Phyre^2

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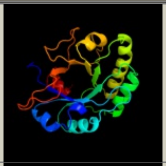
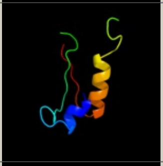
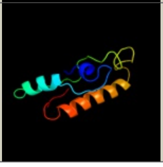
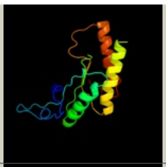
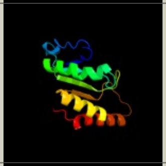
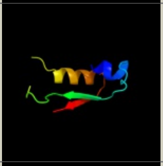
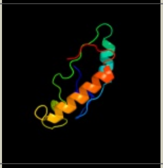
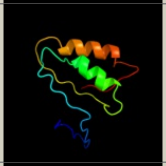
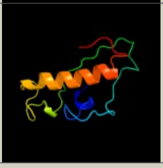
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wagA_	Alignment		100.0	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme, putative; **PDBTitle:** the structure of a family 25 glycosyl hydrolase from2 bacillus anthracis.
2	d1jfxa_	Alignment		100.0	36	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**1,4-beta-N-acetylmuraminidase
3	c2x8rE_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**glycosyl hydrolase; **PDBTitle:** the structure of a family gh25 lysozyme from aspergillus2 fumigatus
4	c2wwcA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1,4-beta-n-acetylmuramidase; **PDBTitle:** 3d-structure of the modular autolysin lytc from2 streptococcus pneumoniae in complex with synthetic3 peptidoglycan ligand
5	c2nw0B_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**plyb; **PDBTitle:** crystal structure of a lysin
6	d2j8ga2	Alignment		100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**1,4-beta-N-acetylmuraminidase
7	c2j8fA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme; **PDBTitle:** crystal structure of the modular cpl-1 endolysin complexed2 with a peptidoglycan analogue (e94q mutant in complex with3 a disaccharide-pentapeptide)
8	d1sfsa_	Alignment		98.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**1,4-beta-N-acetylmuraminidase
9	c1sfsA_	Alignment		98.6	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** 1.07 a crystal structure of an uncharacterized b.2 stearothermophilus protein
10	d1hl9a2	Alignment		64.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Putative alpha-L-fucosidase, catalytic domain
11	d1e4ia_	Alignment		63.8	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase

12	d1hjqa_	Alignment		62.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
13	d1hjsa_	Alignment		62.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
14	c2wvsD_	Alignment		57.5	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**alpha-l-fucosidase; **PDBTitle:** crystal structure of an alpha-l-fucosidase gh29 trapped2 covalent intermediate from bacteroides thetaiotaomicron in3 complex with 2-fluoro-fucosyl fluoride using an e288q4 mutant
15	c3s6dA_	Alignment		56.2	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative triosephosphate isomerase; **PDBTitle:** crystal structure of a putative triosephosphate isomerase from2 coccidioides immitis
16	c3gzaB_	Alignment		54.8	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution
17	c3ahxC_	Alignment		53.4	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-glucosidase a; **PDBTitle:** crystal structure of beta-glucosidase a from bacterium clostridium2 cellulovorans
18	c1hl8B_	Alignment		51.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of thermotoga maritima alpha-fucosidase
19	d1euca2	Alignment		50.5	17	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
20	d2j78a1	Alignment		44.6	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
21	d1tvna1	Alignment	not modelled	44.4	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
22	c3eypB_	Alignment	not modelled	42.2	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase from bacteroides2 thetaiotaomicron
23	c3ebvA_	Alignment	not modelled	39.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**chinitase a; **PDBTitle:** crystal structure of putative chitinase a from streptomyces2 coelicolor.
24	c2jgqB_	Alignment	not modelled	37.5	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** kinetics and structural properties of triosephosphate2 isomerase from helicobacter pylori
25	d1egza_	Alignment	not modelled	37.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
26	d1foba_	Alignment	not modelled	36.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
27	c3mo4B_	Alignment	not modelled	34.6	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-1,3/4-fucosidase; **PDBTitle:** the crystal structure of an alpha-(1-3,4)-fucosidase from2 bifidobacterium longum subsp. infantis atcc 15697
28	c3th6B_	Alignment	not modelled	34.5	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from rhipicephalus2 (boophilus) microplus.
						PDB header:hydrolase

