

## M1 Consensus

Domain	# runs	Description
<b>GH5</b>	17	chitosanase (EC 3.2.1.132); beta-mannosidase (EC 3.2.1.25); Cellulase (EC 3.2.1.4); glucan 1,3-beta-glucosidase (EC 3.2.1.58); licheninase (EC 3.2.1.73); glucan endo-1,6-beta-glucosidase (EC 3.2.1.75); mannan endo-beta-1,4-mannosidase (EC 3.2.1.78); endo-beta-1,4-xylanase (EC 3.2.1.8); cellulose beta-1,4-cellobiosidase (EC 3.2.1.91); beta-1,3-mannanase (EC 3.2.1.-); xyloglucan-specific endo-beta-1,4-glucanase (EC 3.2.1.151); mannan transglycosylase (EC 2.4.1.-); endo-beta-1,6-galactanase (EC 3.2.1.164)
<b>PF00150</b>	18	Cellulase (glycosyl hydrolase family 5)
<b>GH9</b>	18	endoglucanase (EC 3.2.1.4); cellobiohydrolase (EC 3.2.1.91); beta-glucosidase (EC 3.2.1.21); exo-beta-glucosaminidase (EC 3.2.1.165)
<b>PF00759</b>	17	Glycosyl hydrolase family 9
<b>GH10</b>	17	endo-1,4-beta-xylanase (EC 3.2.1.8); endo-1,3-beta-xylanase (EC 3.2.1.32)
<b>PF00331</b>	17	Glycosyl hydrolase family 10
<b>GH26</b>	17	beta-mannanase (EC 3.2.1.78); beta-1,3-xylanase (EC 3.2.1.32)
<b>PF02156</b>	17	Glycosyl hydrolase family 26
<b>GH43</b>	18	beta-xylosidase (EC 3.2.1.37); beta-1,3-xylosidase (EC 3.2.1.-); alpha-L-arabinofuranosidase (EC 3.2.1.55); arabinanase (EC 3.2.1.99); xylanase (EC 3.2.1.8); galactan 1,3-beta-galactosidase (EC 3.2.1.145)
<b>PF04616</b>	17	Glycosyl hydrolases family 43
<b>CBM4</b>	16	Modules of approx. 150 residues found in bacterial enzymes. Binding of these modules has been demonstrated with xylan, beta-1,3-glucan, beta-1,3-1,4-glucan, beta-1,6-glucan and amorphous cellulose but not with crystalline cellulose.
<b>PF02018</b>	17	Carbohydrate binding domain (CBM_4_9)
<b>CBM6</b>	18	Modules of approx. 120 residues. The cellulose-binding function has been demonstrated in one case on amorphous cellulose and beta-1,4-xylan. Some of these modules also bind beta-1,3-glucan, beta-1,3-1,4-glucan, and beta-1,4-glucan.
<b>PF03422</b>	18	Carbohydrate binding module (family 6)
<b>PF02927</b>	17	N-terminal ig-like domain of cellulase
<b>CBM35</b>	17	Modules of approx. 130 residues. A module that is conserved in three Cellvibrio xylan-degrading enzymes binds to xylan and the interaction is calcium dependent, while a module from a Cellvibrio mannanase binds to decorated soluble mannans and mannoooligosaccharides. A module in a
<b>PF00756</b>	13	Putative esterase
<b>PF13472</b>	10	GDSL-like Lipase/Acylhydrolase family

## M1 Histogram

Domain	Description	# runs
PF00150	Cellulase (glycosyl hydrolase family 5)	18
GH43	beta-xylosidase (EC 3.2.1.37); beta-1,3-xylosidase (EC 3.2.1.-); alpha-L-arabin [...]	18
CBM6	Modules of approx. 120 residues. The cellulose-binding function has been demons [...]	18
GH9	endoglucanase (EC 3.2.1.4); cellobiohydrolase (EC 3.2.1.91); beta-glucosidase ( [...]	18
PF03422	Carbohydrate binding module (family 6)	18
GH5	chitosanase (EC 3.2.1.132); beta-mannosidase (EC 3.2.1.25); Cellulase (EC 3.2.1 [...]	17
PF02927	N-terminal ig-like domain of cellulase	17
GH10	endo-1,4-beta-xylanase (EC 3.2.1.8); endo-1,3-beta-xylanase (EC 3.2.1.32)	17
PF00759	Glycosyl hydrolase family 9	17
PF00331	Glycosyl hydrolase family 10	17
PF04616	Glycosyl hydrolases family 43	17
GH26	beta-mannanase (EC 3.2.1.78); beta-1,3-xylanase (EC 3.2.1.32)	17
CBM35	Modules of approx. 130 residues. A module that is conserved in three Cellvibrio [...]	17
PF02018	Carbohydrate binding domain (CBM_4_9)	17
PF02156	Glycosyl hydrolase family 26	17
CBM4	Modules of approx. 150 residues found in bacterial enzymes. Binding of these mo [...]	16
PF00756	Putative esterase	13
PF13472	GDSL-like Lipase/Acylhydrolase family	10
PF00657	GDSL-like Lipase/Acylhydrolase	7
PF00165	Bacterial regulatory helix-turn-helix proteins, AraC family	7
GH94	cellobiose phosphorylase (EC 2.4.1.20); cellodextrin phosphorylase (EC 2.4.1.4 [...]	7
PF06205	Glycosyltransferase 36 associated family	5
PF06165	Glycosyltransferase family 36 (Deleted: now family GH94)	5
GH117	alpha-1,3-L-neoagarooligosaccharide hydrolase (EC 3.2.1.-); alpha-1,3-L-neoagar [...]	5
CBM22	A xylan binding function has been demonstrated in several cases and affinity wi [...]	4
GH16	xyloglucan:xyloglucosyltransferase (EC 2.4.1.207); keratan-sulfate endo-1,4-bet [...]	4
PF06204	Putative carbohydrate binding domain	4
PF01882	Protein of unknown function DUF58	4
GH30	glucosylceramidase (EC 3.2.1.45); beta-1,6-glucanase (EC 3.2.1.75); beta-xylosi [...]	4
PF12833	Helix-turn-helix domain	4
CE3	acetyl xylan esterase (EC 3.1.1.72).	4
PF00722	Glycosyl hydrolases family 16	4
PF06964	Alpha-L-arabinofuranosidase C-terminus	3
GH51	alpha-L-arabinofuranosidase (EC 3.2.1.55); endoglucanase (EC 3.2.1.4)	3
GH8	chitosanase (EC 3.2.1.132); cellulase (EC 3.2.1.4); licheninase (EC 3.2.1.73); [...]	3
GH67	alpha-glucuronidase (EC 3.2.1.139); xylan alpha-1,2-glucuronidase (EC 3.2.1.131)	3
CBM36	Modules of approx. 120-130 residues displaying structural similarities to CBM6 [...]	3
PF01270	Glycosyl hydrolases family 8	3
PF00933	Glycosyl hydrolase family 3 N terminal domain	3
PF08757	CotH protein	2
PF07726	ATPase family associated with various cellular activities (AAA)	2
PF00942	Cellulose binding domain	2
PF13385	Concanavalin A-like lectin/glucanases superfamily	2
GH95	alpha-1,2-L-fucosidase (EC 3.2.1.63); alpha-L-fucosidase (EC 3.2.1.51)	2
GH3	beta-glucosidase (EC 3.2.1.21); xylan 1,4-beta-xylosidase (EC 3.2.1.37); beta-N [...]	2
PF00553	Cellulose binding domain	2
CBM3	Modules of approx. 150 residues found in bacterial enzymes. The cellulose-bindi [...]	2

