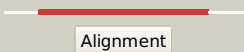

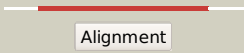



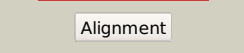



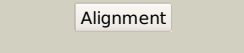

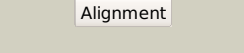



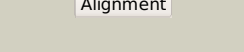

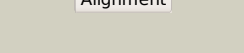

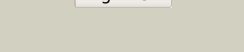








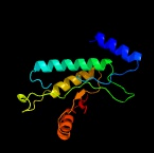












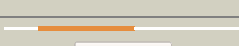
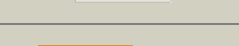
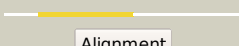

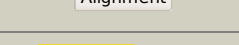
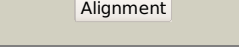


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1188 (- )_1331027_1332016
Date	Wed Jul 31 22:05:27 BST 2019
Unique Job ID	6331907db4380fe4

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2ekgB_</a>			100.0	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> proline dehydrogenase/delta-1-pyrroline-5-carboxylate <b>PDBTitle:</b> structure of thermus thermophilus proline dehydrogenase inactivated by 2 n-propargylglycine
2	<a href="#">c5ur2C_</a>			100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> bifunctional protein puta; <b>PDBTitle:</b> crystal structure of proline utilization a (puta) from bdellovibrio2 bacteriovorus inactivated by n-propargylglycine
3	<a href="#">c4f9iA_</a>			100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> proline dehydrogenase/delta-1-pyrroline-5-carboxylate <b>PDBTitle:</b> crystal structure of proline utilization a (puta) from geobacter2 sulfurreducens pca
4	<a href="#">c4h6rA_</a>			100.0	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> proline dehydrogenase; <b>PDBTitle:</b> structure of reduced deinococcus radiodurans proline dehydrogenase
5	<a href="#">c1k87A_</a>			100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> proline dehydrogenase; <b>PDBTitle:</b> crystal structure of e.coli puta (residues 1-669)
6	<a href="#">c3e2sA_</a>			100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> proline dehydrogenase; <b>PDBTitle:</b> crystal structure reduced puta86-630 mutant y540s complexed with l-2 proline
7	<a href="#">c1tj2A_</a>			100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional puta protein; <b>PDBTitle:</b> crystal structure of e. coli puta proline dehydrogenase domain2 (residues 86-669) complexed with acetate
8	<a href="#">c3hazA_</a>			100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> proline dehydrogenase; <b>PDBTitle:</b> crystal structure of bifunctional proline utilization a2 (puta) protein
9	<a href="#">d1tj1a2</a>			100.0	28	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FAD-linked oxidoreductase <b>Family:</b> Proline dehydrogenase domain of bifunctional PutA protein
10	<a href="#">c5kf6B_</a>			100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein puta; <b>PDBTitle:</b> structure of proline utilization a from sinorhizobium meliloti2 complexed with l-tetrahydrofuroic acid and nad+ in space group p21
11	<a href="#">c5ux5C_</a>			100.0	21	<b>PDB header:</b> oxidoreductase/transferase <b>Chain:</b> C: <b>PDB Molecule:</b> bifunctional protein proline utilization a (puta); <b>PDBTitle:</b> structure of proline utilization a (puta) from corynebacterium2 freiburgense

