

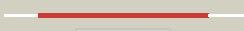





















# Phyre2

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Description	RVBD3520c (- )_3956504_3957547
Date	Fri Aug 9 18:20:19 BST 2019
Unique Job ID	73a5beef4c4b3429

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<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
2	<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
3	<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
4	<a href="#">c5tlcA_</a>	 Alignment		100.0	16	<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
5	<a href="#">d1luca_</a>	 Alignment		100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Bacterial luciferase (alkanal monooxygenase)
6	<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
7	<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)
8	<a href="#">d1rhca_</a>	 Alignment		100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
9	<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 monooxygenase; <b>PDBTitle:</b> type ii baeyer-villiger monooxygenase oxygenating2 constituent of 3,6-diketocamphane 1,6 monooxygenase from3 pseudomonas putida
10	<a href="#">c1tvIA_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> protein ytnj; <b>PDBTitle:</b> structure of ytnj from bacillus subtilis
11	<a href="#">d1tvla_</a>	 Alignment		100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Ssud-like monooxygenases

12	<a href="#">c3sdoB_</a>	Alignment		100.0	16	<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
13	<a href="#">c5dqpA_</a>	Alignment		100.0	15	<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="#">c3raoB_</a>	Alignment		100.0	19	<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.
15	<a href="#">c3b9nB_</a>	Alignment		100.0	16	<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)
16	<a href="#">c6ak1B_</a>	Alignment		100.0	20	<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
17	<a href="#">c3c8nB_</a>	Alignment		100.0	22	<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
18	<a href="#">c6friD_</a>	Alignment		100.0	17	<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
19	<a href="#">d1nqka_</a>	Alignment		100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Ssud-like monooxygenases
20	<a href="#">c2i7gA_</a>	Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monooxygenase; <b>PDBTitle:</b> crystal structure of monooxygenase from agrobacterium tumefaciens
21	<a href="#">c5wanA_</a>	Alignment	not modelled	100.0	16	<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
22	<a href="#">c2b81D_</a>	Alignment	not modelled	100.0	20	<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	17	<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	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="#">c3vniC_</a>	Alignment	not modelled	86.1	18	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> xylose isomerase domain protein tim barrel; <b>PDBTitle:</b> crystal structures of d-psicose 3-epimerase from clostridium2 cellulolyticum h10 and its complex with ketohexose sugars
26	<a href="#">c3qy6A_</a>	Alignment	not modelled	75.7	22	<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
27	<a href="#">d2fiqa1</a>	Alignment	not modelled	73.3	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> GatZ-like
28	<a href="#">c5zfaA</a>	Alignment	not modelled	71.1	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> d-allulose-3-epimerase;

28	<a href="#">c2z18A</a>	Alignment	not modelled	71.1	17	<b>PDBTitle:</b> crystal structure of arthrobacter globiformis m30 sugar epimerase2 which can produce d-allulose from d-fructose <b>PDB header:</b> isomerase
29	<a href="#">c2ou4C</a>	Alignment	not modelled	65.6	15	<b>Chain:</b> C: <b>PDB Molecule:</b> d-tagatose 3-epimerase; <b>PDBTitle:</b> crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
30	<a href="#">d2d69a1</a>	Alignment	not modelled	63.9	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
31	<a href="#">c3cnyA</a>	Alignment	not modelled	63.2	10	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> inositol catabolism protein iole; <b>PDBTitle:</b> crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcf51 at 1.85 a3 resolution
32	<a href="#">c3obeB</a>	Alignment	not modelled	62.8	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> sugar phosphate isomerase/epimerase; <b>PDBTitle:</b> crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution
33	<a href="#">d1xp3a1</a>	Alignment	not modelled	62.7	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Endonuclease IV
34	<a href="#">c3kwsB</a>	Alignment	not modelled	60.1	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative sugar isomerase; <b>PDBTitle:</b> crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution
35	<a href="#">d1m53a2</a>	Alignment	not modelled	59.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
36	<a href="#">d1uoka2</a>	Alignment	not modelled	57.2	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
37	<a href="#">c1bf2A</a>	Alignment	not modelled	56.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isoamylase; <b>PDBTitle:</b> structure of pseudomonas isoamylase
38	<a href="#">d1geha1</a>	Alignment	not modelled	55.3	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
39	<a href="#">d1ykwa1</a>	Alignment	not modelled	55.0	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
40	<a href="#">c1ehaA</a>	Alignment	not modelled	54.8	15	<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
41	<a href="#">c2x7vA</a>	Alignment	not modelled	53.6	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable endonuclease 4; <b>PDBTitle:</b> crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
42	<a href="#">c2d69B</a>	Alignment	not modelled	53.1	8	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase; <b>PDBTitle:</b> crystal structure of the complex of sulfate ion and octameric2 ribulose-1,5-bisphosphate carboxylase/oxygenase (rubisco) from3 pyrococcus horikoshii ot3 (form-2 crystal)
43	<a href="#">c2ze0A</a>	Alignment	not modelled	52.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> alpha-glucosidase gsj
44	<a href="#">d1ea9c3</a>	Alignment	not modelled	51.6	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
45	<a href="#">c5gquA</a>	Alignment	not modelled	51.5	7	<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
46	<a href="#">c2by0A</a>	Alignment	not modelled	51.3	19	<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
47	<a href="#">d1wzla3</a>	Alignment	not modelled	50.9	31	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
48	<a href="#">c5m99A</a>	Alignment	not modelled	50.7	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
49	<a href="#">c3qxbB</a>	Alignment	not modelled	50.4	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative xylose isomerase; <b>PDBTitle:</b> crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution
50	<a href="#">c3wqoB</a>	Alignment	not modelled	49.2	10	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein mj1311; <b>PDBTitle:</b> crystal structure of d-tagatose 3-epimerase-like protein
51	<a href="#">d1g5aa2</a>	Alignment	not modelled	49.2	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
52	<a href="#">c2wjeA</a>	Alignment	not modelled	48.8	18	<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 staphylococcus pneumoniae tigr4.
53	<a href="#">c5kinC</a>	Alignment	not modelled	48.4	15	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha beta

