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Updating the sequence-based classification of glycosyl hydrolases

A classification of glycosyl hydrolases based on amino-acid-sequence similarities was proposed in this Journal a few years ago [1]. This classification originated from the analysis of ~ 300 sequences and their grouping into 35 families designated 1–35. Because such a classification is necessarily sensitive to the sample, it was anticipated that it was incomplete and that new families would be determined when additional sequences would become available. When the number of glycosyl hydrolase sequences reached ~ 480, ten additional families (designated 36–45) could be defined and were added to the classification [2]. There are at present over 950 sequences of glycosyl hydrolases in the data-banks (EMBL/GenBank and SWISS-PROT). Their analysis shows that the vast majority of the ~ 470 additional sequences that have become available since the last update could be classified in the existing families. However, several sequences not fitting the existing families allow the definition of new families (designated 46–57) (Table 1). When the several present genome sequencing projects have reached completion, the number of

Table 1 New families in the classification of glycosyl hydrolases

Family	Enzyme	Organism	SWISS-PROT	EMBL/GenBank
46	Chitosanase	*Bacillus circulans* MH-K1	P33673	D10624
46	Chitosanase	*Streptomyces* sp. N174	P33665	L07779
46	Chitosanase	*Nocardioides* sp.	P48846	L40408
47	α-Mannosidase	*Drosophila melanogaster*		X82641
47	α-Mannosidase 9	Human	P33908	X74837
47	α-Mannosidase	Mouse	P39098	U03458
47	α-Mannosidase	Mouse	P45700	U04299
47	α-Mannosidase	*Penicillium citrinum*		D45839
47	α-Mannosidase	Rabbit	P45701	U04301
47	α-Mannosidase	*Saccharomyces cerevisiae*	P32906	M63598; Z49631
47	Open reading frame	*Caenorhabditis elegans*		Z47073
48	Cellulase CelS	*Clostridium thermocellum*	P38686	S56455
48	Cellulase CelF	*Clostridium cellulolyticum*	P37698	U30321
48	Open reading frame	*Caldocellum saccharolyticum*	P22534	M36063
48	Cellobiohydrolase B	*Cellulomonas fimi*		L38827
49	Dextranase	*Arthrobacter* sp.	P39652	D00834
49	Dextranase	*Penicillium minioluteum*	P48845	L41562
50	Agarase A	*Vibrio* sp.	P48839	D14721
50	Agarase B	*Vibrio* sp.	P48840	D21202
51	Arabinofuranosidase A	*Aspergillus niger*	P42254	L29005
51	Arabinofuranosidase	*Streptomyces lividans*		U04630
52	β-Xylosidase	*Bacillus stearothermophilus* 236	P45704	U15984
52	β-Xylosidase	*Bacillus stearothermophilus* 21	P45702	D28121
53	Galactanase 1	*Aspergillus aculeatus*	P48842	L34599
53	Open reading frame	*Bacillus polymyxa*	P48843	L03425
53	Galactanase	*Pseudomonas fluorescens*	P48841	X91885
54	Arabinofuranosidase B	*Aspergillus niger*	P42255	X74777
54	Arabinofuranosidase/xylanase	*Trichoderma koningii*	P48792	U38661
55	Exo-1,3-β-glucanase	*Cochliobolus carbonum*	P49426	L48994
55	Endo-1,3-β-glucanase	*Trichoderma harzianum*		X84085
56	Hyaluronidase	*Apis mellifera*	Q08169	L10710
56	Hyaluronidase	*Cavia porcellus*	P23613	X56332
56	Hyaluronidase	*Dolichovespula maculata*	P49 371	L34548
56	Hyaluronidase	Human	P38567	L13781
56	Hyaluronidase	*Macaca fascicularis*	P38568	L13780
56	Hyaluronidase	Mouse	P48794	U33958
56	Hyaluronidase	Rabbit	P38566	U09183
56	Hyaluronidase	*Vespula vulgaris*	P49370	L43562
57	α-Amylase 1	*Dictyoglomus thermophilum*	P09961	X07896
57	α-Amylase	*Pyrococcus furiosus*	P49067	L22346

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Family 6
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Description: Endoglucanases (EC 3.2.1.4) and
             cellobiohydrolases (EC 3.2.1.91).
PROSITE: PDOC00563
3D structure status: Available
Reaction stereochemical outcome: Inverted anomeric configuration
Catalytic nucleophile/base: Asp (experimental)
Catalytic proton donor: Asp (experimental)
Clan: None
Known taxonomic range: eukaryotae, prokaryotae.
Note: formerly known as cellulase family B.