12	<a href="#">c3itgA_</a>	 Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein puta; <b>PDBTitle:</b> structure the proline utilization a proline dehydrogenase2 domain (puta86-630) inactivated with n-propargylglycine
13	<a href="#">c5tnvA_</a>	 Alignment		96.3	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ap endonuclease, family protein 2; <b>PDBTitle:</b> crystal structure of a xylose isomerase-like tim barrel protein from2 mycobacterium smegmatis in complex with magnesium
14	<a href="#">d1tz9a_</a>	 Alignment		93.2	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> UxuA-like
15	<a href="#">c4k3zA_</a>	 Alignment		92.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-erythrose 4-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-erythrose 4-phosphate dehydrogenase from2 brucella melitensis, solved by iodide sad
16	<a href="#">c4ovxA_</a>	 Alignment		91.3	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> xylose isomerase domain protein tim barrel; <b>PDBTitle:</b> crystal structure of xylose isomerase domain protein from planctomyces2 limnophilus dsm 3776
17	<a href="#">c3dx5A_</a>	 Alignment		90.7	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein asbf; <b>PDBTitle:</b> crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
18	<a href="#">c3cnyA_</a>	 Alignment		89.7	12	<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
19	<a href="#">c5hmqE_</a>	 Alignment		87.6	16	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-hydroxyphenylpyruvate dioxygenase; <b>PDBTitle:</b> xylose isomerase-like tim barrel/4-hydroxyphenylpyruvate dioxygenase2 fusion protein
20	<a href="#">d1qt1a_</a>	 Alignment		86.1	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
21	<a href="#">c2hk1D_</a>	 Alignment	not modelled	85.8	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
22	<a href="#">d1yx1a1</a>	 Alignment	not modelled	84.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> KguE-like
23	<a href="#">c3vylB_</a>	 Alignment	not modelled	82.6	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> l-ribulose 3-epimerase; <b>PDBTitle:</b> structure of l-ribulose 3-epimerase
24	<a href="#">c2qw5B_</a>	 Alignment	not modelled	81.5	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> xylose isomerase-like tim barrel; <b>PDBTitle:</b> crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
25	<a href="#">c3ktcB_</a>	 Alignment	not modelled	77.3	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> xylose isomerase; <b>PDBTitle:</b> crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
26	<a href="#">d1i60a_</a>	 Alignment	not modelled	77.1	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> lolI-like
27	<a href="#">c5zfsA_</a>	 Alignment	not modelled	76.2	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> d-allulose-3-epimerase; <b>PDBTitle:</b> crystal structure of arthrobacter globiformis m30 sugar epimerase2 which can produce d-allulose from d-fructose
28	<a href="#">c2zdsB_</a>	 Alignment	not modelled	76.0	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> crystal structure of sco6571 from streptomyces coelicolor

