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OVERVIEW

HOW TO USE THIS CATALOGUE?

In this catalogue CAZymes are grouped by enzyme activity. There are > 80 different enzyme categories to list >1000 CAZymes.

Enzyme

Refers to the enzyme name following the suggested nomenclature for CAZymes as described by Henrissat B. *et al.* (1998) FEBS Lett 425:352-354.

EC Number

The Enzyme Commission number (EC number) is a numerical classification scheme for enzymes, based on the chemical reactions they catalyze.

Source Organism

Refers to the host organism from which the enzyme was isolated. All enzymes in this catalogue have a recombinant origin and are produced either in Pichia pastoris or Escherichia coli.

ACETYLGALACTOSAMINIDASES

β-N-Acetylgalactosaminidases are enzymes that participate in the hydrolysis of terminal non-reducing N-acetyl-D-galactosamine residues in N-acetyl-β-D-galactosaminides. α-N-Acetylgalactosaminidases are enzymes that cleave non-reducing 1,3-α-N-acetylgalactosamine residues from human blood group A and AB mucin glycoproteins.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (ºC)	mg/ vial
CZ0515	β-N-Acetylgalactosaminidase 123A	*Paenibacillus sp.*	GH123	3.2.1.53	6.0	37	0.25

Catalogue Number

Specifies the CAZyme catalogue number.

mg/vial

Specifies the number of mg of purified CAZyme provided per vial. NZYTech sells one vial with 1 mL at 158€ and three vials at 349€.

CAZy Architecture

Refers to the CAZy family and enzyme molecular architecture.

Temperature and pH

Reported optima temperature and pH for enzyme activity as described in the literature

NZYTECH CAZYMES ARE AVAILABLE UP TO THE GRAM SCALE AND IN PLATES

NZYTech highly pure CAZymes are provided in the mg scale (1 vial at 158€ or 3 vials at 349€). If you require larger quantities of any of the enzymes listed in this catalogue, up to the 500 gram scale, please contact us. You will have access to large quantities of the enzyme produced and purified to meet the same quality standards.

In case you want to test a large number of enzymes simultaneously, NZYTech can provide a fraction or even all the enzymes listed in this catalogue in plates. Contact us in case you want to receive the enzymes in plates. Price per plate containing 50 µL of 96 enzymes starts at 1.999€.

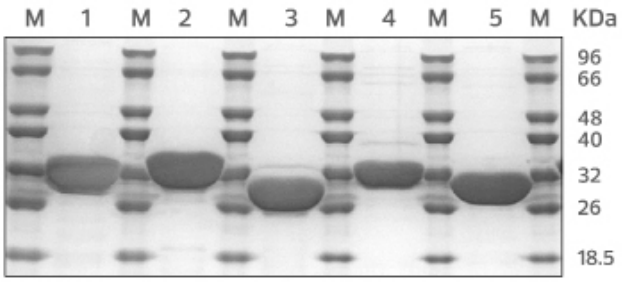
NZYTECH CAZYMES: HIGHLY PURE, STABLE AND OPTIMIZED RESEARCH TOOLS FOR SCIENCE AND INDUSTRY

1. A LARGE AND DIVERSE PORTFOLIO OF RECOMBINANT ENZYMES

NZYTech R&D department, individually or in collaboration with the CAZy community, is building a large and diverse portfolio of research enzymes to foster science and industrial progress. All enzymes have a recombinant origin and are produced and purified from *Pichia pastoris* or *Escherichia coli.* In this catalogue you will find more than 1000 CAZymes, covering >200 CAZy families (www.cazy.com) and >150 EC number activities (www.enzyme.expasy.org).

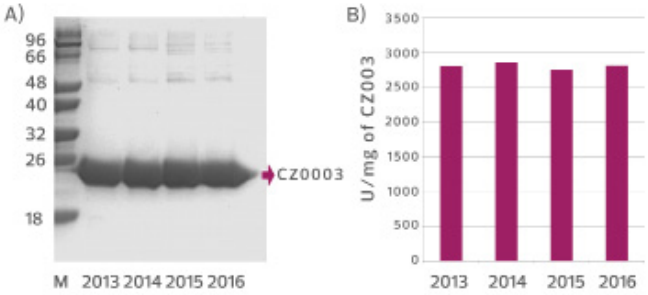
2. ULTRA-PURE ENZYMES FOR A VARIETY OF APPLICATIONS

NZYTech CAZymes are purified using a comprehensive list of chromatography protocols to achieve the highest level of protein purity. As an example, the figure below provides an SDS-PAGE analysis of CAZymes (1)CZ0604, (2) CZ0580, (3) CZ0621, (4) CZ0633, (5) CZ0641 and (M) Low Molecular Weight (LMW) Protein Marker (MB082). Purification level of all CAZymes listed in this catalogue may be found at NZYTech website (www.nzytech.com).



3. REDUCED BATCH-TO-BATCH VARIATION AND LONG STORAGE STABILITY

NZYTech devotes significant efforts to minimize batch to batch variation and improve enzyme stability. In the Figure below 4 batches of Xylanase 11A from *Clostridium thermocellum* (CZ0003), produced in 2013, 2014, 2015 and 2016, were tested in March 2018 for molecular integrity, protein purity and enzyme activity. The data reveals that there is minimal variation in molecular integrity (Panel A) and activity (Panel B) between batches while stability is reflected by retention of full enzyme activity up to 5 years after production (Panel B). Thus, it is important to follow the storage guidelines provided for each enzyme.



4. NZYTECH CAZYMES ARE THROUGHLY CHARACTERIZED AND THEIR BIOCHEMICAL PROPERTIES DESCRIBED IN LITERATURE

The majority of NZYTech CAZymes display well-defined enzyme properties that are described in the literature. Reference of the paper describing the properties of the different enzymes is provided at www.nzytech.com or in the technical instructions that accompany each enzyme. Having available well described enzymes allows you selecting the catalysts that are more suited to your application and/or experiment.

glycoside hydrolases

ACETYLGALACTOSAMINIDASES
ACETYLGLUCOSAMINIDASES
AGARASES
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GALACTANASES
α-GALACTOSIDASES
β-GALACTOSIDASES
PHOSPHO-β-GALACTOSIDASES
β-D-GALACTOSYL-1,4-L-RHAMNOSE PHOSPHORYLASES
GALACTOSYL-N-ACETYLHEXOSAMINE PHOSPHORYLASES
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GLUCANSUCRASES
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GLUCURONIDASES
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LEVANASES
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LICHENASES
LYSOZYMES
α-MANNANASES
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MANNOSYLGLUCOSE PHOSPHORYLASES
OLIGOSACCHARIDE REDUCING-END XYLANASES
PEPTIDOGLYCAN LYTIC EXOTRANSGLYCOSYLASES
POLYGALACTURONASES
PORPHYRANASES
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SIALIDASES
TREHALASES
Δ-4,5-UNSATURATED β-GLUCURONYL HYDROLASES
XYLANASES
XYLOGLUCANASES
XYLOSIDASES
OTHER ACTIVITIES

* Structure of Cellulase 5B from *Bacillus halodurans* (PDB 4V2X), #CZ0476, pg 17

ACETYLGALACTOSAMINIDASES

β-N-Acetylgalactosaminidases are enzymes that participate in the hydrolysis of terminal non-reducing N-acetyl-D-galactosamine residues in N-acetyl-β-D-galactosaminides. α-N-Acetylgalactosaminidases are enzymes that cleave non-reducing 1,3-α-N-acetylgalactosamine residues from human blood group A and AB mucin glycoproteins.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0515	β-N-Acetylgalactosaminidase 123A	*Paenibacillus sp.*	GH123	3.2.1.53	6,0	37	0,25
CZ0543	α-N-Acetylgalactosaminidase 129A	*Bifidobacterium bifidum*	GH129	3.2.1.49	5,0	37	1
CZ0821	α-N-Acetylgalactosaminidase 109A	*Elizabethkingia meningoseptica*	GH109	3.2.1.49	6,8	26	0,25
CZ0955	Endo-α-N-acetylgalactosaminidase 101A	*Clostridium perfringens*	GH101	3.2.1.97	6,0	60	0,5
CZ0969	Endo-α-N-acetylgalactosaminidase 101A	*Bifidobacterium longum*	GH101	3.2.1.97	7,0	30	1

ACETYLGLUCOSAMINIDASES

β-N-Acetylglucosaminidases are highly specific glycoside hydrolases that catalyze the hydrolysis of β-N-acetylglucosamine residues from oligosaccharides and peptidoglycans.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0106	β-Acetylglucosaminidase 18A	*Bacteroides thetaiotaomicron*	GH18	3.2.1.96	7,5	37	1
CZ0229	β-Acetylglucosaminidase 73A	*Clostridium perfringens*	GH73	3.2.1.-	8,0	37	0,25
CZ0428	β-Acetylglucosaminidase 73A	*Lactococcus lactis*	GH73	3.2.1.-	6,8	35	1
CZ0572	Keratan sulfate Endo-N-acetylglucosaminidase 111A	*Bacillus circulans*	GH111	3.2.1.-	6,0	55	0,5
CZ0798	β-N-Acetylglucosaminidase 84A	*Bacteroides thetaiotaomicron*	GH84-CBM32	3.2.1.169	6,0	37	0,5
CZ0824	β-Acetylglucosaminidase 18A	*Elizabethkingia meningoseptica*	GH18	3.2.1.96	7,5	50	0,25
CZ0828	β-Acetylglucosaminidase 18A	*Capnocytophaga canimorsus*	GH18	3.2.1.96	6,5-7,5	37	0,25
CZ0829	β-Acetylglucosaminidase 18A	*Bacillus anthracis*	CBM50-CBM50-GH18	3.2.1.-	6,5-7,5	37	0,25
CZ0830	β-Acetylglucosaminidase 73A	*Streptococcus pneumoniae*	GH73	3.2.1.-	6,5-7,5	37	0,5
CZ0831	β-Acetylglucosaminidase 18A	*Streptococcus pyogenes*	GH18	3.2.1.96	6,5-7,5	37	0,5
CZ0832	β-Acetylglucosaminidase 18A	*Bacillus megaterium*	CBM50-CBM50-GH18	3.2.1.-	6,5-7,5	37	0,25
CZ0833	β-Acetylglucosaminidase 73A	*Clostridium difficile*	GH73	3.2.1.-	8,0	37	0,25
CZ0835	β-Acetylglucosaminidase 73B	*Lactococcus lactis*	GH73	3.2.1.-	4,0-5,0	37	1
CZ0837	β-Acetylglucosaminidase 18A	*Enterococcus faecalis*	GH18	3.2.1.96	6,0-7,0	37	1
CZ0840	β-Acetylglucosaminidase 73A	*Lactobacillus plantarum*	GH73	3.2.1.-	6,5-7,5	37	0,25
CZ0879	β-Acetylglucosaminidase 18A	*Flavobacterium sp.*	GH18	3.2.1.96	6,0-8,0	37	0,5
CZ0891	β-Acetylglucosaminidase 18B	*Streptomyces plicatus*	GH18	3.2.1.96	5,0-6,0	37	1
CZ0893	β-Acetylglucosaminidase 18B	*Elizabethkingia meningoseptica*	GH18	3.2.1.96	7,0-8,0	35	1
CZ0976	β-Acetylglucosaminidase 85A	*Streptococcus pneumoniae*	GH85	3.2.1.96	7,0-8,0	37	1

AGARASES

Agarases are the first enzymes in the agar catabolic pathway and degrade both α or β linkages in agarose.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0407	α-Neoagarobiose hydrolase 117A	*Zobellia galactanivorans*	GH117	3.2.1.-	7,5	20	1
CZ0453	β-Agarase 16D	*Zobellia galactanivorans*	GH16	3.2.1.81	7,0	20-30	0,25
CZ0517	β-Agarase 118A	*Bacteroides plebeius*	GH118	3.2.1.81	6,0	40	0,25
CZ0537	α-Agarase 117A	*Bacteroides plebeius*	GH117	3.2.1.-	7,0	25	1
CZ0538	β-Agarase 16A	*Bacteroides plebeius*	GH16	3.2.1.81	7,0	20	1
CZ0562	β-Agarase 50D	*Saccharophagus degradans*	GH50	3.2.1.81	7,0	30	1
CZ0733	β-Agarase 16B	*Bacteroides uniformis*	GH16	3.2.1.81	8,0	37	1
CZ0736	β-Agarase 16A	*Microbulbifer thermotolerans*	GH16-CBM6	3.2.1.81	7,0	55	0,5
CZ0738	β-Agarase 86A	*Bacteroides uniformis*	GH86	3.2.1.81	8,0	37	1
CZ0739	α-Neoagarobiose hydrolase 117A	*Bacteroides uniformis*	GH117	3.2.1.-	8,0	37	1
CZ0741	β-Agarase 50A	*Bacteroides ovatus*	GH50	3.2.1.81	6,5-7,5	37	1
CZ0743	α-Neoagarobiose hydrolase 117A	*Saccharophagus degradans*	GH117	3.2.1.-	7,5	37	1
CZ0747	β-Agarase 16A	*Janthinobacterium sp.*	GH16	3.2.1.81	7,0	40	0,5
CZ0749	β-Agarase 16B	*Zobellia galactanivorans*	GH16	3.2.1.81	7,0	44	1
CZ0750	α-Neoagarobiose hydrolase 117B	*Zobellia galactanivorans*	GH117	3.2.1.-	6,5-7,5	37	0,5
CZ0751	α-Neoagarobiose hydrolase 117C	*Zobellia galactanivorans*	GH117	3.2.1.-	6,5-7,5	37	1
CZ0764	β-Agarase 50A	*Saccharophagus degradans*	GH50	3.2.1.81	8,0	42	0,5

AMYLASES

Amylases are enzymes that catalyze the hydrolysis of starch and glycogen into sugars by acting on α-glycosidic bonds. Due to the importance of starch as a carbon and energy source, amylases are highly ubiquitous enzymes in nature being produced by animals, plants and microbes.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0152	Glucoamylase 97A	*Bacteroides thetaiotaomicron*	GH97	3.2.1.3	4,0-12,0	45	1
CZ0165	Amylase 13A	*Escherichia coli*	GH13	3.2.1.1	7,0	55	1
CZ0230	Amylase 57C	*Thermotoga maritima*	GH57	3.2.1.1	8,5	90	1
CZ0234	Amylase 126A	*Clostridium perfringens*	GH126	3.2.1.-	7,0	37	1
CZ0263	Amylase 13A	*Streptococcus mutans*	GH13	3.2.1.1	7,5	37	1
CZ0297	Amylase 13A	*Bacillus licheniformis*	GH13	3.2.1.1	7,0-8,0	40	1
CZ0317	Maltogenic α-amylase 13A	*Lactobacillus gasseri*	GH13	3.2.1.133	5,0	55	0,25
CZ0394	Maltogenic α-amylase 13A	*Thermotoga neapolitana*	GH13	3.2.1.133	6,5	75	1
CZ0549	β-Amylase 14A	*Bacillus circulans*	GH14	3.2.1.2	7,0	50	0,5

AMYLASES (CONT.)

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0552	β-Amylase 14B	*Bacillus cereus*	GH14	3.2.1.2	7,0	25	0,5
CZ0561	Amylase 13A	*Paenibacillus polymyxa*	GH13	3.2.1.1	6,0	50	0,25
CZ0758	Amylase 13A	*Thermotoga maritima*	GH13	3.2.1.1	7,0	85-90	1
CZ0759	Amylase 13B	*Thermotoga maritima*	GH13	3.2.1.1	7,0	70	1
CZ0931	Glucoamylase 15A	*Thermoactinomyces vulgaris*	GH15	3.2.1.3	6,5-7,5	60	0,5
CZ0961	Isoamylase 13A	*Escherichia coli*	CBM48-GH13	3.2.1.68	5,0	37	0,25

AMYLOMALTASES

Amylomaltases, also termed 4-α-glucanotransferases, are enzymes that transfer a segment of a 1,4-α-D-glucan to a new position in an acceptor, which may be glucose or a 1,4-α-D-glucan.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0219	Amylomaltase 13B	*Thermotoga maritima*	GH13	2.4.1.25	6,5	85	1
CZ0220	Amylomaltase 13A	*Thermotoga maritima*	GH13	2.4.1.25	7,0-8,0	70	0,25
CZ0254	Amylomaltase 77A	*Thermus thermophilus*	GH77	2.4.1.25	8,0	70	1
CZ0393	Amylomaltase 13A	*Thermotoga neapolitana*	GH13	2.4.1.25	7,0	65	1
CZ0419	Amylomaltase 57A	*Pyrococcus furiosus*	GH57	2.4.1.25	7,0	90-100	1
CZ0690	Amylomaltase 77A	*Saccharophagus degradans*	GH77	2.4.1.25	6,0	40	0,25
CZ0799	Amylomaltase 77A	*Escherichia coli*	GH77	2.4.1.25	7,0	37	1

ARABINANASES

Arabinanases hydrolyze the 1,5-α-linked L-arabinofuranoside backbone of plant cell wall arabinans.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0191	Arabinanase 43A	*Bacteroides thetaiotaomicron*	GH43	3.2.1.99	7,0	37	1
CZ0806	Arabinanase 43A	*Bacillus subtilis*	GH43	3.2.1.99	6,5-7,5	37	1
CZ0844	Arabinanase 51A	*Bacteroides thetaiotaomicron*	CBM22-GH51	3.2.1.99	6,5-7,5	37	1
CZ0902	Arabinanase 43A	*Ruminococcus champanellensis*	GH43-CBM61-doc	3.2.1.99	6,0	37	1
CZ0904	Arabinanase 43D	*Ruminococcus champanellensis*	GH43-CBM13	3.2.1.99	6,0	37	0,5
CZ0968	Arabinanase 43A	*Thermotoga petrophila*	GH43	3.2.1.99	6,0	73	1
CZ1004	Arabinanase 43B	*Bacteroides thetaiotaomicron*	GH43	3.2.1.99	6,5-7,5	37	0,25
CZ1027	Arabinanase 43B	*Bacillus subtilis*	GH43	3.2.1.99	6,6	37	0,25

ARABINOFURANOSIDASES

Arabinofuranosidases are exo-acting enzymes that remove α-L-arabinosides from α-L-arabinofuranosides, α-L-arabinans containing 1,3- and/or 1,5-linkages, arabinoxylans and arabinogalactans.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0024	Arabinofuranosidase 51A	*Clostridium thermocellum*	GH51	3.2.1.55	6,0-8,0	65	1
CZ0136	Arabinofuranosidase 43A	*Bacteroides thetaiotaomicron*	GH43	3.2.1.55	7,0	37	1
CZ0137	Arabinofuranosidase 43B	*Bacteroides thetaiotaomicron*	GH43	3.2.1.55	7,0	37	1
CZ0138	Arabinofuranosidase 43C	*Bacteroides thetaiotaomicron*	GH43	3.2.1.55	7,0	37	0,25
CZ0198	Arabinofuranosidase 43A	*Cellvibrio japonicus*	GH43	3.2.1.-	7,0	37	0,25
CZ0201	Arabinofuranosidase 43D	*Bacteroides thetaiotaomicron*	GH43	3.2.1.-	7,0	37	1
CZ0209	Arabinofuranosidase 43B	*Clostridium thermocellum*	GH43	3.2.1.55	5,0-6,0	50	0,5
CZ0291	Arabinofuranosidase 51A	*Podospora anserina*	GH51	3.2.1.55	4,0-7,0	70	0,5
CZ0292	Arabinofuranosidase 62A	*Ustilago maydis*	GH62	3.2.1.55	4,0-6,0	37	1
CZ0313	Arabinofuranosidase 43A	*Streptomyces avermitilis*	GH43	3.2.1.-	5,0-6,5	45	1
CZ0329	Arabinofuranosidase 43A	*Clostridium stercorarium*	GH43	3.2.1.37 and 3.2.1.55	7,0	65	1
CZ0485	Arabinofuranosidase 43A	*Bacteroides ovatus*	GH43	3.2.1.55	7,2	25	1
CZ0487	Arabinofuranosidase 43B	*Bacteroides ovatus*	GH43	3.2.1.55	7,2	25	0,5
CZ0489	Arabinofuranosidase 43C	*Bacteroides ovatus*	GH43-CBM6	3.2.1.55	7,2	25	1
CZ0490	Arabinofuranosidase 43D	*Bacteroides ovatus*	GH43	3.2.1.55	7,2	25	1
CZ0492	Arabinofuranosidase 43E	*Bacteroides ovatus*	GH43-CBM6	3.2.1.55	7,2	25	1
CZ0554	Arabinofuranosidase 51A	*Cellvibrio japonicus*	GH51	3.2.1.55	5,5	37	1
CZ0557	Arabinofuranosidase 121A	*Bifidobacterium longum*	GH121	3.2.1.-	5,5-6,0	30	0,5
CZ0560	β-L-Arabinofuranosidase 127A	*Bifidobacterium longum*	GH127	3.2.1.185	4,5	35-40	1
CZ0707	Arabinofuranosidase 51B	*Cellvibrio japonicus*	GH51	3.2.1.55	5,5	37-45	0,25
CZ0771	Arabinofuranosidase 51B	*Bacillus subtilis*	GH51	3.2.1.55	7,0	37-60	0,5
CZ0778	Arabinofuranosidase 51A	*Bacteroides ovatus*	GH51	3.2.1.55	6,5-7,5	37	1
CZ0805	Arabinofuranosidase 51A	*Thermotoga maritima*	GH51	3.2.1.55	6,5-7,5	80-90	0,25
CZ0807	Arabinofuranosidase 51A	*Bacillus subtilis*	GH51	3.2.1.55	6,5	35	0,25
CZ0819	Dha hydrolase 143A & β-L-Arabinofuranosidase 142A	*Bacteroides thetaiotaomicron*	GH143-GH142	3.2.1.- and 3.2.1.185	6,5-7,5	37	1
CZ0826	Arabinofuranosidase 43E	*Bacteroides thetaiotaomicron*	GH43	3.2.1.-	6,5-7,5	37	1
CZ0841	Arabinofuranosidase 51A	*Bacteroides thetaiotaomicron*	GH51	3.2.1.55	6,5-7,5	37	1
CZ0842	β-L-Arabinofuranosidase 146B	*Bacteroides thetaiotaomicron*	GH146	3.2.1.185	6,5-7,5	37	1
CZ0882	Arabinofuranosidase 43F	*Bacteroides thetaiotaomicron*	GH43-CBM32	3.2.1.55	6,5-7,5	37	0,5
CZ0903	Arabinofuranosidase 43B	*Ruminococcus champanellensis*	GH43-CBM75	3.2.1.55	6,0	37	1
CZ0943	β-L-Arabinofuranosidase 137A & β-Glucuronidase 2A	*Bacteroides thetaiotaomicron*	GH137-GH2-CBM57-CBM35	3.2.1.185 and 3.2.1.31	6,5-7,5	37	1
CZ0951	Arabinofuranosidase 43A	*Bifidobacterium adolescentis*	GH43	3.2.1.55	6,0	50	1
CZ0995	Xylanase 10BA & Arabinofuranosidase 43B	*Ruminococcus champanellensis*	CBM22-GH10-M22-GH43-CBM6	3.2.1.8 and 3.2.1.55	5,0-6,0	37	0,5
CZ1023	β-L-Arabinofuranosidase 137A	*Bacteroides thetaiotaomicron*	GH137	3.2.1.185	6,5-7,5	37	1
CZ1024	β-L-Arabinofuranosidase 142A	*Bacteroides thetaiotaomicron*	GH142	3.2.1.185	6,5-7,5	37	1

ARABINOPYRANOSIDASES

Arabinopyranosidases are enzymes that display hydrolytic activity towards α-L-arabinopyranoside.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0760	α-L-Arabinopyranosidase 2A	*Bacteroides thetaiotaomicron*	GH2	3.2.1.-	6,5-7,5	37	1

ARABINOXYLANASES

Arabinoxylanases are xylanases that use an arabinose side-chain as a specificity determinant and, thus, only cleave the backbone of arabinoxylans.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0060	Arabinoxylanase 5A	*Clostridium thermocellum*	GH5-CBM6	3.2.1.-	5,0-8,0	60	1
CZ0061	Arabinoxylanase 5A	*Clostridium thermocellum*	GH5-CBM6-CBM13-FN-CBM62	3.2.1.-	5,0-8,0	60	1

CARRAGEENASES

Carrageenases degrade carrageenans, a family of linear sulphated polysaccharides from red edible seaweeds. These enzymes are found in sea and gut bacteria.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0454	K-Carrageenase 16A	*Zobellia galactanivorans*	GH16	3.2.1.83	7,0	20-30	0,25
CZ0753	K-Carrageenase 16A	*Zobellia galactanivorans*	GH16-CBM6	3.2.1.83	6,0	40	0,5

CELLOBIOHYDROLASES

Cellobiohydrolases are cellulases that degrade cellulose by hydrolysing 1,4-β-D-glycosidic bonds in an exo-mode of action, by releasing two to four units of glucose from the polysaccharide ends. Cellobiohydrolases may cleave progressively cellulose from the reducing or non-reducing carbohydrate chain ends.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0017	Cellobiohydrolase 48A	*Clostridium cellulolyticum*	GH48	3.2.1.91	5,5-6,5	37	1
CZ0056	Cellobiohydrolase 48A	*Clostridium thermocellum*	GH48	3.2.1.91	5,5-6,5	60	0,5
CZ0176	Cellobiohydrolase 5A	*Clostridium thermocellum*	CBM3-GH5	3.2.1.91	6,6	65	1
CZ0181	Cellobiohydrolase 9A	*Clostridium thermocellum*	GH9	3.2.1.91	5,0	60	1
CZ0293	Cellobiohydrolase 6A	*Podospora anserina*	CBM1-GH6	3.2.1.91	5,0-9,0	50	0,5
CZ0295	Cellobiohydrolase 6B	*Podospora anserina*	GH6	3.2.1.91	5,0-9,0	30	0,25
CZ0420	Reducing-end cellobiohydrolase 48A	*Clostridium stercorarium*	GH48	3.2.1.176	5,0-6,0	70-75	1
CZ0905	Cellobiohydrolase 48A	*Ruminococcus champanellensis*	GH48	3.2.1.-	5,0	37	0,5
CZ0909	Cellobiohydrolase 6B	*Thermobifida fusca*	CBM2-GH6	3.2.1.91	6,5-7,5	55-60	0,5
CZ0982	Reducing-end cellobiohydrolase 48A	*Thermobifida fusca*	CBM2-GH48	3.2.1.176	5,5-6,0	55-60	1

CELLODEXTRINASES

Cellodextrinases are enzymes that participate in the hydrolysis of 1,4-linkages in 1,4-β-D-glucans, to remove successive glucose units.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0236	Cellodextrinase 5A	*Ruminococcus flavefaciens*	GH5	3.2.1.74	7,0	37	0,25
CZ0768	Cellodextrinase 1A	*Clostridium cellulolyticum*	GH1	3.2.1.74	6,0-7,0	60	1

CELLULASES

Cellulases are highly effective enzymes produced by fungi, bacteria, protozoa and animals (insects) for the decomposition of cellulose, one of the most abundant carbon and energy sources on Earth. These enzymes perform the hydrolysis of the 1,4-β-D-glycosidic linkages in cellulose but also in the hemicelluloses, β-glucan and xyloglucan. Enzymes in this category refer to endo-acting cellulases.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0008	Cellulase 5A	*Cellvibrio mixtus*	GH5	3.2.1.4	7,0-8,0	50	2
CZ0009	Cellulase 5B	*Cellvibrio mixtus*	GH5	3.2.1.4	6,0-8,5	40	3,5
CZ0010	Cellulase 5C & Acetyl xylan esterase 2A	*Clostridium thermocellum*	GH5-CE2	3.2.1.4 and 3.1.1.72	6,5-8,0	60	1
CZ0011	Cellulase 5E	*Clostridium thermocellum*	GH5	3.2.1.4	4,0-6,0	60	2
CZ0013	Lichenase 26A & Cellulase 5E	*Clostridium thermocellum*	GH26-GH5	3.2.1.73 and 3.2.1.4	5,0-7,0	60	2
CZ0014	Cellulase 44A	*Clostridium thermocellum*	GH44	3.2.1.4	4,0-6,0	65	2
CZ0016	Cellulase 8A	*Clostridium thermocellum*	GH8	3.2.1.4	5,0-7,5	60	2,2
CZ0023	Cellulase 5A	*Cellvibrio mixtus x Clostridium thermocellum*	GH5-CBM11	3.2.1.4	7,0-8,0	50	2
CZ0053	Lichenase 26A & Cellulase 5E	*Clostridium thermocellum*	GH26-GH5-CBM11	3.2.1.73 and 3.2.1.4	4,5-8,0	60	0,6
CZ0062	Cellulase 124A	*Clostridium thermocellum*	GH124	3.2.1.4	5,0-7,0	60	1
CZ0102	Cellulase 5A	*Bacillus subtilis*	GH5	3.2.1.4	6,5	60	1
CZ0112	Cellulase 16A	*Bacillus subtilis*	GH16	3.2.1.4	7,5	50	1
CZ0115	Cellulase 48A	*Clostridium thermocellum*	GH48	3.2.1.4	7,0	65	1
CZ0164	Cellulase 8A	*Escherichia coli*	GH8	3.2.1.4	7,0	40	1
CZ0173	Cellulase 5B	*Clostridium thermocellum*	GH5	3.2.1.4	6,0-8,0	65	1
CZ0174	Cellulase 5D	*Clostridium thermocellum*	GH5	3.2.1.4	6,0-6,5	80	1
CZ0180	Cellulase 9A	*Clostridium thermocellum*	GH9	3.2.1.4	6,0	79	1
CZ0183	Cellulase 9B	*Clostridium thermocellum*	GH9	3.2.1.4	6,2	65	1
CZ0203	Cellulase 5E	*Cellvibrio japonicus*	GH5	3.2.1.4	4,5-8,0	37	0,25
CZ0217	Cellulase 12B	*Thermotoga maritima*	GH12	3.2.1.4	6,0	90	1
CZ0218	Cellulase 12A	*Thermotoga maritima*	GH12	3.2.1.4	6,0	85	0,25
CZ0235	Cellulase 5A	*Ruminococcus flavefaciens*	GH5	3.2.1.4	5,0-6,0	37	1
CZ0272	Cellulase 6B	*Thermobifida fusca*	GH6	3.2.1.4	6,0	50	1
CZ0294	Cellulase 6A	*Podospora anserina*	GH6	3.2.1.4	5,0-9,0	40	1
CZ0296	Cellulase 131A	*Podospora anserina*	GH131-CBM1	3.2.1.-	4,5-7,0	40	0,5

CELLULASES (CONT.)

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0306	Cellulase 5A	*Clostridium cellulovorans*	GH5	3.2.1.4	5,2	40	1
CZ0334	Cellulase 5C	*Bacillus licheniformis*	GH5	3.2.1.4	6,0	60	1
CZ0381	Cellulase 5B	*Caldicellulosiruptor saccharolyticus*	GH5	3.2.1.4	6,5	80	1
CZ0390	Cellulase 9W	*Clostridium cellulolyticum*	GH9	3.2.1.4	6,0	37	1
CZ0391	Cellulase 8C	*Clostridium cellulolyticum*	GH8	3.2.1.4	6,0	48	1
CZ0392	Cellulase 9M	*Clostridium cellulolyticum*	GH9	3.2.1.4	6,5	37	1
CZ0403	Cellulase 5D	*Ruminococcus albus*	GH5	3.2.1.4	8,0	37	1
CZ0404	Cellulase 9R	*Clostridium cellulolyticum*	GH9	3.2.1.-	6,0	37	1
CZ0409	Cellulase 12A	*Bacillus licheniformis*	GH12	3.2.1.4 and 3.2.1.151	5,5	55	1
CZ0412	Cellulase 5B	*Clostridium cellulovorans*	GH5	3.2.1.4	6,0	40	1
CZ0413	Cellulase 9A	*Clostridium cellulovorans*	GH9	3.2.1.4	7,0	37	1
CZ0434	Cellulase 44A	*Ruminococcus flavefaciens*	GH44	3.2.1.4	6,8	37	1
CZ0446	Cellulase 9J	*Clostridium cellulolyticum*	GH9	3.2.1.4	6,0	37	1
CZ0447	Cellulase 9Q	*Clostridium cellulolyticum*	GH9	3.2.1.4	6,0	37	1
CZ0451	Cellulase 12A	*Thermotoga neapolitana*	GH12	3.2.1.4	6,0	95	0,25
CZ0461	Cellulase 9T	*Clostridium cellulolyticum*	GH9	3.2.1.-	6,0	37	0,25
CZ0476	Cellulase 5B	*Bacillus halodurans*	GH5-CBM46	3.2.1.4	7,0-8,0	60	0,5
CZ0477	Cellulase 5B	*Ruminococcus flavefaciens*	GH5	3.2.1.4	7,0	37	0,5
CZ0479	Cellulase 5B & Mannanse 5A	*Ruminococcus flavefaciens*	GH5-CBM80-GH5	3.2.1.4	7,0	37	0,5
CZ0564	Cellulase 5A	*Bacillus sp,*	GH5	3.2.1.4	8,6-9,0	45	1
CZ0679	Cellulase 48A	*Caldicellulosiruptor bescii*	GH48	3.2.1.4	5,0	70	1
CZ0843	Cellulase 5C	*Clostridium cellulolyticum*	GH5-doc-doc	3.2.1.4	6,0	50	1
CZ0864	Cellulase 44A	*Clostridium thermocellum*	GH44-CBM44	3.2.1.4	4,0-6,0	65	1
CZ0865	Cellulase 44A	*Clostridium cellulolyticum*	GH44-CBM44	3.2.1.4	4,0-6,0	37	1
CZ0895	Cellulase 5B	*Ruminococcus champanellensis*	GH5	3.2.1.4	5,0	37	0,5
CZ0896	Cellulase 8A	*Ruminococcus champanellensis*	GH8	3.2.1.4	5,0	37	1
CZ0897	Cellulase 9A	*Ruminococcus champanellensis*	GH9	3.2.1.4	5,0	37	1
CZ0899	Cellulase 9E	*Ruminococcus champanellensis*	GH9-CBM3	3.2.1.4	5,0	37	0,5
CZ0906	Cellulase 5A	*Thermobifida fusca*	CBM2-GH5	3.2.1.4	5,0-6,0	65	0,5
CZ0907	Cellulase 5B	*Thermobifida fusca*	GH5-CBM3	3.2.1.4	7,0-8,0	70	1
CZ0908	Cellulase 6A	*Thermobifida fusca*	GH6-CBM2	3.2.1.4	6,5-7,5	55-60	1
CZ0913	Cellulase 5G	*Ruminiclostridium thermocellum*	GH5	3.2.1.4	6,0-7,0	60	1
CZ0914	Cellulase 9R	*Ruminiclostridium thermocellum*	GH9-CBM3	3.2.1.4	6,0	78,5	0,5
CZ0920	Cellulase 5C	*Ruminococcus flavefaciens*	GH5-Doc	3.2.1.4	6,8	37	0,5
CZ0921	Cellulase 5D	*Ruminococcus flavefaciens*	GH5-Doc	3.2.1.4	6,8	37	1

CELLULASES (CONT.)

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0922	Cellulase 8A	*Ruminococcus flavefaciens*	GH8-Doc	3.2.1.4	6,8	37	0,5
CZ0923	Cellulase 9B	*Ruminococcus flavefaciens*	GH9-CBM3-Doc	3.2.1.4	6,8	37	1
CZ0924	Cellulase 9C	*Ruminococcus flavefaciens*	GH9-CBM3-Doc	3.2.1.4	6,8	37	1
CZ0926	Cellulase 124A	*Ruminococcus flavefaciens*	GH124-Doc	3.2.1.4	6,0	37	0,5
CZ0946	Cellulase 9B	*Thermobifida fusca*	CBM4-CBM30-GH9-CBM2	3.2.1.4	5,5-6,0	55-60	1
CZ0947	Cellulase 9G	*Ruminococcus champanellensis*	GH9-CBM3	3.2.1.4	5,0	37	1
CZ0948	Cellulase 9B	*Clostridium clariflavum*	GH9-CBM3-CBM3-doc	3.2.1.4	5,5	60	1
CZ0953	Cellulase 9G	*Clostridium cellulolyticum*	GH9-CBM3-Doc	3.2.1.4	6,5-7,5	37	1
CZ0967	Cellulase 74A	*Thermotoga maritima*	GH74	3.2.1.4	6,0	90	1
CZ0984	Cellulase 9A	*Clostridium papyrosolvens*	GH9-CBM3-doc-doc	3.2.1.4	6,5-7,5	37	0,5
CZ0985	Cellulase 5A	*Caldicellulosiruptor bescii*	GH5-CBM28-S-LH-SLH	3.2.1.4	6,5-7,5	75	1
CZ0986	Cellulase 9E	*Ruminococcus flavefaciens*	GH9-CBM3-Doc	3.2.1.4	6,5-7,5	37	1
CZ0991	Cellulase 5A	*Ruminococcus champanellensis*	GH5	3.2.1.4	5,0-6,0	37	1
CZ0993	Cellulase 9C	*Ruminococcus champanellensis*	GH9-CBM3	3.2.1.4	5,0-6,0	37	1
CZ0994	Cellulase 9F	*Ruminococcus champanellensis*	CBM4-CBM30-GH9	3.2.1.4	5,0-6,0	37	1
CZ0999	Cellulase 9K	*Ruminiclostridium thermocellum*	CBM4-CBM30-GH9-doc	3.2.1.4	6,0	65	0,5
CZ1001	Cellulase 9C	*Clostridium clariflavum*	GH9-CBM3-doc-doc	3.2.1.4	5,5	60	0,5
CZ1006	Cellulase 5A	*Clostridium papyrosolvens*	GH5	3.2.1.4	6,5-7,5	37	0,5
CZ1042	Cellulase 9F	*Ruminococcus flavefaciens*	CBM4-GH9	3.2.1.4	6,5-7,5	37	0,5

CHITINASES

Chitinases are hydrolytic enzymes that break down the 1,4-β-D-glucosaminide linkages in chitin, a component of the cell walls of fungi and the exoskeletal elements of some animals (including worms and arthropods).

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0030	Chitinase 18A	*Clostridium thermocellum*	GH18	3.2.1.14	5,0-7,0	60	1
CZ0298	Chitinase 18A	*Bacillus licheniformis*	GH18	3.2.1.14	7,5	45-55	1
CZ0438	Chitinase 18A	*Bacillus cereus*	GH18	3.2.1.14	6,5	65	1
CZ0731	Chitinase 19A	*Streptomyces coelicolor*	GH19	3.2.1.14	6,0	25	1
CZ0742	Chitinase 18A	*Bacteroides thetaiotaomicron*	GH18	3.2.1.14	6,5-7,5	37	1
CZ0748	Chitinase 19A	*Streptomyces thermoviolaceus*	GH19	3.2.1.14	4,0	60	1
CZ0763	Chitinase 18A	*Saccharophagus degradans*	GH18	3.2.1.14 and 3.2.1.-	7,5	37	1

CHITOSANASES

Chitosanases participate in the endo-hydrolysis of 1,4-β-linkages between D-glucosamine residues in partly acetylated chitosan. Chitosan is a linear polysaccharide composed of randomly distributed β-1-4-linked D-glucosamine (deacetylated unit) and N-acetyl-D-glucosamine (acetylated unit).

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0125	Chitosanase 46A	*Bacillus subtilis*	GH46	3.2.1.132	4,0-7.0	50	1
CZ0437	Chitosanase 8B	*Bacillus cereus*	GH8	3.2.1.132	6,0	60	1
CZ0745	Chitosanase 5A	*Streptomyces griseus*	GH5	3.2.1.132	5,7	60	0,5

DEXTRANASES

Dextranases participate in the endo-hydrolysis of 1,6-α-D-glucosidic linkages in dextran. Dextran 1,6-α-isomaltotriosidases are enzymes that participate in the hydrolysis of 1,6-α-D-glucosidic linkages in dextrans, to remove successive isomaltotriose units from the non-reducing ends of the chains.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0569	Dextran 1,6-α-isomaltotriosidase 49A	*Brevibacterium fuscum*	GH49	3.2.1.95	7,5	37	0,5
CZ0720	Dextranase 49A	*Arthrobacter oxydans*	GH49	3.2.1.11	7,0	40	0,5
CZ0965	Dextranase 66A	*Streptococcus mutans*	GH66	3.2.1.11	5,5	37	0,25
CZ0978	Isomalto-dextranase 27A	*Arthrobacter dextranolyticus*	GH27-CBM35	3.2.1.94	3,5	60	1

FRUCTANASES

Fructanases are enzymes that participate in the hydrolysis of fructans, including inulin and levan.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0426	Fructan 2,1-β-fructosidase 32A	*Paenibacillus polymyxa*	GH32	3.2.1.153	7,0	35	1
CZ0526	Fructanase 32A	*Lactobacillus paracasei*	GH32	3.2.1.80	5.0-5.5	49	1
CZ0692	Fructanase 32A	*Streptococcus mutans*	CBM66-GH32	3.2.1.80	5,5	37	0,25

FRUCTOFURANOSIDASES

β-Fructofuranosidases are enzymes that participate in the hydrolysis of terminal non-reducing β-D-fructofuranoside residues in β-D-fructofuranosides.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0547	β-Fructofuranosidase 68A	*Arthrobacter sp.*	GH68	3.2.1.26	8,0-9,0	35	1
CZ0676	β-Fructofuranosidase 100B	*Nostoc sp.*	GH100	3.2.1.26	7,5-7,8	30	0,5
CZ0780	β-Fructofuranosidase 32A	*Bacteroides thetaiotaomicron*	GH32	3.2.1.26, 3.2.1.64 and 3.2.1.80	8,0	37	1
CZ0781	β-Fructofuranosidase 32B	*Bacteroides thetaiotaomicron*	GH32	3.2.1.26, 3.2.1.64 and 3.2.1.80	8,0	37	0,5

FUCOSIDASES

Fucosidases cleave fucosidic bonds in oligosaccharides and glycoconjugates.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0511	Fucosidase 95A	*Bifidobacterium longum*	GH95	3.2.1.51	6,0-7,5	37	1
CZ0566	Fucosidase 29A	*Lactobacillus casei*	GH29	3.2.1.51	7,0	42	0,5
CZ0754	Fucosidase 29A	*Bacteroides thetaiotaomicron*	GH29	3.2.1.51	6,5-7,5	37	1
CZ0761	Methyl-fucosidase 139A	*Bacteroides thetaiotaomicron*	GH139	3.2.1.-	6,5-7,5	37	1
CZ0792	Fucosidase 141A	*Bacteroides thetaiotaomicron*	GH141	3.2.1.51	6,5-7,5	37	1
CZ0804	Fucosidase 29A	*Thermotoga maritima*	GH29	3.2.1.51	4,5-5,0	60	0,5
CZ0963	β-D-Fucosidase 30A	*Prevotella bryantii*	GH30	3.2.1.38	5,0	37	1
CZ0989	Fucosidase 95A	*Clostridium perfringens*	GH95	3.2.1.63	6,5-7,5	37	1
CZ1054	Fucosidase 95A	*Zobellia galactanivorans*	GH95	3.2.1.51	6,5-7,5	37	0,25
CZ1055	Fucosidase 95B	*Zobellia galactanivorans*	GH95	3.2.1.51	6,5-7,5	37	1
CZ1056	Fucosidase 95C	*Zobellia galactanivorans*	GH95	3.2.1.51	6,5-7,5	37	0,5
CZ1057	Fucosidase 95D	*Zobellia galactanivorans*	GH95	3.2.1.51	6,5-7,5	37	0,5
CZ1058	Fucosidase 29E	*Zobellia galactanivorans*	GH29-CBM32	3.2.1.51	6,5-7,5	37	0,25
CZ1059	Fucosidase 29F	*Zobellia galactanivorans*	GH29	3.2.1.51	6,5-7,5	37	0,25
CZ1087	Fucosidase 29A	*Zobellia galactanivorans*	GH29	3.2.1.51	6,5-7,5	37	0,25
CZ1088	Fucosidase 29B	*Zobellia galactanivorans*	GH29	3.2.1.51	6,5-7,5	37	0,25

GALACTANASES

Galactanases are enzymes that specifically hydrolyze β-D-galactosidic linkages in galactans and arabinogalactans.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0028	Galactanase 53A	*Clostridium thermocellum*	GH53	3.2.1.89	5,0-7,5	65	1,5
CZ0029	Exo-1,3-β-Galactanase 43A	*Clostridium thermocellum*	GH43	3.2.1.145	3,0-10,0	50	2
CZ0054	Galactanase 53A	*Cellvibrio japonicus*	GH53	3.2.1.89	6,5-8,0	37	1
CZ0127	Galactanase 53A	*Bacillus subtilis*	GH53	3.2.1.89	6,0-10,0	60	1
CZ0178	Galactanase 53A	*Bacteroides thetaiotaomicron*	GH53	3.2.1.89	7,0	37	1
CZ0299	Galactanase 53A	*Bacillus licheniformis*	GH53	3.2.1.89	6,5	37	1

α-GALACTOSIDASES

α-Galactosidases are enzymes that participate in the hydrolysis of terminal, non-reducing α-D-galactose residues in α-D-galactosides, including galactose oligosaccharides, galactomannans and galactolipids.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0026	α-Galactosidase 27A	*Cellvibrio mixtus*	GH27	3.2.1.22	8,0-9,5	37	1,2
CZ0153	α-Galactosidase 97A	*Bacteroides thetaiotaomicron*	GH97	3.2.1.22	4,0-12,0	45	1
CZ0155	α-Galactosidase 110A	*Bacteroides thetaiotaomicron*	GH110	3.2.1.22	6,5	37	1
CZ0196	α-Galactosidase 97B	*Bacteroides thetaiotaomicron*	GH97	3.2.1.22	7,0	37	1
CZ0200	α-Galactosidase 27A	*Clostridium cellulolyticum*	GH27	3.2.1.22	7,0	37	1
CZ0322	α-Galactosidase 110A	*Bacteroides fragilis*	GH110	3.2.1.-	6,8	26	1
CZ0399	α-Galactosidase 4A	*Bacillus halodurans*	GH4	3.2.1.22	7,4	37	1
CZ0493	α-Galactosidase 95A	*Bacteroides ovatus*	GH95	3.2.1.22	7,2	25	0,25
CZ0684	α-Galactosidase 110A	*Bifidobacterium bifidum*	GH110	3.2.1.-	6,0-6,5	30	1
CZ0701	α-Galactosidase 95A	*Bacteroides thetaiotaomicron*	GH95	3.2.1.-	6,5-7,5	37	1
CZ0705	α-Galactosidase 4A	*Escherichia coli*	GH4	3.2.1.22	8,0	37	0,25
CZ0710	α-Galactosidase 36A	*Thermotoga maritima*	GH36	3.2.1.22	5,0	37	0,5
CZ0782	α-Galactosidase 36A	*Bifidobacterium longum*	GH36	3.2.1.22	6,5	30-37	1
CZ1050	α-Galactosidase 110B	*Bacteroides fragilis*	GH110	3.2.1.-	6,5-7,5	25	0,5
CZ1064	α-Galactosidase 110A	*Zobellia galactanivorans*	GH110	3.2.1.22	6,5-7,5	37	0,5

β–GALACTOSIDASES

β-Galactosidases are enzymes that specifically hydrolyze terminal non-reducing β-D-galactose residues in β-D-galactosides. Blood-group endo-β-galactosidases are enzymes that hydrolyze the 1,4-β-D-galactosyl linkages adjacent to a 1,3-α-D-galactosyl or N-acetylgalactosaminyl residues and a 1,2-α-D-fucosyl residue.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0195	β-Galactosidase 2A	*Bacteroides thetaiotaomicron*	GH2	3.2.1.23	7,0	37	1
CZ0199	β-Galactosidase 2B	*Bacteroides thetaiotaomicron*	GH2	3.2.1.23	7,0	37	1
CZ0223	β-Galactosidase 42A	*Thermotoga maritima*	GH42	3.2.1.23	5,5	80	0,25
CZ0225	N-Acetylglucosamine endo-β-galactosidase 16C	*Clostridium perfringens*	GH16	3.2.1.-	6,0	37	1
CZ0238	Blood-group endo-β-galactosidase 98A	*Streptococcus pneumoniae*	GH98	3.2.1.102	7,4	37	1
CZ0384	β-Galactosidase 42A	*Caldicellulosiruptor saccharolyticus*	GH42	3.2.1.23	6,5	80	1
CZ0411	β-Galactosidase 42A	*Bifidobacterium longum*	GH42	3.2.1.23	6,5	30	1
CZ0414	β-Galactosidase 1A	*Sulfolobus solfataricus*	GH1	3.2.1.23	4,5-7,0	50	1
CZ0516	β-Galactosidase 50A	*Victivallis vadensis*	GH50	3.2.1.23	7,0	40	0,5
CZ0555	β-Galactosidase 42A	*Bacillus subtilis*	GH42	3.2.1.23	7,0-7,5	28-30	0,5

β–GALACTOSIDASES (CONT.)