<b>GH39</b>	alpha-L-iduronidase (EC 3.2.1.76); beta-xylosidase (EC 3.2.1.37).	2
<b>PF01915</b>	Glycosyl hydrolase family 3 C-terminal domain	2
<b>PF07477</b>	Glycosyl hydrolase family 67 C-terminus	2
<b>PF07488</b>	Glycosyl hydrolase family 67 middle domain	2
<b>GH2</b>	beta-galactosidase (EC 3.2.1.23) ; beta-mannosidase (EC 3.2.1.25); beta-glucuro [...]	2
<b>PL1</b>	pectate lyase (EC 4.2.2.2); exo-pectate lyase (EC 4.2.2.9); pectin lyase (EC 4. [...]	2
<b>CBM2</b>	Modules of approx. 100 residues and which are found in a large number of bacter [...]	2
<b>PF02837</b>	Glycosyl hydrolases family 2, sugar binding domain	2
<b>CE2</b>	acetyl xylan esterase (EC 3.1.1.72).	2
<b>PF01055</b>	Glycosyl hydrolases family 31	1
<b>GH124</b>	endoglucanase (EC 3.2.1.4)	1
<b>PF13377</b>	Periplasmic binding protein-like domain	1
<b>GH36</b>	alpha-galactosidase (EC 3.2.1.22); alpha-N-acetylgalactosaminidase (EC 3.2.1.49 [...]	1
<b>PF07745</b>	Glycosyl hydrolase family 53	1
<b>PF00703</b>	Glycosyl hydrolases family 2	1
<b>dockerin</b>		1
<b>PF13407</b>	Periplasmic binding protein domain	1
<b>GH53</b>	endo-beta-1,4-galactanase (EC 3.2.1.89).	1
<b>PF01243</b>	Pyridoxamine 5'-phosphate oxidase	1
<b>PF01841</b>	Transglutaminase-like superfamily	1
<b>GH31</b>	alpha-glucosidase (EC 3.2.1.20); alpha-1,3-glucosidase (EC 3.2.1.84); sucrase-i [...]	1
<b>GH32</b>	invertase (EC 3.2.1.26); endo-inulinase (EC 3.2.1.7); beta-2,6-fructan 6-levanb [...]	1
<b>PF07691</b>	PA14 domain	1
<b>PF00544</b>	Pectate lyase	1
<b>PF02836</b>	Glycosyl hydrolases family 2, TIM barrel domain	1
<b>PF00457</b>	Glycosyl hydrolases family 11	1
<b>PF14310</b>	Fibronectin type III-like domain	1
<b>PF00404</b>	Dockerin type I repeat	1
<b>GH11</b>	xylanase (EC 3.2.1.8)	1
<b>PF00532</b>	Periplasmic binding proteins and sugar binding domain of LacI family	1