GUNA_CELFI (P07984), GUNB_FUSOX (P46236), GUNA_MICBI (P26414),
GUNA_STRHA (P33682), GUN1_STRSQ (P13933), GUN2_THEFU (P26222),
GUX2_TRIRE (P07987)
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Figure 1 Example of a section of the glycosyl hydrolase classification document

The text in **bold** denotes hypertext links to other electronic servers (ENZYME, PROSITE and SWISS-PROT).

glycosyl hydrolase sequences will probably increase dramatically. There are two major problems with keeping the classification: (i) how to make it available *in toto*, and (ii) how to disclose the new families when they are discovered. One way is the publication in scientific journals of papers whose interest decreases as they become progressively similar to stamp collections. Another way is the use of more adapted media such as electronic databases.

We are happy to announce that a permanently updated version of the classification is now available through the ExPASy WWW server [3] at the URL: 'http://expasy.hcuge.ch/cgi-bin/lists?glycosid.txt'. For each family of glycosyl hydrolases, a section of the document exists (Figure 1) that briefly lists the main enzymes that belong to this family. This section includes links to the relevant SWISS-PROT [4] protein-sequence entries. Links are also provided to the relevant EC numbers in the ENZYME [5] nomenclature database as well as to PROSITE [6] entries (which currently exist for more than half of the known glycosyl hydrolase families). This electronic classification should answer the need for rapid updates and availability *in toto* or family by family and allow users to navigate seamlessly between various types of network resources providing information on these enzymes.

There are two major mechanisms for glycosyl hydrolases, leading to overall retention or inversion of the stereochemistry at the cleavage point [7]. The mechanism appears to be conserved within each family [8]. The following families have been found to act with a retaining mechanism : 1, 2, 5, 7, 10, 11, 12, 13, 16, 17, 22, 30, 31, 32, 33, 34, 35, 39 and 42 (the mechanism of families 30, 35 and 42 was inferred from sequence similarities [9]). The inverting mechanism prevails in families 6, 8, 9, 14, 15, 19, 24, 37, 43, 44, 45, 46, 47 and 48. The electronic classification indicates the type of mechanism for each family where it is known.

The three-dimensional structure is now known for at least one member of families 1, 2, 5, 6, 7, 9, 10, 11, 13, 14, 15, 16, 17, 18, 19, 20, 22, 23, 24, 33, 34, 45 and 46 (for a review, see [10]). The availability of a three-dimensional structure is indicated in the electronic version of the classification.

A 'clan' is a group of families that are thought to have a common ancestry and are recognized by significant similarities in tertiary structure together with conservation of the catalytic residues and catalytic mechanism. The growing number of three-dimensional structures solved for glycosyl hydrolases and/or improved sequence comparison strategies have revealed the relationship between some glycosyl hydrolases families which can be grouped in clans (Table 2).

Table 2 Clan grouping of glycosyl hydrolase families

Clan	Families grouped	Reference
GH-A	1, 2, 5, 10, 17, 30, 35, 39, 42	[9,11]
GH-B	7, 16	[12]
GH-C	11, 12	[13]
GH-D	27, 36	[14,15]
GH-E	33, 34	[16]

The grouping into clans is also indicated in the electronic classification. Families 19, 22, 23 and 24 have been proposed to be related on the basis of weak local three-dimensional similarities [17]. However, since family 22 acts with a retaining mechanism while families 19 and 24 use the inverting mechanism, and since the mechanism of family 23 is not yet known, we feel it is safer to consider these families as independent until a stronger evidence for their grouping is available.

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