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0730	Endo-1,4-β-galactosidase 98A	*Streptococcus pneumoniae*	GH98	3.2.1.102	7,4	37	1
CZ0774	β-Galactosidase 2A	*Bacteroides fragilis*	GH2	3.2.1.23	7,4	37	1
CZ0783	β-Galactosidase 2A	*Bifidobacterium longum*	GH2	3.2.1.23	5,0	45-55	0,5
CZ0788	β-Galactosidase 2C	*Bacteroides thetaiotaomicron*	GH2	3.2.1.23	6,5-7,5	37	0,5
CZ0808	β-Galactosidase 2A	*Bacteroides ovatus*	GH2	3.2.1.23	7,0-8,0	37	0,5
CZ0850	β-Galactosidase 2D	*Bacteroides thetaiotaomicron*	GH2	3.2.1.23	6,5-7,5	37	1
CZ0851	β-Galactosidase 42A	*Bacteroides thetaiotaomicron*	GH43-GH42	3.2.1.23	6,5-7,5	37	1
CZ0854	β-Galactosidase 35A	*Bacteroides thetaiotaomicron*	GH35	3.2.1.23	6,5-7,5	37	1
CZ0927	β-Galactosidase 35A	*Paenibacillus thiaminolyticus*	GH35	3.2.1.23 and 3.2.1.38	5,5	65	1
CZ0966	β-Galactosidase 35A	*Streptococcus pneumoniae*	GH35	3.2.1.23	5,5-8,0	37	1
CZ0974	β-Galactosidase 42A	*Alicyclobacillus acidocaldarius*	GH42	3.2.1.23	4,0	65	1

PHOSPHO-β-GALACTOSIDASES

Phospho-β-galactosidases are enzymes that hydrolyze the β-glycosidic bond between a terminal nonreducing galactose-6-phosphate and other organic molecules.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0261	Phospho-β-Galactosidase 1B	*Streptococcus mutans*	GH1	3.2.1.85	8,0	37	1
CZ0314	Phospho-β-Galactosidase 1A	*Lactobacillus gasseri*	GH1	3.2.1.85	6,0-7,0	40	1
CZ0323	Phospho-β-Galactosidase 1A	*Lactococcus lactis*	GH1	3.2.1.85	5,5-6,5	37	1
CZ0333	Phospho-β-Galactosidase 1B	*Lactobacillus gasseri*	GH1	3.2.1.85	5,5-6,0	50	1

β-D-GALACTOSYL-1,4-L-RHAMNOSE PHOSPHORYLASES

These enzymes are particular β-galactoside phosphorylases acting specifically on D-galactosyl-1,4-β-L-rhamnose (GalRha). GalRha is found in rhamnogalacturonan I (RG-I) where one galactose residue binds L-Rha in the main chain of RG-I.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0542	β-D-Galactosyl-1,4-L-rhamnose phosphorylase 112A	*Lachnoclostridium phytofermentans*	GH112	2.4.1.247	6,5	37	1
CZ0970	β-D-Galactosyl-1,4-L-rhamnose phosphorylase 112A	*Opitutus terrae*	GH112	2.4.1.247	6,0-70	45	0,5

GALACTOSYL-N-ACETYLHEXOSAMINE PHOSPHORYLASES

These enzymes are β-galactoside phosphorylases specifically attacking β-D-galactopyranosyl-1,3-N-acetyl-D-glucosamine. Phosphorylases, which reversibly phosphorolyze oligosaccharides to produce monosaccharide 1-phosphate are generally intracellular enzymes showing strict substrate specificity.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0767	1,3-β-Galactosyl-N-acetylhexosamine phosphorylase 112A	*Bifidobacterium longum*	GH112	2.4.1.211	8,5	40	1
CZ0928	1,3-β-Galactosyl-N-acetylhexosamine phosphorylase 112A	*Clostridium phytofermentans*	GH112	2.4.1.211	6,0-7,0	37	0,5

GALACTURONIDASES

Galacturonidases are enzymes that attack homo and rhamno galacturonans.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0775	β-D-Galacturonidase 2A	*Bacteroides thetaiotaomicron*	GH2	3.2.1.-	6,5-7,5	37	0,5
CZ0847	Exo-α-galacturonidase 28A	*Bacteroides thetaiotaomicron*	GH28	3.2.1.-	6,5-7,5	37	0,5
CZ0849	Exo-α-galacturonidase 28B	*Bacteroides thetaiotaomicron*	GH28	3.2.1.-	6,5-7,5	37	1
CZ0852	Exo-α-galacturonidase 28C	*Bacteroides thetaiotaomicron*	GH28	3.2.1.-	6,5-7,5	37	0,5
CZ0853	Exo-α-galacturonidase 28D	*Bacteroides thetaiotaomicron*	GH28	3.2.1.-	6,5-7,5	37	1
CZ1005	Exo-α-galacturonidase 28E	*Bacteroides thetaiotaomicron*	GH28	3.2.1.-	6,5-7,5	37	1

GLUCANSUCRASES

Glucansucrases are enzymes that convert sucrose into α-glucan polysaccharides with 1,2-α, 1,3-α, 1,4-α and/or 1,6-α-glycosidic bonds.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0265	Glucansucrase 70B	*Streptococcus mutans*	GH70	2.4.1.5	6,0	37	1
CZ0266	Glucansucrase 70C	*Streptococcus mutans*	GH70	2.4.1.5	6,0	37	1
CZ0267	Glucansucrase 70D	*Streptococcus mutans*	GH70	2.4.1.5	6,0	37	1
CZ0545	Glucansucrase 70A	*Lactobacillus reuteri*	GH70	2.4.4.-	5,5	37	0,5
CZ0546	Glucansucrase 70A	*Lactobacillus animalis*	GH70	2.4.1.5	5,8	22-59	0,5

GLUCOSAMINIDASES

Exo-β-Glucosaminidases are enzymes that participate in the hydrolysis of chitosan or chitosan oligosaccharides to remove successive D-glucosamine residues from the non-reducing termini of the carbohydrate chain.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0523	Exo-β-Glucosaminidase 9A	*Photobacterium profundum*	GH9	3.2.1.165	7,0	50	0,5
CZ0567	Exo-β-Glucosaminidase 35A	*Thermococcus kodakarensis*	GH35	3.2.1.165	6,0	80	0,5
CZ0674	Exo-β-Glucosaminidase 35A	*Pyrococcus horikoshii*	GH35	3.2.1.165	6,0	90	0,25

α-GLUCOSIDASES

α-Glucosidases are enzymes that cleave the glycosidic bond between two glucose molecules, occurring as α- configurations. 1,3-α-Glucosidases participate in endohydrolysis of 1,3-α-D-glucosidic linkages in isolichenin, pseudonigeran and nigeran. Oligo-1,6-αGlucosidases are enzymes that participate in hydrolysis of 1,6-α-D-glucosidic linkages in 1,6-α-D-glucans and derived oligosaccharides. They participate in hydrolysis of 1,6-α-D-glucosidic linkages in some oligosaccharides produced from starch and glycogen by α-amylases and isomaltose.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0101	Phospho-α-Glucosidase 4A	*Bacillus subtilis*	GH4	3.2.1.122	5,5-9,0	37	1
CZ0111	Oligo-1,6-α-Glucosidase 13B	*Bacillus subtilis*	GH13	3.2.1.10	7,0	25	0,25
CZ0264	α-Glucosidase 13A	*Streptococcus mutans*	GH13	3.2.1.70	7,5	37	1
CZ0328	Oligo-1,6-α-Glucosidase 13A	*Bacillus cereus*	GH13	3.2.1.10	7,0	35	1
CZ0387	Oligo-1,6-α-Glucosidase 13A	*Bifidobacterium adolescentis*	GH13	3.2.1.10	6,5	37	1
CZ0524	α-Glucosidase 97A	*Tannerella forsythia*	GH97	3.2.1.20	7,5	37	0,5
CZ0551	1,3-α-Glucosidase 87A	*Bacillus circulans*	GH87	3.2.1.59	6,5	30	0,25
CZ0811	α-Glucosidase 31A	*Bacteroides thetaiotaomicron*	GH31	3.2.1.20	6,5	37	0,5
CZ0812	α-Glucosidase 31B	*Bacteroides thetaiotaomicron*	GH31	3.2.1.20	6,5	37	0,5
CZ0952	Phospho-α-Glucosidase 4A	*Clostridium acetobutylicum*	GH4	3.2.1.122	7,5	37	1
CZ0958	α-Glucosidase 13A	*Escherichia coli*	CBM34-GH13	3.2.1.20	7,0	37	0,25
CZ0962	α-Glucosidase 63A	*Escherichia coli*	GH63	3.2.1.20 and 3.2.1.84	5,0	37	0,5
CZ1011	α-Glucosidase 31A	*Sulfolobus solfataricus*	GH31	3.2.1.20	5,0-6,0	85	0,25

β-GLUCOSIDASES

β-Glucosidases are enzymes that participate in the hydrolysis of terminal, non-reducing β-D-glucosyl residues with release of β-D-glucose.

SKU	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0019	β-Glucosidase 1A	*Clostridium thermocellum*	GH1	3.2.1.21	5,5-7,0	60	3
CZ0211	β-Glucosidase 1A	*Thermotoga maritima*	GH1	3.2.1.21	6,5	45-50	0,25
CZ0252	β-Glucosidase 1A	*Thermus thermophilus*	GH1	3.2.1.21	6,5	45-50	1
CZ0268	β-Glucosidase 1A	*Thermobifida fusca*	GH1	3.2.1.21	7,0	50	1
CZ0301	β-Glucosidase 1A	*Saccharophagus degradans*	GH1	3.2.1.21	5,0-8,0	37	0,25
CZ0318	β-Glucosidase 1B	*Paenibacillus polymyxa*	GH1	3.2.1.21	7,0	37	1

β-GLUCOSIDASES (CONT.)

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0319	β-Glucosidase 1A	*Paenibacillus polymyxa*	GH1	3.2.1.21	7,0	30	1
CZ0396	β-Glucosidase 1C	*Pectobacterium carotovorum*	GH1	3.2.1.21	7,0	40	1
CZ0397	β-Glucosidase 1A	*Pectobacterium carotovorum*	GH1	3.2.1.86 and 3.2.1.21	7,0	40	1
CZ0418	β-Glucosidase 1A	*Pyrococcus furiosus*	GH1	3.2.1.21	5,0	100-110	1
CZ0441	β-Glucosidase 1A	*Thermotoga petrophila*	GH1	3.2.1.21	7,0	90	1
CZ0444	β-Glucosidase 1A	*Clostridium cellulovorans*	GH1	3.2.1.21	6,0	50	1
CZ0449	β-Glucosidase 1A	*Caldicellulosiruptor saccharolyticus*	GH1	3.2.1.21	6,0-6,5	70	0,25
CZ0455	β-Glucosidase 1G	*Pectobacterium carotovorum*	GH1	3.2.1.21	5,0	40	0,25
CZ0457	β-Glucosidase 1A	*Bacillus halodurans*	GH1	3.2.1.21	8,0	45	0,25
CZ0510	β-Glucosidase 3A	*Saccharophagus degradans*	GH3	3.2.1.21	7,0	25-50	0,25
CZ0525	β-Glucosidase 1A	*bacterium enrichment culture clone*	GH1	3.2.1.21	6,0	40	1
CZ0772	β-Glucosidase 3A	*Bacteroides fragilis*	GH3	3.2.1.21	5,0-7,0	37	0,5
CZ0777	β-Glucosidase 3B	*Bacteroides ovatus*	GH3	3.2.1.21	6,0-6,5	37	1
CZ0786	β-Glucosidase 3B	*Cellvibrio japonicus*	GH3	3.2.1.21	7,5	37	1
CZ0818	β-Glucosidase 3A	*Ruminococcus albus*	GH3	3.2.1.21	6,5-7,5	30	0,5
CZ0894	β-Glucosidase 3A	*Clostridium cellulolyticum*	GH3	3.2.1.21	6,0	37	0,25
CZ0919	β-Glucosidase 1A	*Caldicellulosiruptor bescii*	GH1	3.2.1.21	6,8	85	0,5
CZ0973	β-Glucosidase 1A	*Alicyclobacillus acidocaldarius*	GH1	3.2.1.21	5,5	65	0,5
CZ0980	β-Glucosidase 3A	*Prevotella bryantii*	GH3	3.2.1.21 and 3.2.1.74	6,0	39	1

PHOSPHO-β-GLUCOSIDASES

Phospho-β-glucosidases catalyze the hydrolysis of 1,4-β-linked cellobiose 6-phosphate to yield glucose and glucose 6-phosphate.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0097	Phospho-β-Glucosidase 1A	*Bacillus subtilis*	GH1	3.2.1.86	7,0-8,0	37	1
CZ0098	Phospho-β-Glucosidase 1B	*Bacillus subtilis*	GH1	3.2.1.86	7,0-7,9	37	1
CZ0099	Phospho-β-Glucosidase 1C	*Bacillus subtilis*	GH1	3.2.1.86	7,0-8,0	37	1
CZ0100	Phospho-β-Glucosidase 4A	*Bacillus subtilis*	GH4	3.2.1.86	6,5-7,5	37	1
CZ0160	Phospho-β-Glucosidase 1A	*Escherichia coli*	GH1	3.2.1.86	7,5	25	1
CZ0161	Phospho-β-Glucosidase 1B	*Escherichia coli*	GH1	3.2.1.86	6,8	35	1
CZ0163	Phospho-β-Glucosidase 4A	*Escherichia coli*	GH4	3.2.1.86	7,5	37	1
CZ0212	Phospho-β-Glucosidase 4A	*Thermotoga maritima*	GH4	3.2.1.86	6,5-10,0	37	1
CZ0259	Phospho-β-Glucosidase 1A	*Streptococcus mutans*	GH1	3.2.1.86	8,0	37	1
CZ0260	Phospho-β-Glucosidase 1B	*Streptococcus mutans*	GH1	3.2.1.86	8,0	37	1
CZ0262	Phospho-β-Glucosidase 1D	*Streptococcus mutans*	GH1	3.2.1.86	8,0	37	1

PHOSPHO-β-GLUCOSIDASES (CONT.)

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0277	Phospho-β-Glucosidase 1A	*Streptococcus pneumoniae*	GH1	3.2.1.86	7,5	37	1
CZ0315	Phospho-β-Glucosidase 1A	*Lactobacillus gasseri*	GH1	3.2.1.86	6,0-7,0	40	1
CZ0316	Phospho-β-Glucosidase 1B	*Lactobacillus gasseri*	GH1	3.2.1.86	6,0-7,0	40	1
CZ0330	Phospho-β-Glucosidase 1B	*Streptococcus pyogenes*	GH1	3.2.1.86	7,0	37	1
CZ0416	Phospho-β-Glucosidase 1C	*Erwinia chrysanthemi*	GH1	3.2.1.86	8,8	37	1

GLUCURONIDASES

Glucuronidases are enzymes that act on α- or β-D-glucuronosides to release D-glucuronic acid residues.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0020	Glucuronidase 67A	*Cellvibrio japonicus*	GH67	3.2.1.131	5,0-8,0	45	2
CZ0213	α-Glucuronidase 4A	*Thermotoga maritima*	GH4	3.2.1.139	5,0-11,0	60	0,25
CZ0232	α-Glucuronidase 4B	*Thermotoga maritima*	GH4	3.2.1.139	7,5	80	0,25
CZ0311	α-Methyl-glucuronidase 115A	*Bacteroides ovatus*	GH115	3.2.1.-	7,0	37	1
CZ0494	α-Glucuronidase 67A	*Bacteroides ovatus*	GH67	3.2.1.131	7,2	25	1
CZ0714	α-Glucuronidase 115A	*Bacteroides ovatus*	GH115	3.2.1.131	7,2	37	1
CZ0729	α-Glucuronidase 67A	*Geobacillus stearothermophilus*	GH67	3.2.1.139	6,5	40	1
CZ0795	β-Glucuronidase 2A	*Escherichia coli*	GH2	3.2.1.31	6,5-7,5	37	1
CZ0855	β-Glucuronidase 2A	*Bacteroides thetaiotaomicron*	GH2	3.2.1.31	6,5-7,5	37	1
CZ0868	β-Glucuronidase 2A	*Lactobacillus brevis*	GH2	3.2.1.31	5,0	37	1
CZ0869	β-Glucuronidase 2A	*Ruminococcus gnavus*	GH2	3.2.1.31	6,5-7,5	37	1
CZ0933	β-Glucuronidase 79A	*Acidobacterium capsulatum*	GH79	3.2.1.31	2,6-3,5	25	1
CZ0943	β-L-Arabinofuranosidase 137A & β-Glucuronidase 2A	*Bacteroides thetaiotaomicron*	GH137-GH2-CBM57-CBM35	3.2.1.185 and 3.2.1.31	6,5-7,5	37	1
CZ0972	β-Glucuronidase 2A	*Sulfolobus solfataricus P2*	GH2	3.2.1.31	4,5-8,0	80	0,25

GLUCURONOXYLANASES

Glucuronoxylanases are enzymes that participate in endohydrolysis of the backbone of glucuronoxylans and thus display a specificity determinant for the glucurono side chain.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0445	Glucuronoxylanase 30A	*Clostridium thermocellum*	GH30	3.2.1.136	7,0	50	0,5
CZ0709	Glucuronoxylanase 30A	*Bacteroides ovatus*	GH30	3.2.1.136	7,2	37	0,25
CZ0916	Glucuronoxylanase 30A	*Clostridium clariflavum*	GH30	3.2.1.136	6,0	37	0,5
CZ0917	Glucuronoxylanase 30B	*Clostridium clariflavum*	GH30-CBM6	3.2.1.136	6,0	37	0,5

HEXOSAMINIDASES

Hexosaminidases are enzymes that are involved in the hydrolysis of terminal N-acetyl-D-hexoxamine residues in N-acetyl-β-D-hexosaminides.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0278	Hexosaminidase 20A	*Streptococcus pneumoniae*	GH20	3.2.1.52	5,0	37	1
CZ0279	Hexosaminidase 20B	*Streptococcus pneumoniae*	GH20	3.2.1.52	5,0	37	1
CZ0302	Hexosaminidase 3C	*Saccharophagus degradans*	GH3	3.2.1.52	5,0-8,0	37	1
CZ0450	Hexosaminidase 3A	*Thermotoga neapolitana*	GH3	3.2.1.52	7,0-8,0	65-75	0,25
CZ0689	Hexosaminidase 84A	*Clostridium perfringens*	GH84-CBM32	3.2.1.52	5,5	20	0,25
CZ0708	Hexosaminidase 3A	*Thermotoga maritima*	GH3	3.2.1.52	7,0-8,0	65-75	0,25
CZ0793	Hexosaminidase 3A	*Escherichia coli*	GH3	3.2.1.52	6,5-7,5	37	0,5
CZ0822	Hexosaminidase 20A	*Bifidobacterium longum*	GH20	3.2.1.52	5,0	37	0,5
CZ0823	Hexosaminidase 20A	*Saccharophagus degradans*	GH20	3.2.1.52	7,5	37	0,5
CZ0825	Hexosaminidase 3A	*Vibrio furnissii*	GH3	3.2.1.52	7,0	45	1
CZ0827	Hexosaminidase 3A	*Clostridium paraputrificum*	GH3	3.2.1.52	7,0	50	0,25
CZ0839	Hexosaminidase 20A	*Lactobacillus casei*	GH20	3.2.1.52	5,0-5,5	37-40	0,5
CZ0977	Hexosaminidase 3A	*Pseudomonas aeruginosa*	GH3	3.2.1.52	7,4	37	1

HYALURONIDASES

Hyaluronidases are enzymes that participate in random hydrolysis of 1,4-linkages between N-acetyl-β-D-glucosamine and D-glucuronate residues in hyaluronate.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0717	Hyaluronidase 84A	*Clostridium perfringens*	GH84	3.2.1.35	6,4	37	0,5
CZ0732	Hyaluronidase 84B	*Clostridium perfringens*	GH84-CBM32-CBM32	3.2.1.35	6,4	37	0,25

INULASES

Inulin fructotransferases are enzymes that produce α-D-fructofuranose β-D-fructofuranose 1,2':2,3'-dianhydride (DFA III) by successively eliminating the diminishing 2-1-β-D-fructan (inulin) chain from the terminal D-fructosyl-D-fructosyl disaccharide.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0677	Inulin fructotransferase 91A	*Bacillus sp.*	GH91	4.2.2.18	5,0-6,0	40	0,5
CZ0678	Inulin fructotransferase 91A	*Nonomuraea sp.*	GH91	4.2.2.18	5,6	65	1

LAMINARINASES

Laminarinases are generally endo-acting enzymes that break down 1,3-β-glucans such as laminarin, callose or curdlan. 1,3-β-glucans are abundant in the plant cell walls of algae, plants and fungi.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0018	Laminarinase 81A	*Clostridium thermocellum*	GH81	3.2.1.39	5,5-6,5	65	3
CZ0222	Laminarinase 16A	*Thermotoga maritima*	GH16	3.2.1.39	7,0	45	1
CZ0305	Laminarinase 16A	*Pyrococcus furiosus*	GH16	3.2.1.39	6,5	70-80	1
CZ0331	Laminarinase 16A	*Thermotoga petrophila*	GH16	3.2.1.39	5,0-7,0	78-95	1
CZ0406	Laminarinase 16A	*Thermotoga neapolitana*	GH16	3.2.1.39	6,2	85-95	1
CZ0452	Laminarinase 16A	*Zobellia galactanivorans*	GH16	3.2.1.39	8,5	40	0,25
CZ0459	Laminarinase 81A	*Bacillus halodurans*	GH81	3.2.1.39	6,0-8,0	60	0,25
CZ0571	Laminarinase 55A	*Arthrobacter sp.*	GH55	3.2.1.39	5,0	45	1
CZ0675	Laminarinase 64A	*Lysobacter enzymogenes*	GH64	3.2.1.39	4,5-5,0	41	1
CZ0757	Laminarinase 16C	*Zobellia galactanivorans*	GH16-CBM6	3.2.1.39	5,0	40	1
CZ0858	Laminarinase 64A	*Paenibacillus sp.*	GH64	3.2.1.39	6,5	37	1
CZ0861	Laminarinase 16A	*Paenibacillus sp.*	GH16	3.2.1.39	6,5	37	1
CZ0863	Laminarinase 16A	*Paenibacillus sp.*	GH16-CBM56	3.2.1.39	6,5	37	1
CZ1052	Laminarinase 157A	*Labilibaculum antarcticum*	GH157	3.2.1.39	6,5-7,5	37	1
CZ1053	Laminarinase 157A	*Polaribacter sp.*	GH157	3.2.1.39	6,5-7,5	37	1
CZ1060	Laminarinase 64A	*Zobellia galactanivorans*	GH64-CBM6	3.2.1.39	6,5-7,5	37	0,5

LEVANASES

Levanases are enzymes that participate in random hydrolysis of 2,6-β-D-fructofuranosidic linkages in 2,6-β-D-fructans (levans) containing more than 3 fructose units.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0124	Levanase 32A	*Bacillus subtilis*	GH32	3.2.1.65	6,0	30	1
CZ0135	Levanase 32A	*Bacteroides thetaiotaomicron*	GH32	3.2.1.65	8,0	37	1
CZ0508	Levanase 32B	*Bacillus subtilis*	GH32-CBM66	3.2.1.65	7,0	37	0,5
CZ0509	Levanase 32B	*Bacillus subtilis*	GH32	3.2.1.65	7,0	37	0,5

LEVANSUCRASES

Levansucrases are fructosyltransferases that transfer β-D-frutosyl residue from sucrose to a levan chain.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0128	Fructosyltransferase 68A	*Bacillus subtilis*	GH68	2.4.1.10	6,0	37	1
CZ0514	Fructosyltransferase 68A	*Streptococcus mutans*	GH68	2.4.1.10	7,0	25	0,5
CZ0519	Fructosyltransferase 68A	*Gluconacetobacter xylinus*	GH68	2.4.1.10	4,5	30	1

LICHENASES

Lichenases are enzymes that participate in the endo-hydrolysis of 1,3-1,4-β-D-glucans when the glucose residue, whose reducing group which is involved in the linkage to be hydrolyzed is itself substituted at C-3 (EC number 3.2.1.6) or C-4 (EC number 3.2.1.73).

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0012	Lichenase 26A	*Clostridium thermocellum*	GH26	3.2.1.73	6,0-8,0	60	3
CZ0013	Lichenase 26A & Cellulase 5E	*Clostridium thermocellum*	GH26-GH5	3.2.1.73 and 3.2.1.4	5,0-7,0	60	2
CZ0015	Lichenase 16A	*Clostridium thermocellum*	GH16	3.2.1.73	5,5-7,0	65	1,5
CZ0053	Lichenase 26A & Cellulase 5E	*Clostridium thermocellum*	GH26-GH5-CBM11	3.2.1.73 and 3.2.1.4	4,5-8,0	60	0,6
CZ0214	Lichenase 5A	*Thermotoga maritima*	GH5	3.2.1.73	6,0	80	0,25
CZ0326	Lichenase 16D	*Ruminococcus flavefaciens*	GH16	3.2.1.73	6,8	37	1
CZ0423	Lichenase 16A	*Paenibacillus polymyxa*	GH16	3.2.1.73	7,0	30	1
CZ0458	Lichenase 16A	*Bacillus halodurans*	GH16	3.2.1.6	6,0-8,0	60	0,25
CZ0480	Lichenase 16A	*Ruminococcus flavefaciens*	GH16-GH16-GH16	3.2.1.73	7,0	37	0,5
CZ0548	Lichenase 8A	*Bacillus circulans*	GH8	3.2.1.73	5,0	37	1
CZ0898	Lichenase 16A	*Ruminococcus champanellensis*	GH16	3.2.1.73	5,0	37	1

LYSOZYMES

Lysozymes are enzymes that participate in the hydrolysis of 1,4-β-linkages between N-acetylmuramic acid and N-acetyl-glucosamine residues in a peptidoglycan and between N-acetyl-D-glucosamine residues in chitodextrins.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0117	Lysozyme 23A	*Bacillus subtilis*	GH23	3.2.1.17	6,0-7,0	32	1
CZ0273	Lysozyme 25A	*Streptococcus pneumoniae*	GH25	3.2.1.17	5,0	37	1
CZ0713	Lysozyme 25A	*Clostridium perfringens*	GH25	3.2.1.17	5,0	37	0,25
CZ0719	Lysozyme 24B	*Escherichia coli*	GH24	3.2.1.17	7,5	25	0,5

α-MANNANASES

α-Mannanases participate in the hydrolysis of α-mannan, a cell wall polysaccharide found in yeasts. This type of mannan has a 1,6-α linked backbone and 1,2-α and 1,3-α linked branches.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0146	α-Mannanase 76A	*Bacteroides thetaiotaomicron*	GH76	3.2.1.101	7,0	37	1
CZ0202	α-Mannanase 76B	*Bacteroides thetaiotaomicron*	GH76	3.2.1.101	7,0	37	1
CZ0550	α-Mannanase 76A	*Bacillus circulans*	GH76	3.2.1.101	6,0	50	1

β-MANNANASES

β-Mannanases are enzymes that participate in the random hydrolysis of 1,4-β-D-mannosidic linkages in mannans, galactomannans and glucomannans. Plant mannans have 1,4-β-linkages and are storage polysaccharides. Ivory nut is a source of mannan.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0025	β-Mannanase 26B	*Clostridium thermocellum*	GH26	3.2.1.78	6,0-8,0	65	1
CZ0055	β-Mannanase 5A	*Cellvibrio japonicus*	GH5	3.2.1.78	6,5-8,0	37	1,8
CZ0063	β-Mannanase 5A	*Clostridium thermocellum*	GH5	3.2.1.78	5,0-7,0	60	1
CZ0064	β-Mannanase 5A	*Clostridium thermocellum*	GH5-CBM32	3.2.1.78	5,0-7,1	60	1
CZ0123	β-Mannanase 26E	*Bacillus subtilis*	GH26	3.2.1.78	7,0	37	0,25
CZ0147	β-Mannanase 26C	*Clostridium thermocellum*	GH26	3.2.1.78	6,0-7,0	50	0,5
CZ0205	β-Mannanase 26A	*Cellvibrio japonicus*	GH26	3.2.1.78	6,5	37	1
CZ0215	β-Mannanase 5B	*Thermotoga maritima*	GH5	3.2.1.78	7,0	90	1
CZ0270	β-Mannanase 5A	*Thermobifida fusca*	GH5	3.2.1.78	7,0-8,0	80	1
CZ0288	β-Mannanase 5A	*Podospora anserina*	GH5	3.2.1.78	3,0-6,0	60	1
CZ0289	β-Mannanase 26A	*Podospora anserina*	CBM35-GH26	3.2.1.78	4,0-6,0	40	1
CZ0307	β-Mannanase 5A	*Clostridium cellulovorans*	GH5	3.2.1.78	7,0	45	1
CZ0308	β-Mannanase 26B	*Clostridium cellulovorans*	GH26	3.2.1.78	7,0	40	1
CZ0425	β-Mannanase 26A	*Paenibacillus polymyxa*	GH26	3.2.1.78	7,0	30	1
CZ0442	β-Mannanase 5A	*Thermotoga petrophila*	GH5	3.2.1.78	4,5-6,5	81-93	1
CZ0464	β-Mannanase 5B	*Clostridium cellulolyticum*	GH5	3.2.1.78	6,0	37	0,25
CZ0478	Mannanse 5A	*Ruminococcus flavefaciens*	GH5	3.2.1.78	7,0	37	0,5
CZ0479	Cellulase 5B & Mannanse 5A	*Ruminococcus flavefaciens*	GH5-CBM80-GH5	3.2.1.4	7,0	37	0,5
CZ0565	β-Mannanase 5A	*Bacillus sp.*	GH5	3.2.1.78	9,5	50	1
CZ0681	β-Mannanase 113A	*Alicyclobacillus acidocaldarius*	GH113	3.2.1.78	5,5	65	1
CZ0901	β-Mannanase 26B	*Ruminococcus champanellensis*	CBM35-GH26	3.2.1.78	5,0	37	1
CZ0942	β-Mannanase 134A	*Streptomyces sp.*	CBM10-GH134	3.2.1.78	5,0	37	0,5
CZ0992	β-Mannanase 5A	*Ruminococcus champanellensis*	CBM23-GH5	3.2.1.78	5,0-6,0	37	1
CZ0997	β-Mannanase 26A	*Ruminococcus champanellensis*	CBM35-GH26-CBM35	3.2.1.78	5,0-6,0	37	1
CZ1007	β-Mannanase 134A	*Streptomyces sp.*	GH134	3.2.1.78	5,0	37	0,5

α-MANNOSIDASES

α-Mannosidases are enzymes that participate in the hydrolysis of terminal, non-reducing α-D-mannose residues in α-D-mannosides.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0109	α-Mannosidase 92M	*Bacteroides thetaiotaomicron*	GH92	3.2.1.113	7,5	37	1
CZ0139	α-Mannosidase 92C	*Bacteroides thetaiotaomicron*	GH92	3.2.1.-	6,5	37	0,5
CZ0140	α-Mannosidase 92D	*Bacteroides thetaiotaomicron*	GH92	3.2.1.-	6,5	37	1
CZ0141	α-Mannosidase 92A	*Bacteroides thetaiotaomicron*	GH92	3.2.1.113	6,5	37	1
CZ0144	α-Mannosidase 92E	*Bacteroides thetaiotaomicron*	GH92	3.2.1.-	7,5	37	1
CZ0145	α-Mannosidase 38A	*Bacteroides thetaiotaomicron*	GH38	3.2.1.113 and 3.2.1.-	7,5	37	1
CZ0148	α-Mannosidase 92F	*Bacteroides thetaiotaomicron*	GH92	3.2.1.-	7,0	37	1
CZ0149	α-Mannosidase 92G	*Bacteroides thetaiotaomicron*	GH92	3.2.1.-	6,5	37	1
CZ0151	α-Mannosidase 92H	*Bacteroides thetaiotaomicron*	GH92	3.2.1.-	6,5	37	1
CZ0154	α-Mannosidase 99B	*Bacteroides thetaiotaomicron*	GH99	3.2.1.130	5,5-7,5	37	1
CZ0166	α-Mannosidase 92I	*Bacteroides thetaiotaomicron*	GH92	3.2.1.-	6,5	37	1
CZ0167	α-Mannosidase 92J	*Bacteroides thetaiotaomicron*	GH92	3.2.1.-	6,5	37	1
CZ0168	α-Mannosidase 92L	*Bacteroides thetaiotaomicron*	GH92	3.2.1.-	6,5	37	0,25
CZ0172	α-Mannosidase 125A	*Bacteroides thetaiotaomicron*	GH125	3.2.1.-	7,0	37	1
CZ0175	α-Mannosidase 92O	*Bacteroides thetaiotaomicron*	GH92	3.2.1.113	7,0	37	1
CZ0233	α-Mannosidase 125A	*Clostridium perfringens*	GH125	3.2.1.-	7,4	37	1
CZ0239	α-Mannosidase 125A	*Streptococcus pneumoniae*	GH125	3.2.1.-	7,4	37	1
CZ0440	α-Mannosidase 38A	*Streptococcus pyogenes*	GH38	3.2.1.-	7,0	37	1
CZ0556	α-Mannosidase 92S	*Bacteroides thetaiotaomicron*	GH92	3.2.1.-	7,0	37	0,5
CZ0568	α-Mannosidase 47A	*Caulobacter sp.*	GH47	3.2.1.113	7,0	25	0,25
CZ0700	1,3-α-Mannosidase 92A	*Bacteroides thetaiotaomicron*	GH92	3.2.1.-	7,0	37	0,25
CZ0950	α-Mannosidase 92B	*Bacteroides thetaiotaomicron*	GH92-GH92	3.2.1.24	7,0	37	0,5

β-MANNOSIDASES

β-Mannosidases are enzymes with activity exo-1,4-β-mannosidase that removes mannose residues from the non-reducing ends of oligosaccharides or carbohydrates.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0027	β-Mannosidase 5A	*Cellvibrio mixtus*	GH5	3.2.1.25	6,5-7,5	37	3
CZ0320	β-Mannosidase 26A	*Bacteroides fragilis*	GH26	3.2.1.100	7,0	50	1
CZ0332	β-Mannosidase 1A	*Pyrococcus furiosus*	GH1	3.2.1.25	7,0	95	0,25
CZ0694	β-Mannosidase 1B	*Pyrococcus furiosus*	GH1	3.2.1.25	5,0	90	0,25
CZ0810	β-Mannosidase 2A	*Bacteroides thetaiotaomicron*	GH2	3.2.1.25	5,6	37	1
CZ1082	β-Mannosidase 2A	*Thermotoga maritima*	GH2	3.2.1.25	6,5-7,5	37	0,5

MANNOSYLGLUCOSE PHOSPHORYLASES

Mannosylglucose phosphorylases are enzymes that convert D-mannopyranosyl-1,4-β-D-glucopyranose (Man-Glc) to D-mannose-1-phosphate (M1P) and D-glucose (Glc) in an inverting manner.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0773	Mannosylglucose phosphorylase 130A	*Bacteroides fragilis*	GH130	2.4.1.281	7,0	40	0,5
CZ0880	Mannosylglucose phosphorylase 130A	*Ruminococcus albus*	GH130	2.4.1.281	4,5-10,5	50	1

OLIGOSACCHARIDE REDUCING-END XYLANASES

Oligosaccharide reducing-end xylanases are enzymes that participate in the hydrolysis of 1,4-β-xylose residues from the reducing end of oligosaccharides.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0385	Oligosaccharide reducing-end xylanase 8A	*Bifidobacterium adolescentis*	GH8	3.2.1.156	6,0	40	1
CZ0400	Oligosaccharide reducing-end xylanase 8A	*Bacillus halodurans*	GH8	3.2.1.156	7,0-7,5	40	1

PEPTIDOGLYCAN LYTIC EXOTRANSGLYCOSYLASES

Peptidoglycan lytic exotransglycosylases are enzymes that participate in the exolytic cleavage of the 1-4-β-glycosidic linkage between N-acetylmuramic acid (MurNAc) and N-acetylglucosamine (GlcNAc) residues in peptidoglycans with the concomitant formation of a 1,6-anhydrobond in the MurNAc residue.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0193	Peptidoglycan lytic exotransglycosylase 102A	*Escherichia coli*	GH102	4.2.2.n1	4,0-4,5	30	0,25
CZ0687	Peptidoglycan lytic exotransglycosylase 23A	*Escherichia coli*	GH23	4.2.2.n1	6,0	37	0,5
CZ0696	Peptidoglycan lytic exotransglycosylase 23A	*Bacillus subtilis*	GH23	4.2.2.n1	6,0-6,5	37-40	0,25
CZ0794	Peptidoglycan lytic exotransglycosylase 103A	*Escherichia coli*	GH103	4.2.2.n1	6,5-7,5	37	1