29	c3qr3B_	Alignment	not modelled	29.2	8	**Chain:** B: **PDB Molecule:**endoglucanase eg-ii; **PDBTitle:** crystal structure of cel5a (eg2) from hypocrea jecorina (trichoderma2 reesei)
30	d1o5xa_	Alignment	not modelled	28.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
31	c3krsB_	Alignment	not modelled	28.2	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** structure of triosephosphate isomerase from cryptosporidium parvum at2 1.55a resolution
32	d1ur4a_	Alignment	not modelled	27.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
33	c3ianA_	Alignment	not modelled	25.4	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** crystal structure of a chitinase from lactococcus lactis2 subsp. lactis
34	d1wkya2	Alignment	not modelled	21.0	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
35	c2xucA_	Alignment	not modelled	20.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** natural product-guided discovery of a fungal chitinase2 inhibitor
36	c3c65A_	Alignment	not modelled	20.3	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of bacillus stearothermophilus uvrc 5'2 endonuclease domain
37	d1gnxa_	Alignment	not modelled	19.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
38	d1f61a_	Alignment	not modelled	17.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
39	c3e5bB_	Alignment	not modelled	16.9	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**isocitrate lyase; **PDBTitle:** 2.4 a crystal structure of isocitrate lyase from brucella2 melitensis
40	d1ktba2	Alignment	not modelled	16.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
41	c2g3nA_	Alignment	not modelled	15.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** crystal structure of the sulfolobus solfataricus alpha-2 glucosidase mala in complex with beta-octyl-glucopyranoside
42	c2pt7G_	Alignment	not modelled	15.3	12	**PDB header:**hydrolase/protein binding **Chain:** G: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of cag virb11 (hp0525) and an inhibitory protein2 (hp1451)
43	d1b9ba_	Alignment	not modelled	13.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
44	c3mmwB_	Alignment	not modelled	13.3	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase cel5a from the hyperthermophilic2 thermotoga maritima
45	d1q1ra3	Alignment	not modelled	13.3	22	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
46	c2dskA_	Alignment	not modelled	13.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** crystal structure of catalytic domain of hyperthermophilic chitinase2 from pyrococcus furiosus
47	d1qcrd2	Alignment	not modelled	13.0	22	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Cytochrome bc1 domain
48	d1mo0a_	Alignment	not modelled	12.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
49	c3ffjA_	Alignment	not modelled	12.2	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hydrolase (family 31); **PDBTitle:** the crystal structure of the glycosyl hydrolase (family 31) from2 ruminococcus obeum atcc 29174
50	c2qmjA_	Alignment	not modelled	12.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltase-glucoamylase, intestinal; **PDBTitle:** crystral structure of the n-terminal subunit of human maltase-2 glucoamylase in complex with acarbose
51	c3lecA_	Alignment	not modelled	11.9	18	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**nadb-rossmann superfamily protein; **PDBTitle:** the crystal structure of a protein in the nadb-rossmann2 superfamily from streptococcus agalactiae to 1.8a
52	d1trea_	Alignment	not modelled	11.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
53	d1o0sa2	Alignment	not modelled	11.6	28	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Malic enzyme N-domain
54	c1qcrD_	Alignment	not modelled	11.5	21	**PDB header:** **PDB COMPND:**
55	d1suxa_	Alignment	not modelled	11.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM)