					a3(2)
29	<a href="#">c3ju2A</a>	Alignment	not modelled	74.4	13 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein smc04130; <b>PDBTitle:</b> crystal structure of protein smc04130 from sinorhizobium melloti 1021
30	<a href="#">d2glka1</a>	Alignment	not modelled	73.3	18 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
31	<a href="#">c2ou4C</a>	Alignment	not modelled	71.9	14 <b>PDB header:</b> isomerase <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
32	<a href="#">d1xima</a>	Alignment	not modelled	71.3	19 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
33	<a href="#">c3vniC</a>	Alignment	not modelled	68.2	13 <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
34	<a href="#">d1kkoa1</a>	Alignment	not modelled	66.9	17 <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="#">c3qxbB</a>	Alignment	not modelled	66.0	12 <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
36	<a href="#">c1kczA</a>	Alignment	not modelled	62.7	19 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-methylaspartase; <b>PDBTitle:</b> crystal structure of beta-methylaspartase from clostridium2 tetanomorphum. mg-complex.
37	<a href="#">d2q02a1</a>	Alignment	not modelled	61.6	8 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> lolI-like
38	<a href="#">d1bxba</a>	Alignment	not modelled	60.9	18 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
39	<a href="#">c2qpuB</a>	Alignment	not modelled	60.3	14 <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
40	<a href="#">c3bdkB</a>	Alignment	not modelled	58.5	18 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> d-mannonate dehydratase; <b>PDBTitle:</b> crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
41	<a href="#">c3wqoB</a>	Alignment	not modelled	56.6	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
42	<a href="#">d2pb1a1</a>	Alignment	not modelled	56.4	11 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
43	<a href="#">c3icgD</a>	Alignment	not modelled	52.2	11 <b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> endoglucanase d; <b>PDBTitle:</b> crystal structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
44	<a href="#">c3p6IA</a>	Alignment	not modelled	52.0	6 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> sugar phosphate isomerase/epimerase; <b>PDBTitle:</b> crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distansis atcc 8503 at 1.85 a resolution
45	<a href="#">d1bxca</a>	Alignment	not modelled	51.5	19 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
46	<a href="#">c3kwsB</a>	Alignment	not modelled	49.0	17 <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 distansis atcc 8503 at 1.68 a resolution
47	<a href="#">d1ht6a2</a>	Alignment	not modelled	48.3	13 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
48	<a href="#">d2guya2</a>	Alignment	not modelled	45.7	16 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
49	<a href="#">d1avaa2</a>	Alignment	not modelled	44.0	13 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
50	<a href="#">d1k77a</a>	Alignment	not modelled	43.3	13 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Hypothetical protein YgbM (EC1530)
51	<a href="#">c5oydA</a>	Alignment	not modelled	42.6	13 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulase, putative, cel5d; <b>PDBTitle:</b> gh5 endo-xyloglucanase from cellvibrio japonicus
52	<a href="#">c4w8aA</a>	Alignment	not modelled	41.7	11 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exo-xyloglucanase; <b>PDBTitle:</b> crystal structure of xeg5b, a gh5 xyloglucan-specific beta-1,4-2 glucanase from ruminal metagenomic library, in the native form
53	<a href="#">c3l23A</a>	Alignment	not modelled	38.3	10 <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
54	<a href="#">d1muwa_</a>	Alignment	not modelled	33.6	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
55	<a href="#">c3l55B_</a>	Alignment	not modelled	32.0	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> b-1,4-endoglucanase/cellulase; <b>PDBTitle:</b> crystal structure of a putative beta-1,4-endoglucanase / cellulase2 from prevotella bryantii
56	<a href="#">c3cqkB_</a>	Alignment	not modelled	30.4	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> l-ribose-5-phosphate 3-epimerase ulae; <b>PDBTitle:</b> crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
57	<a href="#">c1uz4A_</a>	Alignment	not modelled	29.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> man5a; <b>PDBTitle:</b> common inhibition of beta-glucosidase and beta-mannosidase2 by isofagomine lactam reflects different conformational3 itineraries for glucoside and mannoside hydrolysis
58	<a href="#">d1uuqa_</a>	Alignment	not modelled	29.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
59	<a href="#">c6nbmB_</a>	Alignment	not modelled	29.0	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> crystal structure of enolase from legionella pneumophila bound to2 phosphate and magnesium
60	<a href="#">d1mxga2</a>	Alignment	not modelled	28.2	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
61	<a href="#">c2oylB_</a>	Alignment	not modelled	27.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endoglycoceramidase ii; <b>PDBTitle:</b> endo-glycoceramidase ii from rhodococcus sp.: cellobiose-like2 imidazole complex
62	<a href="#">c4m0xB_</a>	Alignment	not modelled	27.6	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> chloromuconate cycloisomerase; <b>PDBTitle:</b> crystal structure of 2-chloromuconate cycloisomerase from rhodococcus2 opacus1cp
63	<a href="#">c4e8gA_</a>	Alignment	not modelled	27.4	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme, n-terminal <b>PDBTitle:</b> crystal structure of an enolase (mandelate racemase subgroup) from2 paracoccus denitrificans pd1222 (target nysgrc-012907) with bound mg
64	<a href="#">d1vjza_</a>	Alignment	not modelled	27.2	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
65	<a href="#">d1edga_</a>	Alignment	not modelled	26.9	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
66	<a href="#">c2zvrA_</a>	Alignment	not modelled	26.6	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein tm_0416; <b>PDBTitle:</b> crystal structure of a d-tagatose 3-epimerase-related protein from2 thermotoga maritima
67	<a href="#">c2yl8A_</a>	Alignment	not modelled	26.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-n-acetylhexosaminidase; <b>PDBTitle:</b> inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
68	<a href="#">c3zviB_</a>	Alignment	not modelled	25.8	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> methylaspartate ammonia-lyase; <b>PDBTitle:</b> methylaspartate ammonia lyase from clostridium tetanomorphum mutant2 l384a
69	<a href="#">d1ur4a_</a>	Alignment	not modelled	25.8	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
70	<a href="#">c4nf7A_</a>	Alignment	not modelled	25.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-1,4-beta-glucanase cel5c; <b>PDBTitle:</b> crystal structure of the gh5 family catalytic domain of endo-1,4-beta-2 glucanase cel5c from butyrivibrio proteoclasticus.
71	<a href="#">c1qhoA_</a>	Alignment	not modelled	25.4	23	<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
72	<a href="#">c4yheB_</a>	Alignment	not modelled	25.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gh5; <b>PDBTitle:</b> native bacteroidetes-affiliated gh5 cellulase linked with a2 polysaccharide utilization locus
73	<a href="#">c3bmwA_</a>	Alignment	not modelled	25.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclomalto-dextrin glucanotransferase; <b>PDBTitle:</b> cyclodextrin glycosyl transferase from thermoanaerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
74	<a href="#">c4x0vH_</a>	Alignment	not modelled	24.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> beta-1,3-1,4-glucanase; <b>PDBTitle:</b> structure of a gh5 family lichenase from caldicellulosiruptor sp. f32
75	<a href="#">c3sjnB_</a>	Alignment	not modelled	24.3	24	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing protein; <b>PDBTitle:</b> crystal structure of enolase spea_3858 (target efi-500646) from2 shewanella pealeana with magnesium bound
76	<a href="#">d1hx0a2</a>	Alignment	not modelled	24.1	32	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
77	<a href="#">c3t8qA_</a>	Alignment	not modelled	24.1	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme family <b>PDBTitle:</b> crystal structure of mandelate racemase/muconate lactonizing enzyme2 family protein from hoeflea phototrophica
78	<a href="#">d1cgta4</a>	Alignment	not modelled	24.1	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases

						<b>Family:</b> Amylase, catalytic domain
79	<a href="#">c5ccuA_</a>	Alignment	not modelled	23.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative secreted endoglycosylceramidase; <b>PDBTitle:</b> crystal structure of endoglycoceramidase i from rhodococ-cus equi
80	<a href="#">c1cygA_</a>	Alignment	not modelled	23.8	23	<b>PDB header:</b> glycosyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclodextrin glucanotransferase; <b>PDBTitle:</b> cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
81	<a href="#">c3aysA_</a>	Alignment	not modelled	23.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> gh5 endoglucanase from a ruminal fungus in complex with cellotriase
82	<a href="#">c2zunB_</a>	Alignment	not modelled	23.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 458aa long hypothetical endo-1,4-beta-glucanase; <b>PDBTitle:</b> functional analysis of hyperthermophilic endocellulase from2 the archaeon pyrococcus horikoshii
83	<a href="#">c2jepB_</a>	Alignment	not modelled	23.3	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xyloglucanase; <b>PDBTitle:</b> native family 5 xyloglucanase from paenibacillus pabuli
84	<a href="#">c3ncoA_</a>	Alignment	not modelled	23.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase fncel5a; <b>PDBTitle:</b> crystal structure of fncel5a from f. nodosum rt17-b1
85	<a href="#">c2bg5C_</a>	Alignment	not modelled	22.9	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoenolpyruvate-protein kinase; <b>PDBTitle:</b> crystal structure of the phosphoenolpyruvate-binding enzyme i-domain2 from the thermoanaerobacter tengcongensis pep: sugar3 phosphotransferase system (pts)
86	<a href="#">d1jpmA1</a>	Alignment	not modelled	22.4	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
87	<a href="#">c2y8kA_</a>	Alignment	not modelled	22.3	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate binding family 6; <b>PDBTitle:</b> structure of ctgh5-cbm6, an arabinoxylan-specific xylanase.
88	<a href="#">c4ee9A_</a>	Alignment	not modelled	22.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> crystal structure of the rbccl1 endo-1,4-glucanase
89	<a href="#">c1kkoB_</a>	Alignment	not modelled	21.8	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-methylaspartate ammonia-lyase; <b>PDBTitle:</b> crystal structure of citrobacter amalonaticus2 methylaspartate ammonia lyase
90	<a href="#">c5y6tA_</a>	Alignment	not modelled	21.8	10	<b>PDB header:</b> carbohydrate <b>Chain:</b> A: <b>PDB Molecule:</b> endo-1,4-beta-mannanase; <b>PDBTitle:</b> crystal structure of endo-1,4-beta-mannanase from eisenia fetida
91	<a href="#">d1cxlA4</a>	Alignment	not modelled	21.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
92	<a href="#">c5zxgB_</a>	Alignment	not modelled	21.4	23	<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
93	<a href="#">d1gcya2</a>	Alignment	not modelled	21.4	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
94	<a href="#">c5dlcC_</a>	Alignment	not modelled	21.0	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pyridoxine 5'-phosphate synthase; <b>PDBTitle:</b> x-ray crystal structure of a pyridoxine 5-prime-phosphate synthase2 from pseudomonas aeruginosa
95	<a href="#">d2ffca1</a>	Alignment	not modelled	20.3	6	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
96	<a href="#">d1ob0a2</a>	Alignment	not modelled	20.2	9	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
97	<a href="#">d2g0wa1</a>	Alignment	not modelled	20.0	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> loll-like
98	<a href="#">d1pama4</a>	Alignment	not modelled	19.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
99	<a href="#">d1wu7a1</a>	Alignment	not modelled	19.2	13	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS