A</a>	Alignment	not modelled	57.9	26	<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
90	<a href="#">c5do8A</a>	Alignment	not modelled	57.7	19	<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
91	<a href="#">d1e43a2</a>	Alignment	not modelled	57.5	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
92	<a href="#">c2ya1A</a>	Alignment	not modelled	57.3	19	<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
93	<a href="#">c1m7xC</a>	Alignment	not modelled	57.3	19	<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
94	<a href="#">c4aieA</a>	Alignment	not modelled	57.2	23	<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
95	<a href="#">c1bagA</a>	Alignment	not modelled	56.8	19	<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
96	<a href="#">c4e2oA</a>	Alignment	not modelled	56.5	22	<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
97	<a href="#">d1ud2a2</a>	Alignment	not modelled	56.5	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
98	<a href="#">c6gyaA</a>	Alignment	not modelled	56.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> a-amylase; <b>PDBTitle:</b> amylase in complex with branched ligand
99	<a href="#">c3e96B</a>	Alignment	not modelled	55.5	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
100	<a href="#">c3vndD</a>	Alignment	not modelled	55.3	20	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
101	<a href="#">c5h06C</a>	Alignment	not modelled	55.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> amyp; <b>PDBTitle:</b> crystal structure of amyp in complex with maltose
102	<a href="#">c1zjaB</a>	Alignment	not modelled	55.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> trehalulose synthase; <b>PDBTitle:</b> crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
103	<a href="#">d1h3ga3</a>	Alignment	not modelled	54.7	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
104	<a href="#">d1gjwa2</a>	Alignment	not modelled	54.7	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
105	<a href="#">c2ehhE</a>	Alignment	not modelled	54.6	11	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
106	<a href="#">c5zcbA</a>	Alignment	not modelled	54.5	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> crystal structure of alpha-glucosidase
107	<a href="#">c3fkkA</a>	Alianment	not modelled	54.2	9	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-2-keto-3-deoxyarabonate dehydratase;

						<b>PDBTitle:</b> structure of l-2-keto-3-deoxyarabonate dehydratase
108	<a href="#">c2dh3A_</a>	Alignment	not modelled	53.5	15	<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
109	<a href="#">c2zidA_</a>	Alignment	not modelled	53.3	15	<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
110	<a href="#">d1yeya1</a>	Alignment	not modelled	53.1	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
111	<a href="#">c1bplA_</a>	Alignment	not modelled	52.9	22	<b>PDB header:</b> glycosyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-1,4-glucan-4-glucanohydrolase; <b>PDBTitle:</b> glycosyltransferase
112	<a href="#">c3vm7A_</a>	Alignment	not modelled	52.2	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> structure of an alpha-amylase from malbranchea cinnamomea
113	<a href="#">c2vncB_</a>	Alignment	not modelled	50.9	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
114	<a href="#">c2oztA_</a>	Alignment	not modelled	50.9	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tlr1174 protein; <b>PDBTitle:</b> crystal structure of o-succinylbenzoate synthase from2 thermosynechococcus elongatus bp-1
115	<a href="#">d1gcya2</a>	Alignment	not modelled	50.4	7	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
116	<a href="#">c2r8wB_</a>	Alignment	not modelled	50.0	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> agr_c_1641p; <b>PDBTitle:</b> the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
117	<a href="#">c2ze3A_</a>	Alignment	not modelled	49.7	42	<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
118	<a href="#">c5gquA_</a>	Alignment	not modelled	49.5	22	<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 cyanothecce sp. atcc 51142
119	<a href="#">c2qpuB_</a>	Alignment	not modelled	49.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-amylase type a isozyme; <b>PDBTitle:</b> sugar tongs mutant s378p in complex with acarbose
120	<a href="#">c6ahuj_</a>	Alignment	not modelled	49.4	18	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> J: <b>PDB Molecule:</b> ribonuclease p protein subunit p30; <b>PDBTitle:</b> cryo-em structure of human ribonuclease p with mature trna