## M2 Consensus

Domain	# runs	Description
<b>GH16</b>	16	xyloglucan:xyloglucosyltransferase (EC 2.4.1.207); keratan-sulfate endo-1,4-beta-galactosidase (EC 3.2.1.103); endo-1,3-beta-glucanase (EC 3.2.1.39); endo-1,3(4)-beta-glucanase (EC 3.2.1.6); licheninase (EC 3.2.1.73); beta-agarase (EC 3.2.1.81); kappa;-carrageenase (EC 3.2.1.83); xyloglucanase (EC 3.2.1.151)
<b>PF00722</b>	17	Glycosyl hydrolases family 16
<b>GH30</b>	10	glucosylceramidase (EC 3.2.1.45); beta-1,6-glucanase (EC 3.2.1.75); beta-xylosidase (EC 3.2.1.37); beta-fucosidase (EC 3.2.1.38); beta-glucosidase (3.2.1.21); endo-beta-1,6-galactanase (EC:3.2.1.164)
<b>CBM6</b>	18	Modules of approx. 120 residues. The cellulose-binding function has been demonstrated in one case on amorphous cellulose and beta-1,4-xylan. Some of these modules also bind beta-1,3-glucan, beta-1,3-1,4-glucan, and beta-1,4-glucan.
<b>PF03422</b>	18	Carbohydrate binding module (family 6)
<b>CBM16</b>	16	Carbohydrate-binding module 16. Binding to cellulose and glucomannan demonstrated [B. Bae et al (2008) J Biol Chem. 283:12415-25 (PMID: 18025086)]
<b>CBM35</b>	18	Modules of approx. 130 residues. A module that is conserved in three Cellvibrio xylan-degrading enzymes binds to xylan and the interaction is calcium dependent, while a module from a Cellvibrio mannanase binds to decorated soluble mannans and mannoooligosaccharides. A module in a
<b>CBM61</b>	17	Modules of approx. 150 residues found appended to GH16, GH30, GH31, GH43, GH53 and GH66 catalytic domains. A beta-1,4-galactan binding function has been demonstrated for the CBM60 of <i>Thermotoga maritima</i> GH53 galactanase [PMID: 20826814].
<b>CBM47</b>	17	Modules of approx 150 residues. Fucose-binding activity demonstrated
<b>CBM32</b>	17	Binding to galactose and lactose has been demonstrated for the module of <i>Micromonospora viridifaciens</i> sialidase (PMID: 16239725). Binding to polygalacturonic acid has been shown for a <i>Yersinia</i> member (PMID: 17292916). Binding to LacNAc (beta-D-galactosyl-1,4-beta-D-N-acetylglucosamine) has been shown for an N-acetylglucosaminidase from <i>Clostridium perfringens</i> (PMID: 16990278). (Distantly related to CBM6 modules and to <i>Anguilla anguilla</i> agglutinin.)
<b>CBM13</b>	11	Modules of approx. 150 residues which always appear as a threefold internal repeat. The only apparent exception to this, xylanase II of <i>Actinomadura</i> sp. FC7 (GenBank U08894), is in fact not completely sequenced. These modules were first identified in several plant lectins such as ricin or agglutinin of <i>Ricinus communis</i> which bind galactose residues. The three-dimensional structure of a plant lectin has been determined and displays a pseudo-threefold symmetry in accord with the observed sequence threefold repeat. These modules have since been found in a number of other proteins of various functions including glycoside hydrolases and glycosyltransferases. While in the plant lectins this module binds mannose, binding to xylan has been demonstrated in the <i>Streptomyces lividans</i> xylanase A and arabinofuranosidase B. Binding to GalNAc has been shown for the corresponding module of GalNAc transferase 4. For the other proteins, the binding specificity of these modules has not been established. The pseudo three-fold symmetry of the CBM13 module has now been confirmed in the 3-D structure of the intact, two-domain, xylanase of <i>Streptomyces olivaceoviridis</i> .
<b>PF14200</b>	11	Ricin-type beta-trefoil lectin domain-like
<b>PF00652</b>	11	Ricin-type beta-trefoil lectin domain
<b>GH87</b>	17	mycodextranase (EC 3.2.1.61); alpha-1,3-glucanase (EC 3.2.1.59)
<b>PF00754</b>	17	F5/8 type C domain
<b>PF00041</b>	17	Fibronectin type III domain
<b>GH119</b>	17	alpha-amylase (EC 3.2.1.1) (Distantly related to family GH57)

<b>PF12708</b>	14	Pectate lyase superfamily protein
<b>PF02311</b>	13	AraC-like ligand binding domain
<b>PF02018</b>	13	Carbohydrate binding domain (CBM_4_9)
<b>GH55</b>	12	exo-beta-1,3-glucanase (EC 3.2.1.58); endo-beta-1,3-glucanase (EC 3.2.1.39).
<b>PF13483</b>	9	Beta-lactamase superfamily domain

## M2 Histogram

Domain	Description	# runs
<b>CBM6</b>	Modules of approx. 120 residues. The cellulose-binding function has been demons [...]	18
<b>PF03422</b>	Carbohydrate binding module (family 6)	18
<b>CBM35</b>	Modules of approx. 130 residues. A module that is conserved in three Cellvibrio [...]	18
<b>PF00754</b>	F5/8 type C domain	17
<b>CBM47</b>	Modules of approx 150 residues. Fucose-binding activity demonstrated	17
<b>CBM32</b>	Binding to galactose and lactose has been demonstrated for the module of Microm [...]	17
<b>GH87</b>	mycodextranase (EC 3.2.1.61); alpha-1,3-glucanase (EC 3.2.1.59)	17
<b>PF00041</b>	Fibronectin type III domain	17
<b>PF00722</b>	Glycosyl hydrolases family 16	17
<b>GH119</b>	alpha-amylase (EC 3.2.1.1) (Distantly related to family GH57)	17
<b>CBM61</b>	Modules of approx. 150 residues found appended to GH16, GH30, GH31, GH43, GH53 [...]	17
<b>GH16</b>	xyloglucan:xyloglucosyltransferase (EC 2.4.1.207); keratan-sulfate endo-1,4-bet [...]	16
<b>CBM16</b>	Carbohydrate-binding module 16. Binding to cellulose and glucomannan demonstrat [...]	16
<b>PF12708</b>	Pectate lyase superfamily protein	14
<b>PF02311</b>	AraC-like ligand binding domain	13
<b>PF02018</b>	Carbohydrate binding domain (CBM_4_9)	13
<b>GH55</b>	exo-beta-1,3-glucanase (EC 3.2.1.58); endo-beta-1,3-glucanase (EC 3.2.1.39).	12
<b>PF14200</b>	Ricin-type beta-trefoil lectin domain-like	11
<b>CBM13</b>	Modules of approx. 150 residues which always appear as a threefold internal rep [...]	11
<b>PF00652</b>	Ricin-type beta-trefoil lectin domain	11
<b>GH30</b>	glucosylceramidase (EC 3.2.1.45); beta-1,6-glucanase (EC 3.2.1.75); beta-xylosi [...]	10
<b>PF13483</b>	Beta-lactamase superfamily domain	9
<b>GH18</b>	chitinase (EC 3.2.1.14); endo-beta-N-acetylglucosaminidase (EC 3.2.1.96); xylan [...]	8
<b>PF00704</b>	Glycosyl hydrolases family 18	8
<b>GH109</b>	alpha-N-acetylgalactosaminidase (EC 3.2.1.49)	6
<b>PF02894</b>	Oxidoreductase family, C-terminal alpha/beta domain	6
<b>PF13385</b>	Concanavalin A-like lectin/glucanases superfamily	6
<b>PF13229</b>	Right handed beta helix region	6
<b>PF02055</b>	O-Glycosyl hydrolase family 30	5
<b>PF06271</b>	RDD family	5
<b>PF13527</b>	Acetyltransferase (GNAT) domain	4
<b>PF00801</b>	PKD domain	3
<b>PF00553</b>	Cellulose binding domain	3
<b>PF05721</b>	Phytanoyl-CoA dioxygenase (PhyH)	3
<b>CBM2</b>	Modules of approx. 100 residues and which are found in a large number of bacter [...]	3
<b>CBM4</b>	Modules of approx. 150 residues found in bacterial enzymes. Binding of these mo [...]	3
<b>GH5</b>	chitosanase (EC 3.2.1.132); beta-mannosidase (EC 3.2.1.25); Cellulase (EC 3.2.1 [...]	2
<b>PF01638</b>	HxIR-like helix-turn-helix	2
<b>PF13463</b>	Winged helix DNA-binding domain	2
<b>GH3</b>	beta-glucosidase (EC 3.2.1.21); xylan 1,4-beta-xylosidase (EC 3.2.1.37); beta-N [...]	2
<b>CE3</b>	acetyl xylan esterase (EC 3.1.1.72).	2
<b>PF00165</b>	Bacterial regulatory helix-turn-helix proteins, AraC family	2
<b>PF00933</b>	Glycosyl hydrolase family 3 N terminal domain	2
<b>GH2</b>	beta-galactosidase (EC 3.2.1.23) ; beta-mannosidase (EC 3.2.1.25); beta-glucuro [...]	2
<b>PL9</b>	pectate lyase (EC 4.2.2.2); exopolygalacturonate lyase (EC 4.2.2.9); thiopeptid [...]	2
<b>CBM22</b>	A xylan binding function has been demonstrated in several cases and affinity wi [...]	1
<b>PF08757</b>	CotH protein	1
<b>GH92</b>	mannosyl-oligosaccharide alpha-1,2-mannosidase (EC 3.2.1.113); mannosyl-oligosa [...]	1

<b>PF06205</b>	Glycosyltransferase 36 associated family	1
<b>PF06165</b>	Glycosyltransferase family 36 (Deleted: now family GH94)	1
<b>PF00150</b>	Cellulase (glycosyl hydrolase family 5)	1
<b>PF13377</b>	Periplasmic binding protein-like domain	1
<b>PF00480</b>	ROK family	1
<b>PF06204</b>	Putative carbohydrate binding domain	1
<b>PF00756</b>	Putative esterase	1
<b>PF02927</b>	N-terminal ig-like domain of cellulase	1
<b>GH10</b>	endo-1,4-beta-xylanase (EC 3.2.1.8); endo-1,3-beta-xylanase (EC 3.2.1.32)	1
<b>PF12679</b>	ABC-2 family transporter protein	1
<b>PF00144</b>	Beta-lactamase	1
<b>PF00759</b>	Glycosyl hydrolase family 9	1
<b>PF07971</b>	Glycosyl hydrolase family 92	1
<b>PF00657</b>	GDSL-like Lipase/Acylhydrolase	1
<b>PF00331</b>	Glycosyl hydrolase family 10	1
<b>GH43</b>	beta-xylosidase (EC 3.2.1.37); beta-1,3-xylosidase (EC 3.2.1.-); alpha-L-arabin [...]	1
<b>PF13407</b>	Periplasmic binding protein domain	1
<b>CBM5</b>	Modules of approx. 60 residues found in bacterial enzymes. Chitin-binding descr [...]	1
<b>PF13472</b>	GDSL-like Lipase/Acylhydrolase family	1
<b>PF01522</b>	Polysaccharide deacetylase	1
<b>GT41</b>	UDP-GlcNAc: peptide beta-N-acetylglucosaminyltransferase (EC 2.4.1.94)	1
<b>GH9</b>	endoglucanase (EC 3.2.1.4); cellobiohydrolase (EC 3.2.1.91); beta-glucosidase ( [...]	1
<b>PF03935</b>	Beta-glucan synthesis-associated protein (SKN1)	1
<b>PF13519</b>	von Willebrand factor type A domain	1
<b>CE4</b>	acetyl xylan esterase (EC 3.1.1.72); chitin deacetylase (EC 3.5.1.41); chitool [...]	1
<b>CBM44</b>	The C-terminal CBM44 module of the Clostridium thermocellum enzyme has been dem [...]	1
<b>CBM12</b>	Modules of approx. 40-60 residues. The majority of these modules is found among [...]	1
<b>PF12833</b>	Helix-turn-helix domain	1
<b>PF04616</b>	Glycosyl hydrolases family 43	1
<b>GH94</b>	cellobiose phosphorylase (EC 2.4.1.20); cellodextrin phosphorylase (EC 2.4.1.4 [...]	1
<b>PF01915</b>	Glycosyl hydrolase family 3 C-terminal domain	1
<b>GH26</b>	beta-mannanase (EC 3.2.1.78); beta-1,3-xylanase (EC 3.2.1.32)	1
<b>PF02839</b>	Carbohydrate binding domain	1
<b>GH59</b>	galactocerebrosidase (EC 3.2.1.46)	1
<b>PF00532</b>	Periplasmic binding proteins and sugar binding domain of LacI family	1
<b>PF02156</b>	Glycosyl hydrolase family 26	1
<b>CE7</b>	acetyl xylan esterase (EC 3.1.1.72); cephalosporin-C deacetylase (EC 3.1.1.41).	1
<b>PF00082</b>	Subtilase family	1

### M3 Consensus

Domain	# runs	Description
<b>GH5</b>	18	chitosanase (EC 3.2.1.132); beta-mannosidase (EC 3.2.1.25); Cellulase (EC 3.2.1.4); glucan 1,3-beta-glucosidase (EC 3.2.1.58); licheninase (EC 3.2.1.73); glucan endo-1,6-beta-glucosidase (EC 3.2.1.75); mannan endo-beta-1,4-mannosidase (EC 3.2.1.78); endo-beta-1,4-xylanase (EC 3.2.1.8); cellulose beta-1,4-cellobiosidase (EC 3.2.1.91); beta-1,3-mannanase (EC 3.2.1.-); xyloglucan-specific endo-beta-1,4-glucanase (EC 3.2.1.151); mannan transglycosylase (EC 2.4.1.-); endo-beta-1,6-galactanase (EC 3.2.1.164)
<b>GH43</b>	12	beta-xylosidase (EC 3.2.1.37); beta-1,3-xylosidase (EC 3.2.1.-); alpha-L-arabinofuranosidase (EC 3.2.1.55); arabinanase (EC 3.2.1.99); xylanase (EC 3.2.1.8); galactan 1,3-beta-galactosidase (EC 3.2.1.145)
<b>PF04616</b>	12	Glycosyl hydrolases family 43
<b>PF03629</b>	17	Domain of unknown function (DUF303)
<b>PF01095</b>	18	Pectinesterase
<b>PL1</b>	18	pectate lyase (EC 4.2.2.2); exo-pectate lyase (EC 4.2.2.9); pectin lyase (EC 4.2.2.10).
<b>PF12708</b>	18	Pectate lyase superfamily protein
<b>GH28</b>	18	polygalacturonase (EC 3.2.1.15); exo-polygalacturonase (EC 3.2.1.67); exo-polygalacturonosidase (EC 3.2.1.82); rhamnogalacturonase (EC 3.2.1.-); endo-xylogalacturonan hydrolase (EC 3.2.1.-); rhamnogalacturonan alpha-L-rhamnopyranohydrolase (EC 3.2.1.40)
<b>PF00295</b>	18	Glycosyl hydrolases family 28
<b>CE6</b>	12	acetyl xylan esterase (EC 3.1.1.72).
<b>CE7</b>	18	acetyl xylan esterase (EC 3.1.1.72); cephalosporin-C deacetylase (EC 3.1.1.41).
<b>CE8</b>	18	pectin methylesterase (EC 3.1.1.11).
<b>CE12</b>	18	pectin acetylerase (EC 3.1.1.-); rhamnogalacturonan acetylerase (EC 3.1.1.-); acetyl xylan esterase (EC 3.1.1.72)
<b>PL9</b>	13	pectate lyase (EC 4.2.2.2); exopolygalacturonate lyase (EC 4.2.2.9); thiopeptidoglycan lyase (EC 4.2.2.-).
<b>GH106</b>	16	alpha-L-rhamnosidase (EC 3.2.1.40)
<b>GH88</b>	14	d-4,5 unsaturated beta-glucuronyl hydrolase (EC 3.2.1.-)
<b>PF07470</b>	18	Glycosyl Hydrolase Family 88
<b>GH105</b>	18	unsaturated rhamnogalacturonyl hydrolase (EC 3.2.1.-)
<b>PF00657</b>	18	GDSL-like Lipase/Acylhydrolase
<b>PF13229</b>	18	Right handed beta helix region
<b>GH95</b>	17	alpha-1,2-L-fucosidase (EC 3.2.1.63); alpha-L-fucosidase (EC 3.2.1.51)
<b>PF13472</b>	15	GDSL-like Lipase/Acylhydrolase family
<b>PF13524</b>	13	Glycosyl transferases group 1



### M3 Histogram

Domain	Description	# runs
PF01095	Pectinesterase	18
GH5	chitosanase (EC 3.2.1.132); beta-mannosidase (EC 3.2.1.25); Cellulase (EC 3.2.1 [...]	18
CE12	pectin acetylerase (EC 3.1.1.-); rhamnogalacturonan acetylerase (EC 3.1.1 [...]	18
GH28	polygalacturonase (EC 3.2.1.15); exo-polygalacturonase (EC 3.2.1.67); exo-polyg [...]	18
GH105	unsaturated rhamnogalacturonyl hydrolase (EC 3.2.1.-)	18
PF00657	GDSL-like Lipase/Acylhydrolase	18
PF00295	Glycosyl hydrolases family 28	18
PF07470	Glycosyl Hydrolase Family 88	18
PL1	pectate lyase (EC 4.2.2.2); exo-pectate lyase (EC 4.2.2.9); pectin lyase (EC 4. [...]	18
PF12708	Pectate lyase superfamily protein	18
PF13229	Right handed beta helix region	18
CE7	acetyl xylan esterase (EC 3.1.1.72); cephalosporin-C deacetylase (EC 3.1.1.41).	18
CE8	pectin methylesterase (EC 3.1.1.11).	18
GH95	alpha-1,2-L-fucosidase (EC 3.2.1.63); alpha-L-fucosidase (EC 3.2.1.51)	17
PF03629	Domain of unknown function (DUF303)	17
GH106	alpha-L-rhamnosidase (EC 3.2.1.40)	16
PF13472	GDSL-like Lipase/Acylhydrolase family	15
GH88	d-4,5 unsaturated beta-glucuronyl hydrolase (EC 3.2.1.-)	14
PF13524	Glycosyl transferases group 1	13
PL9	pectate lyase (EC 4.2.2.2); exopolygalacturonate lyase (EC 4.2.2.9); thiopeptid [...]	13
PF04616	Glycosyl hydrolases family 43	12
CE6	acetyl xylan esterase (EC 3.1.1.72).	12
GH43	beta-xylosidase (EC 3.2.1.37); beta-1,3-xylosidase (EC 3.2.1.-); alpha-L-arabin [...]	12
PL11	rhamnogalacturonan lyase (EC 4.2.2.-); exo-unsaturated rhamnogalacturonan lyase [...]	8
PF07944	Putative glycosyl hydrolase of unknown function (DUF1680)	8
GH115	xylan alpha-1,2-glucuronidase (3.2.1.131); alpha-(4-O-methyl)-glucuronidase (3. [...]	7
GH32	invertase (EC 3.2.1.26); endo-inulinase (EC 3.2.1.7); beta-2,6-fructan 6-levanb [...]	6
GH117	alpha-1,3-L-neoagarooligosaccharide hydrolase (EC 3.2.1.-); alpha-1,3-L-neoagar [...]	6
PF13632	Glycosyl transferase family group 2	6
PF07940	Heparinase II/III-like protein	5
GH78	alpha-L-rhamnosidase (EC 3.2.1.40)	5
PF05448	Acetyl xylan esterase (AXE1)	4
GH51	alpha-L-arabinofuranosidase (EC 3.2.1.55); endoglucanase (EC 3.2.1.4)	4
PF06964	Alpha-L-arabinofuranosidase C-terminus	3
PF05592	Bacterial alpha-L-rhamnosidase	3
PF00532	Periplasmic binding proteins and sugar binding domain of LacI family	3
PL12	heparin-sulfate lyase (EC 4.2.2.8)	2
PF00703	Glycosyl hydrolases family 2	2
CBM32	Binding to galactose and lactose has been demonstrated for the module of Microm [...]	2
PF07495	Y_Y_Y domain	2
GH97	alpha-glucosidase (EC 3.2.1.20); alpha-galactosidase (EC 3.2.1.22)	2
PF00756	Putative esterase	1
PF08666	SAF domain	1
PF02836	Glycosyl hydrolases family 2, TIM barrel domain	1
PF01263	Aldose 1-epimerase	1
GH55	exo-beta-1,3-glucanase (EC 3.2.1.58); endo-beta-1,3-glucanase (EC 3.2.1.39).	1
GH2	beta-galactosidase (EC 3.2.1.23) ; beta-mannosidase (EC 3.2.1.25); beta-glucuro [...]	1