						complex from2 streptococcus pneumoniae
54	<a href="#">c6aavA</a>	Alignment	not modelled	48.3	15	<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
55	<a href="#">c2ya0A</a>	Alignment	not modelled	48.3	15	<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
56	<a href="#">c3m07A</a>	Alignment	not modelled	47.0	19	<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.
57	<a href="#">c5zxB</a>	Alignment	not modelled	46.8	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
58	<a href="#">d2guya2</a>	Alignment	not modelled	46.5	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
59	<a href="#">c3ez4B</a>	Alignment	not modelled	46.3	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-methyl-2-oxobutanoate hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of 3-methyl-2-oxobutanoate hydroxymethyltransferase2 from burkholderia pseudomallei
60	<a href="#">c3wy3A</a>	Alignment	not modelled	46.3	12	<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
61	<a href="#">c3zoaB</a>	Alignment	not modelled	46.1	15	<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
62	<a href="#">d1gvia3</a>	Alignment	not modelled	45.8	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
63	<a href="#">c3fk4A</a>	Alignment	not modelled	45.5	9	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> rubisco-like protein; <b>PDBTitle:</b> crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
64	<a href="#">c2aaaA</a>	Alignment	not modelled	45.4	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
65	<a href="#">c1uokA</a>	Alignment	not modelled	44.9	12	<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
66	<a href="#">c1qhoA</a>	Alignment	not modelled	44.7	27	<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
67	<a href="#">d1qhoa4</a>	Alignment	not modelled	44.5	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
68	<a href="#">c3czkA</a>	Alignment	not modelled	43.7	16	<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
69	<a href="#">c3qfeB</a>	Alignment	not modelled	43.3	11	<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
70	<a href="#">c3l23A</a>	Alignment	not modelled	43.1	27	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> sugar phosphate isomerase/epimerase; <b>PDBTitle:</b> crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution
71	<a href="#">d2bhua3</a>	Alignment	not modelled	42.9	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
72	<a href="#">c5brgA</a>	Alignment	not modelled	42.8	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)
73	<a href="#">c2qygC</a>	Alignment	not modelled	42.4	12	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> ribulose biphosphate carboxylase-like protein 2; <b>PDBTitle:</b> crystal structure of a rubisco-like protein rlp2 from rhodospseudomonas2 palustris
74	<a href="#">d1eh9a3</a>	Alignment	not modelled	42.3	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
75	<a href="#">c3faxA</a>	Alignment	not modelled	42.2	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
76	<a href="#">c1jgiA</a>	Alignment	not modelled	42.0	15	<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
77	<a href="#">c3k1dA</a>	Alignment	not modelled	41.9	8	<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
78	<a href="#">c4mb1A</a>	Alignment	not modelled	41.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oligo-1,6-glucosidase 1;

78	<a href="#">c4m01A</a>	Alignment	not modelled	41.7	15	<b>PDBTitle:</b> the structure of mall mutant enzyme g202p from bacillus subtilus <b>PDB header:</b> lyase
79	<a href="#">c3thaB</a>	Alignment	not modelled	41.7	16	<b>Chain:</b> B; <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> tryptophan synthase subunit alpha from campylobacter jejuni.
80	<a href="#">d1rbla1</a>	Alignment	not modelled	41.6	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
81	<a href="#">c5ykbB</a>	Alignment	not modelled	41.6	15	<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
82	<a href="#">d1j0ha3</a>	Alignment	not modelled	40.9	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
83	<a href="#">c4e2oA</a>	Alignment	not modelled	40.9	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
84	<a href="#">c1jpkA</a>	Alignment	not modelled	40.8	9	<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
85	<a href="#">c2z1kA</a>	Alignment	not modelled	40.7	15	<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
86	<a href="#">c3fa4D</a>	Alignment	not modelled	40.3	14	<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
87	<a href="#">c3uccA</a>	Alignment	not modelled	40.2	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> amylsucrase; <b>PDBTitle:</b> crystal structure of amylsucrase from deinococcus geothermalis
88	<a href="#">c5do8A</a>	Alignment	not modelled	40.1	23	<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
89	<a href="#">d1r3sa</a>	Alignment	not modelled	40.0	9	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MetE-like <b>Family:</b> Uroporphyrinogen decarboxylase, UROD
90	<a href="#">c1gehE</a>	Alignment	not modelled	39.8	12	<b>PDB header:</b> lyase <b>Chain:</b> E; <b>PDB Molecule:</b> ribulose-1,5-bisphosphate carboxylase/oxygenase; <b>PDBTitle:</b> crystal structure of archaeal rubisco (ribulose 1,5-bisphosphate2 carboxylase/oxygenase)
91	<a href="#">c4j7rA</a>	Alignment	not modelled	39.7	12	<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)
92	<a href="#">d1ej7l1</a>	Alignment	not modelled	39.6	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
93	<a href="#">c4aieA</a>	Alignment	not modelled	39.5	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
94	<a href="#">c5x7uA</a>	Alignment	not modelled	39.4	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> trehalose synthase; <b>PDBTitle:</b> trehalose synthase from thermobaculum terrenum
95	<a href="#">d1bf2a3</a>	Alignment	not modelled	39.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
96	<a href="#">c3fkkA</a>	Alignment	not modelled	39.1	14	<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
97	<a href="#">c3eegB</a>	Alignment	not modelled	39.1	17	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
98	<a href="#">c2ehhE</a>	Alignment	not modelled	38.9	12	<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
99	<a href="#">d1gcya2</a>	Alignment	not modelled	38.8	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
100	<a href="#">c1telA</a>	Alignment	not modelled	38.6	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> ribulose bisphosphate carboxylase, large subunit; <b>PDBTitle:</b> crystal structure of a rubisco-like protein from chlorobium2 tepidum
101	<a href="#">c1m53A</a>	Alignment	not modelled	38.6	15	<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
102	<a href="#">c4aefB</a>	Alignment	not modelled	38.3	16	<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
103	<a href="#">c2hk1D</a>	Alignment	not modelled	38.3	13	<b>PDB header:</b> isomerase <b>Chain:</b> D; <b>PDB Molecule:</b> d-psicose 3-epimerase; <b>PDBTitle:</b> crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose <b>PDB header:</b> hydrolase

104	<a href="#">c2wcsA</a>	Alignment	not modelled	38.1	15	<b>Chain:</b> A: <b>PDB Molecule:</b> alpha amylase, catalytic region; <b>PDBTitle:</b> crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
105	<a href="#">c1jibA</a>	Alignment	not modelled	38.0	31	<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.
106	<a href="#">c3eool</a>	Alignment	not modelled	37.9	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
107	<a href="#">c3vndD</a>	Alignment	not modelled	37.8	24	<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
108	<a href="#">d1o5ka</a>	Alignment	not modelled	37.8	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
109	<a href="#">d1m5wa</a>	Alignment	not modelled	37.7	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Pyridoxine 5'-phosphate synthase <b>Family:</b> Pyridoxine 5'-phosphate synthase
110	<a href="#">d1nvma2</a>	Alignment	not modelled	37.6	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> HMGL-like
111	<a href="#">d2aaaa2</a>	Alignment	not modelled	37.5	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
112	<a href="#">d1j93a</a>	Alignment	not modelled	37.3	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MetE-like <b>Family:</b> Uroporphyrinogen decarboxylase, UROD
113	<a href="#">c2p0oA</a>	Alignment	not modelled	37.2	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein duf871; <b>PDBTitle:</b> crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
114	<a href="#">d1fa2a</a>	Alignment	not modelled	36.8	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
115	<a href="#">c3qfwB</a>	Alignment	not modelled	36.7	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> ribulose-1,5-bisphosphate carboxylase/oxygenase large <b>PDBTitle:</b> crystal structure of rubisco-like protein from rhodospseudomonas2 palustris
116	<a href="#">c3k8kB</a>	Alignment	not modelled	36.7	19	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-amylase, susg; <b>PDBTitle:</b> crystal structure of susg
117	<a href="#">d1h3ga3</a>	Alignment	not modelled	36.4	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
118	<a href="#">c4mwaA</a>	Alignment	not modelled	36.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; <b>PDBTitle:</b> 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis
119	<a href="#">c2zidA</a>	Alignment	not modelled	36.1	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
120	<a href="#">d1ujqa</a>	Alignment	not modelled	35.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like