						Family: Triosephosphate isomerase (TIM)
56	c2rirA_	Alignment	not modelled	10.9	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase, a chain; **PDBTitle:** crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
57	c3lppA_	Alignment	not modelled	10.8	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sucrase-isomaltase; **PDBTitle:** crystal complex of n-terminal sucrase-isomaltase with kotalanol
58	d1qoxa_	Alignment	not modelled	10.8	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
59	d1aw1a_	Alignment	not modelled	10.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
60	c3gnoA_	Alignment	not modelled	10.6	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**os03g0212800 protein; **PDBTitle:** crystal structure of a rice os3bglu6 beta-glucosidase
61	d1nqua_	Alignment	not modelled	10.2	14	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
62	d1pj3a2	Alignment	not modelled	10.2	18	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Malic enzyme N-domain
63	d1neya_	Alignment	not modelled	10.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
64	c2dp3A_	Alignment	not modelled	10.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of a double mutant (c202a/a198v) of triosephosphate2 isomerase from giardia lamblia
65	d1eg7a_	Alignment	not modelled	9.9	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
66	d1kv5a_	Alignment	not modelled	9.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
67	c2rgmA_	Alignment	not modelled	9.5	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** rice bglu1 beta-glucosidase, a plant exoglucanase/beta-glucosidase
68	c3kxqB_	Alignment	not modelled	9.4	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from bartonella2 henselae at 1.6a resolution
69	d2btma_	Alignment	not modelled	9.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
70	c3civA_	Alignment	not modelled	9.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-beta-1,4-mannanase; **PDBTitle:** crystal structure of the endo-beta-1,4-mannanase from2 alicyclobacillus acidocaldarius
71	c2h6rG_	Alignment	not modelled	8.9	15	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
72	c2j75A_	Alignment	not modelled	8.8	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase a; **PDBTitle:** beta-glucosidase from thermotoga maritima in complex with2 noeuromycin
73	d2ebna_	Alignment	not modelled	8.8	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
74	c2r94B_	Alignment	not modelled	8.6	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxy-(6-phospho-)gluconate aldolase; **PDBTitle:** crystal structure of kd(p)ga from t.tenax
75	c1yyaA_	Alignment	not modelled	8.5	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of tt0473, putative triosephosphate isomerase from2 thermus thermophilus hb8
76	c3bghB_	Alignment	not modelled	8.5	35	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative neuraminyllactose-binding hemagglutinin homolog; **PDBTitle:** crystal structure of putative neuraminyllactose-binding hemagglutinin2 homolog from helicobacter pylori
77	c3d4oA_	Alignment	not modelled	8.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit a; **PDBTitle:** crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
78	c1zrtD_	Alignment	not modelled	8.1	19	**PDB header:**oxidoreductase/metal transport **Chain:** D: **PDB Molecule:**cytochrome c1; **PDBTitle:** rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
79	c3jugA_	Alignment	not modelled	8.1	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-mannanase; **PDBTitle:** crystal structure of endo-beta-1,4-mannanase from the alkaliphilic2 bacillus sp. n16-5
80	c2nrzB_	Alignment	not modelled	8.0	50	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of the c-terminal half of uvrc bound to2 its catalytic divalent cation
81	c3cz8A_	Alignment	not modelled	7.9	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sporulation-specific glycosylase ydhd;

						PDBTitle: crystal structure of putative sporulation-specific glycosylase ydhd2 from bacillus subtilis
82	c2dgaA_	Alignment	not modelled	7.6	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** crystal structure of hexameric beta-glucosidase in wheat
83	d1oa3a_	Alignment	not modelled	7.5	19	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Xylanase/endoglucanase 11/12
84	c3d5hA_	Alignment	not modelled	7.2	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**haementhin; **PDBTitle:** crystal structure of haementhin from haemanthus multiflorus2 at 2.0a resolution: formation of a novel loop on a tim3 barrel fold and its functional significance
85	d1pbga_	Alignment	not modelled	7.2	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
86	d2i9ia1	Alignment	not modelled	7.1	19	**Fold:**Anticodon-binding domain-like **Superfamily:**XCC0632-like **Family:**NLBH-like
87	c2i9iA_	Alignment	not modelled	7.1	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of helicobacter pylori protein hp0492
88	c1wkyA_	Alignment	not modelled	7.1	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-beta-1,4-mannanase; **PDBTitle:** crystal structure of alkaline mannanase from bacillus sp. strain jamb-2 602: catalytic domain and its carbohydrate binding module
89	d1u83a_	Alignment	not modelled	7.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
90	c1u83A_	Alignment	not modelled	7.1	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphosulfolactate synthase; **PDBTitle:** psl synthase from bacillus subtilis
91	d1ta3a_	Alignment	not modelled	7.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
92	c2fpgA_	Alignment	not modelled	6.9	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**succinyl-coa ligase [gdp-forming] alpha-chain, **PDBTitle:** crystal structure of pig gtp-specific succinyl-coa2 synthetase in complex with gdp
93	d1edta_	Alignment	not modelled	6.9	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
94	d1rvv1_	Alignment	not modelled	6.7	14	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
95	d1r2ra_	Alignment	not modelled	6.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
96	c2uy2A_	Alignment	not modelled	6.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endochitinase; **PDBTitle:** sccts1_apo crystal structure
97	d1m6ja_	Alignment	not modelled	6.6	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
98	c3thdD_	Alignment	not modelled	6.6	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of human beta-galactosidase in complex with 1-2 deoxygalactonojirimycin
99	c3topA_	Alignment	not modelled	6.6	6	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**maltase-glucoamylase, intestinal; **PDBTitle:** crystral structure of the c-terminal subunit of human maltase-2 glucoamylase in complex with acarbose