<b>PL17</b>	alginate lyase (EC 4.2.2.3).	1
<b>PF02837</b>	Glycosyl hydrolases family 2, sugar binding domain	1
<b>PF08531</b>	Alpha-L-rhamnosidase N-terminal domain	1
<b>PF13407</b>	Periplasmic binding protein domain	1

#### M4 Consensus

Domain	# runs	Description
<b>GH5</b>	18	chitosanase (EC 3.2.1.132); beta-mannosidase (EC 3.2.1.25); Cellulase (EC 3.2.1.4); glucan 1,3-beta-glucosidase (EC 3.2.1.58); licheninase (EC 3.2.1.73); glucan endo-1,6-beta-glucosidase (EC 3.2.1.75); mannan endo-beta-1,4-mannosidase (EC 3.2.1.78); endo-beta-1,4-xylanase (EC 3.2.1.8); cellulose beta-1,4-cellobiosidase (EC 3.2.1.91); beta-1,3-mannanase (EC 3.2.1.-); xyloglucan-specific endo-beta-1,4-glucanase (EC 3.2.1.151); mannan transglycosylase (EC 2.4.1.-); endo-beta-1,6-galactanase (EC 3.2.1.164)
<b>PF00150</b>	13	Cellulase (glycosyl hydrolase family 5)
<b>GH43</b>	16	beta-xylosidase (EC 3.2.1.37); beta-1,3-xylosidase (EC 3.2.1.-); alpha-L-arabinofuranosidase (EC 3.2.1.55); arabinanase (EC 3.2.1.99); xylanase (EC 3.2.1.8); galactan 1,3-beta-galactosidase (EC 3.2.1.145)
<b>PF04616</b>	15	Glycosyl hydrolases family 43
<b>GH2</b>	18	beta-galactosidase (EC 3.2.1.23) ; beta-mannosidase (EC 3.2.1.25); beta-glucuronidase (EC 3.2.1.31); mannosylglycoprotein endo-beta-mannosidase (EC 3.2.1.152); exo-beta-glucosaminidase (EC 3.2.1.165)
<b>PF02836</b>	18	Glycosyl hydrolases family 2, TIM barrel domain
<b>PF00703</b>	18	Glycosyl hydrolases family 2
<b>PF02837</b>	18	Glycosyl hydrolases family 2, sugar binding domain
<b>GH3</b>	18	beta-glucosidase (EC 3.2.1.21); xylan 1,4-beta-xylosidase (EC 3.2.1.37); beta-N-acetylhexosaminidase (EC 3.2.1.52); glucan 1,3-beta-glucosidase (EC 3.2.1.58); glucan 1,4-beta-glucosidase (EC 3.2.1.74); exo-1,3,1,4-glucanase (EC 3.2.1.-); alpha-L-arabinofuranosidase (EC 3.2.1.55).
<b>PF01915</b>	18	Glycosyl hydrolase family 3 C-terminal domain
<b>PF00933</b>	18	Glycosyl hydrolase family 3 N terminal domain
<b>GH35</b>	9	beta-galactosidase (EC 3.2.1.23); exo-beta-glucosaminidase (EC 3.2.1.165)
<b>PF02449</b>	10	Beta-galactosidase
<b>GH42</b>	10	beta-galactosidase (EC 3.2.1.23)
<b>PF02065</b>	17	Melibiose (GH27) [GH-D clan, a superfamily of alpha-galactosidases]
<b>GH31</b>	18	alpha-glucosidase (EC 3.2.1.20); alpha-1,3-glucosidase (EC 3.2.1.84); sucrase-isomaltase (EC 3.2.1.48) (EC 3.2.1.10); alpha-xylosidase (EC 3.2.1.-); alpha-glucan lyase (EC 4.2.2.13); isomaltosyltransferase (EC 2.4.1.-). [GH-D clan, a superfamily of alpha-galactosidases]
<b>PF01055</b>	18	Glycosyl hydrolases family 31
<b>GH36</b>	17	alpha-galactosidase (EC 3.2.1.22); alpha-N-acetylgalactosaminidase (EC 3.2.1.49); stachyose synthase (EC 2.4.1.67); raffinose synthase (EC 2.4.1.82) [GH-D clan, a superfamily of alpha-galactosidases]
<b>PF14310</b>	18	Fibronectin type III-like domain
<b>PF07859</b>	15	alpha/beta hydrolase fold
<b>CE10</b>	14	arylesterase (EC 3.1.1.-); carboxyl esterase (EC 3.1.1.3); acetylcholinesterase (EC 3.1.1.7); cholinesterase (EC 3.1.1.8); sterol esterase (EC 3.1.1.13); brefeldin A esterase (EC 3.1.1.-).
<b>GH32</b>	12	invertase (EC 3.2.1.26); endo-inulinase (EC 3.2.1.7); beta-2,6-fructan 6-levanbiohydrolase (EC 3.2.1.64); endo-levanase (EC 3.2.1.65); exo-inulinase (EC 3.2.1.80); fructan beta-(2,1)-fructosidase/1-exohydrolase (EC 3.2.1.153); fructan beta-(2,6)-fructosidase/6-exohydrolase (EC 3.2.1.154); sucrose:sucrose 1-fructosyltransferase (EC 2.4.1.99); fructan:fructan 1-fructosyltransferase (EC 2.4.1.100); sucrose:fructan 6-fructosyltransferase (EC 2.4.1.10); fructan:fructan 6G-fructosyltransferase (EC 2.4.1.243); levan fructosyltransferase (EC 2.4.1.-)
<b>PF00135</b>	10	Carboxylesterase family
<b>PF13802</b>	9	Galactose mutarotase-like
<b>GH106</b>	9	alpha-L-rhamnosidase (EC 3.2.1.40)

## M4 Histogram

Domain	Description	# runs
PF01055	Glycosyl hydrolases family 31	18
GH5	chitinase (EC 3.2.1.132); beta-mannosidase (EC 3.2.1.25); Cellulase (EC 3.2.1 [...]	18
GH31	alpha-glucosidase (EC 3.2.1.20); alpha-1,3-glucosidase (EC 3.2.1.84); sucrase-i [...]	18
PF02836	Glycosyl hydrolases family 2, TIM barrel domain	18
PF01915	Glycosyl hydrolase family 3 C-terminal domain	18
PF00933	Glycosyl hydrolase family 3 N terminal domain	18
PF00703	Glycosyl hydrolases family 2	18
GH2	beta-galactosidase (EC 3.2.1.23) ; beta-mannosidase (EC 3.2.1.25); beta-glucuro [...]	18
PF14310	Fibronectin type III-like domain	18
GH3	beta-glucosidase (EC 3.2.1.21); xylan 1,4-beta-xylosidase (EC 3.2.1.37); beta-N [...]	18
PF02837	Glycosyl hydrolases family 2, sugar binding domain	18
PF02065	Melibiose (GH27) [GH-D clan, a superfamily of alpha-galactosidases]	17
GH36	alpha-galactosidase (EC 3.2.1.22); alpha-N-acetylgalactosaminidase (EC 3.2.1.49 [...]	17
GH43	beta-xylosidase (EC 3.2.1.37); beta-1,3-xylosidase (EC 3.2.1.-); alpha-L-arabin [...]	16
PF04616	Glycosyl hydrolases family 43	15
PF07859	alpha/beta hydrolase fold	15
CE10	arylesterase (EC 3.1.1.-); carboxyl esterase (EC 3.1.1.3); acetylcholinesteras [...]	14
PF00150	Cellulase (glycosyl hydrolase family 5)	13
GH32	invertase (EC 3.2.1.26); endo-inulinase (EC 3.2.1.7); beta-2,6-fructan 6-levanb [...]	12
PF02449	Beta-galactosidase	10
GH42	beta-galactosidase (EC 3.2.1.23)	10
PF00135	Carboxylesterase family	10
PF13802	Galactose mutarotase-like	9
GH35	beta-galactosidase (EC 3.2.1.23); exo-beta-glucosaminidase (EC 3.2.1.165)	9
GH106	alpha-L-rhamnosidase (EC 3.2.1.40)	9
PF08532	Beta-galactosidase trimerisation domain	8
PF00165	Bacterial regulatory helix-turn-helix proteins, AraC family	7
GH51	alpha-L-arabinofuranosidase (EC 3.2.1.55); endoglucanase (EC 3.2.1.4)	7
GH78	alpha-L-rhamnosidase (EC 3.2.1.40)	7
GH27	alpha-galactosidase (EC 3.2.1.22); alpha-N-acetylgalactosaminidase (EC 3.2.1.49 [...]	7
PF02929	Beta galactosidase small chain	7
PF06964	Alpha-L-arabinofuranosidase C-terminus	6
PF12833	Helix-turn-helix domain	6
PF05592	Bacterial alpha-L-rhamnosidase	6
PF02311	AraC-like ligand binding domain	6
PF08533	Beta-galactosidase C-terminal domain	5
PF07944	Putative glycosyl hydrolase of unknown function (DUF1680)	5
PF08531	Alpha-L-rhamnosidase N-terminal domain	5
GH39	alpha-L-iduronidase (EC 3.2.1.76); beta-xylosidase (EC 3.2.1.37).	4
PF00532	Periplasmic binding proteins and sugar binding domain of LacI family	4
PF13407	Periplasmic binding protein domain	4
PF00596	Class II Aldolase and Adducin N-terminal domain	3
PF13377	Periplasmic binding protein-like domain	3
PF01301	Glycosyl hydrolases family 35	3
GH1	beta-glucosidase (EC 3.2.1.21); beta-galactosidase (EC 3.2.1.23); beta-mannosid [...]	3
PF00356	Bacterial regulatory proteins, lacI family	3
PF00480	ROK family	2

<b>PF00756</b>	Putative esterase	2
<b>PF00251</b>	Glycosyl hydrolases family 32 N-terminal domain	2
<b>PF00232</b>	Glycosyl hydrolase family 1	2
<b>PF04397</b>	LytTr DNA-binding domain	2
<b>PF10509</b>	Galactokinase galactose-binding signature	1
<b>PF02397</b>	Bacterial sugar transferase	1
<b>PF01074</b>	Glycosyl hydrolases family 38 N-terminal domain	1
<b>GH117</b>	alpha-1,3-L-neoagarooligosaccharide hydrolase (EC 3.2.1.-); alpha-1,3-L-neoagar [...]	1
<b>PF09261</b>	Alpha mannosidase, middle domain	1
<b>PF01757</b>	Acyltransferase family	1
<b>PF13524</b>	Glycosyl transferases group 1	1
<b>PF01663</b>	Type I phosphodiesterase / nucleotide pyrophosphatase	1
<b>PF01263</b>	Aldose 1-epimerase	1
<b>PF02614</b>	Glucuronate isomerase	1
<b>PF07748</b>	Glycosyl hydrolases family 38 C-terminal domain	1
<b>GH38</b>	alpha-mannosidase (EC 3.2.1.24) ; mannosyl-oligosaccharide alpha-1,3-1,6-mannos [...]	1
<b>PF06580</b>	Histidine kinase	1
<b>PF13472</b>	GDSL-like Lipase/Acylhydrolase family	1

## M5 Consensus

Domain	# runs	Description
<b>PF00942</b>	16	Cellulose binding domain
<b>GH124</b>	16	endoglucanase (EC 3.2.1.4)
<b>CBM3</b>	16	Modules of approx. 150 residues found in bacterial enzymes. The cellulose-binding function has been demonstrated in many cases. In one instance binding to chitin has been reported.
<b>dockerin</b>		
<b>PF00404</b>	16	Dockerin type I repeat
<b>cohesin</b>		
<b>PF00963</b>	16	Cohesin domain
<b>PF07591</b>	16	Pretoxin HINT domain
<b>PF13186</b>	16	Domain of unknown function (DUF4008)
<b>CBM36</b>	15	Modules of approx. 120-130 residues displaying structural similarities to CBM6 modules. The only CBM36 currently characterised, that from <i>Paenbacillus polymyxa</i> xylanase 43A, shows calcium-dependent binding of xylans and xylooligosaccharides. X-ray crystallography shows that there is a direct interaction between calcium and ligand.
<b>PF05593</b>	12	RHS Repeat
<b>PF07238</b>	10	PilZ domain
<b>PF13403</b>	9	Hint domain

## M5 Histogram

Domain	Description	# runs
<b>PF00942</b>	Cellulose binding domain	16
<b>GH124</b>	endoglucanase (EC 3.2.1.4)	16
<b>PF00404</b>	Dockerin type I repeat	16
<b>CBM3</b>	Modules of approx. 150 residues found in bacterial enzymes. The cellulose-bindi [...]	16
<b>dockerin</b>		16
<b>cohesin</b>		16
<b>PF07591</b>	Pretoxin HINT domain	16
<b>PF13186</b>	Domain of unknown function (DUF4008)	16
<b>PF00963</b>	Cohesin domain	16
<b>CBM36</b>	Modules of approx. 120-130 residues displaying structural similarities to CBM6 [...]	15
<b>PF05593</b>	RHS Repeat	12
<b>PF07238</b>	PilZ domain	10
<b>PF13403</b>	Hint domain	9
<b>PF00759</b>	Glycosyl hydrolase family 9	7
<b>GH9</b>	endoglucanase (EC 3.2.1.4); cellobiohydrolase (EC 3.2.1.91); beta-glucosidase ( [...]	7
<b>PF01584</b>	CheW-like domain	5
<b>PF12791</b>	Anti-sigma factor N-terminus	5
<b>CBM35</b>	Modules of approx. 130 residues. A module that is conserved in three Cellvibrio [...]	5
<b>PF12833</b>	Helix-turn-helix domain	4
<b>PF03422</b>	Carbohydrate binding module (family 6)	2
<b>PF12730</b>	ABC-2 family transporter protein	2
<b>PF00150</b>	Cellulase (glycosyl hydrolase family 5)	2
<b>GH5</b>	chitosanase (EC 3.2.1.132); beta-mannosidase (EC 3.2.1.25); Cellulase (EC 3.2.1 [...]	2
<b>PF00239</b>	Resolvase, N terminal domain	2
<b>PF02018</b>	Carbohydrate binding domain (CBM_4_9)	2
<b>PF13231</b>	Dolichyl-phosphate-mannose-protein mannosyltransferase	2
<b>CBM6</b>	Modules of approx. 120 residues. The cellulose-binding function has been demons [...]	1
<b>PF07508</b>	Recombinase	1
<b>PF01797</b>	Transposase IS200 like	1

### PUL module consensus

Domain	# runs	Description
<b>PF07980</b>	17	SusD family
<b>PF00593</b>	17	TonB dependent receptor
<b>PF07715</b>	17	TonB-dependent Receptor Plug Domain
<b>PF14322</b>	17	Starch-binding associating with outer membrane
<b>PF13715</b>	17	Cna protein B-type domain
<b>PF13620</b>	16	Carboxypeptidase regulatory-like domain
<b>PF13568</b>	13	Outer membrane protein beta-barrel domain
<b>PF00691</b>	13	OmpA family
<b>PF13505</b>	12	Outer membrane protein beta-barrel domain
<b>PF02321</b>	11	Outer membrane efflux protein



## PUL module histogram

Domain	Description	# runs
PF07980	SusD family	17
PF00593	TonB dependent receptor	17
PF07715	TonB-dependent Receptor Plug Domain	17
PF14322	Starch-binding associating with outer membrane	17
PF13715	Cna protein B-type domain	17
PF13620	Carboxypeptidase regulatory-like domain	16
PF13568	Outer membrane protein beta-barrel domain	13
PF00691	OmpA family	13
PF13505	Outer membrane protein beta-barrel domain	12
PF02321	Outer membrane efflux protein	11
PF12833	Helix-turn-helix domain	7
PF01551	Peptidase family M23	5
PF00165	Bacterial regulatory helix-turn-helix proteins, AraC family	5
PF03544	Gram-negative bacterial tonB protein	4
GT41	UDP-GlcNAc: peptide beta-N-acetylglucosaminyltransferase (EC 2.4.1.94)	4
PF13437	HlyD family secretion protein	4
PF12700	HlyD family secretion protein	4
CE10	arylesterase (EC 3.1.1.-); carboxyl esterase (EC 3.1.1.3); acetylcholinesteras [...]	3
PF13533	Biotin-lipoyl like	2
PF00529	HlyD family secretion protein	1
PF14289	Domain of unknown function (DUF4369)	1
PF13187	4Fe-4S dicluster domain	1
PF00873	AcrB/AcrD/AcrF family	1
PF12771	Starch-binding associating with outer membrane	1
PF03572	Peptidase family S41	1
PF00196	Bacterial regulatory proteins, luxR family	1
PF12741	Susd and RagB outer membrane lipoprotein	1
PF00082	Subtilase family	1