POLYGALACTURONASES

Polygalacturonases, also known as pectins depolymerases, are enzymes that hydrolyze the 1,4-α-glycosidic bonds between galacturonic acid residues in polygalacturonan, a significant carbohydrate component of the pectin network of plant cell walls.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0116	Polygalacturonase 4A	*Bacillus subtilis*	GH4	3.2.1.67	7,2-7,8	37	0,25
CZ0244	Polygalacturonosidase 28A	*Dickeya dadantii*	GH28	3.2.1.82	6,0	37	1
CZ0245	Endopolygalacturonase 28A	*Dickeya dadantii*	GH28	3.2.1.15	6,0	37	1
CZ0688	Polygalacturonase 28A	*Thermotoga maritima*	GH28	3.2.1.67	6,0	95	0,25
CZ0816	Endopolygalacturonase 28A	*Bacteroides thetaiotaomicron*	GH28	3.2.1.15	6,5-7,5	37	1
CZ1066	Polygalacturonase 28A	*Zobellia galactanivorans*	GH28	3.2.1.67	6,5-7,5	37	1
CZ1067	Polygalacturonase 28B	*Zobellia galactanivorans*	GH28	3.2.1.67	6,5-7,5	37	0,25

PORPHYRANASES

Porphyranases are enzymes that perform the hydrolysis of β-D-galactopyranose-1,4-α-L-galactopyranose-6-sulfate linkages in porphyran. The backbone of porphyran consists largely (~70%) of (1->3)-linked β-D-galactopyranose, followed by (1->4)-linked α-L-galactopyranose-6-sulphate.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0395	β-Porphyranase 16A	*Zobellia galactanivorans*	GH16	3.2.1.178	7,5	30	1
CZ0734	β-Porphyranase 16C	*Bacteroides uniformis*	GH16	3.2.1.178	8,0	37	0,5
CZ0735	β-Porphyranase 16B	*Bacteroides plebeius*	GH16	3.2.1.178	6,5-7,5	30	0,5
CZ0737	β-Porphyranase 86A	*Bacteroides plebeius*	GH86	3.2.1.178	6,5-7,5	30	1

PULLULANASES

Pullulanases are enzymes that participate in the hydrolysis of 1,6-α-D-glucosidic linkages in pullulan, amylopectin and glycogen, and in α- and β-limit dextrins of amylopectin and glycogen.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0221	Pullulanase 13A	*Thermotoga maritima*	GH13	3.2.1.41	5,9	90	0,25
CZ0779	Neopullulanase 13A	*Bacteroides thetaiotaomicron*	GH13	3.2.1.135	6,5-7,5	37	1
CZ0867	Neopullulanase 13A	*Geobacillus stearothermophilus*	CBM34-GH13	3.2.1.135	6,0	55	0,5

RHAMNOGALACTURONASES

Rhamnogalacturonases are enzymes that participate in the endo-hydrolysis of rhamnogalacturonans releasing oligosaccharides with β-D-galacturonate at the reducing end. Rhamnogalacturonans are a group of closely related cell wall pectic polysaccharides that contain a backbone of the repeating disaccharide: 1,4-α-D-GalpA-1,2-α-L-Rhap-1.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0129	Unsaturated rhamnogalacturonyl hydrolase 105A	*Bacillus subtilis*	GH105	3.2.1.172	4,0	30	1
CZ0179	α-Rhamnosidase 78A	*Streptomyces avermitilis*	GH78	3.2.1.40	5,0	40	1
CZ0194	Unsaturated rhamnogalacturonyl hydrolase 105A	*Bacteroides thetaiotaomicron*	GH105	3.2.1.172	7,0	37	1
CZ0680	α-Rhamnosidase 106A	*Sphingomonas paucimobilis*	GH106	3.2.1.40	7,8	45	1
CZ0724	Unsaturated rhamnogalacturonyl hydrolase 105B	*Bacteroides thetaiotaomicron*	GH105	3.2.1.172	7,0	37	1
CZ0762	α-Rhamnosidase 78C	*Bacteroides thetaiotaomicron*	CBM67-GH78	3.2.1.40	6,5-7,5	37	1
CZ0770	α-Rhamnosidase 106A	*Bacteroides thetaiotaomicron*	GH106	3.2.1.-	6,5-7,5	37	1
CZ0790	α-Rhamnosidase 78A	*Bacteroides thetaiotaomicron*	GH78	3.2.1.-	6,5-7,5	37	1
CZ0883	Unsaturated rhamnogalacturonyl hydrolase 105C	*Bacteroides thetaiotaomicron*	GH105	3.2.1.-	6,5-7,5	37	1
CZ0884	α-Rhamnosidase 78B & Kdo hydrolase 33A	*Bacteroides thetaiotaomicron*	CBM67-GH78-GH33	3.2.1.40 and 3.2.1.-	6,5-7,5	37	1
CZ1012	Unsaturated rhamnogalacturonyl hydrolase 105D	*Bacteroides thetaiotaomicron*	GH105	3.2.1.172	6,5-7,5	37	0,5
CZ1044	α-Rhamnosidase 78B	*Bacteroides thetaiotaomicron*	GH78	3.2.1.40	6,5-7,5	37	0,5
CZ1061	α-Rhamnosidase 78A	*Zobellia galactanivorans*	CBM67-GH78	3.2.1.40	6,5-7,5	37	0,25

RHAMNOGALACTURONASES (CONT.)

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ1071	Unsaturated rhamnogalacturonyl hydrolase 105A	*Zobellia galactanivorans*	GH105	3.2.1.172	6,5-7,5	37	0,5
CZ1075	Unsaturated rhamnogalacturonyl hydrolase 105A	*Mariniflexile sp.*	GH105	3.2.1.172	6,5-7,5	37	1
CZ1076	Unsaturated rhamnogalacturonyl hydrolase 105B	*Mariniflexile sp.*	GH105	3.2.1.172	6,5-7,5	37	1

SIALIDASES

Sialidases hydrolyze 2,3-α, 2,6-α and 2,8-α-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates. Sialidases may act as pathogenic factors in microbial infections.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0226	Sialidase 33B	*Clostridium perfringens*	GH33	3.2.1.18	6,0	37	0,25
CZ0228	Sialidase 33D	*Clostridium perfringens*	GH33	3.2.1.18	6,0	30	0,25
CZ0231	Sialidase 33A	*Clostridium perfringens*	GH33	3.2.1.18	7,5	37	0,25
CZ0237	Sialidase 33A	*Streptococcus pneumoniae*	CBM40-GH33a-GH33b	3.2.1.18	7,5	37	1
CZ0481	Sialidase 33A	*Bacteroides fragilis*	GH33	3.2.1.18	7,0	37	0,25
CZ1049	Sialidase 33A	*Streptococcus pneumoniae*	GH33a-GH33b	3.2.1.18	7,5	37	0,5

TREHALASES

Trehalases are enzymes that catalyze the conversion of trehalose, a natural α-linked disaccharide formed by an α,α-1,1-glucoside bond between two α-glucose units, to glucose.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0532	Trehalose synthase 13A	*Deinococcus deserti*	GH13	5.4.99.16	9,0	45	0,5
CZ0533	Trehalose synthase 13A	*Mycobacterium smegmatis*	GH13	5.4.99.16	7,0	40	0,25
CZ0544	α-Phosphotrehalase 13A	*Lactobacillus acidophilus*	GH13	3.2.1.93	6,5	37	1
CZ0559	α-Phosphotrehalase 13A	*Bacillus licheniformis*	GH13	3.2.1.93	8,0	30	1
CZ0673	Trehalase 15A	*Mycobacterium smegmatis*	GH15	3.2.1.28	7,1	37	1
CZ0703	Trehalase 37A	*Escherichia coli*	GH37	3.2.1.28	7,2	25	1
CZ0765	Malto-oligosyltrehalose trehalohydrolase 13A	*Sulfolobus solfataricus*	CBM48-GH13	3.2.1.141	5,0	80	0,25
CZ0769	α-Phosphotrehalase 13A	*Escherichia coli*	GH13	3.2.1.93	7,5	25	1
CZ0797	Trehalase 37B	*Escherichia coli*	GH37	3.2.1.28	7,4	25	1
CZ0870	Malto-oligosyltrehalose trehalohydrolase 13A	*Rhizobium sp.*	CBM48-GH13	3.2.1.141	6,5-7,5	25	1
CZ0871	Malto-oligosyltrehalose trehalohydrolase 13A	*Nostoc punctiforme*	CBM48-GH13	3.2.1.141	7,0-7,5	25	0,5
CZ0936	Malto-oligosyltrehalose synthase 13A	*Arthrobacter sp.*	GH13	5.4.99.15	6,0-9,5	40	0,25
CZ0990	α-Trehalose phosphorylase 65A	*Thermoanaerobacter brockii*	GH65	2.4.1.64	6,5-7,5	60	0,25

Δ-4,5-UNSATURATED β-GLUCURONYL HYDROLASES

Catalyze the hydrolysis of the glycosidic bond in an unsaturated saccharide between the unsaturated glucuronyl residue at the non-reducing terminus and the saccharide linked to the residue.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0443	Δ-4,5-unsaturated β-glucuronyl hydrolase 88A	*Pedobacter heparinus*	GH88	3.2.1.-	5,0-6,0	30	1
CZ0845	Δ-4,5-Unsaturated β-glucuronyl hydrolase 105A	*Bacteroides thetaiotaomicron*	GH105	3.2.1.-	6,5-7,5	37	1
CZ0856	Δ-4,5-Unsaturated β-glucuronyl hydrolase 88A	*Bacteroides thetaiotaomicron*	GH88	3.2.1.-	6,5	37	1
CZ0939	Δ-4,5-Unsaturated β-glucuronyl hydrolase 105A	*Nonlabens ulvanivorans*	GH105	3.2.1.-	6,5-9,0	20-55	1
CZ0954	Δ-4,5-Unsaturated β-glucuronyl hydrolase 88A	*Clostridium perfringens*	GH88	3.2.1.-	6,6	37	0,5
CZ1065	Δ-4,5-unsaturated β-glucuronyl hydrolase 88A	*Zobellia galactanivorans*	GH88	3.2.1.-	6,5-7,5	37	0,5
CZ1068	Δ-4,5-unsaturated β-glucuronyl hydrolase 88B	*Zobellia galactanivorans*	GH88	3.2.1.-	6,5-7,5	37	1

XYLANASES

Xylanases are enzymes that degrade the linear polysaccharide 1,4-β-xylan into xylo-oligosaccharides. Xylan is one of the most abundant hemicelluloses found in plant cell walls and some algae. Xylans are usually decorated with acetyl, arabinose and glucuronic acid side chains. Xylooligosaccharides produced from hydrolysis are considered as "functional food" or dietary fibers.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0001	Xylanase 10B	*Clostridium thermocellum*	GH10	3.2.1.8	5,0-8,0	65	1
CZ0002	Xylanase 10B	*Clostridium thermocellum*	GH10-CBM22	3.2.1.8	5,0-8,0	65	1
CZ0003	Xylanase 11A	*Clostridium thermocellum*	GH11	3.2.1.8	4,5-8,0	65	1
CZ0004	Xylanase 11A	*Clostridium thermocellum*	GH11-CBM6	3.2.1.8	4,5-8,0	65	1,5
CZ0005	Xylanase 10C	*Clostridium thermocellum*	CBM22-GH10	3.2.1.8	4,0-11,0	65	1
CZ0006	Xylanase 10C	*Cellvibrio mixtus*	GH10	3.2.1.8	7,0-8,0	37	1,5
CZ0007	Xylanase 10A	*Cellvibrio japonicus*	CBM22-GH10	3.2.1.8	7,0-8,0	37	1,5
CZ0022	Xylanase 10B	*Clostridium thermocellum*	CBM22-GH10-CBM22	3.2.1.8	5,0-7,5	65	2
CZ0051	Xylanase 11A & Acetyl xylan esterase 4A	*Clostridium thermocellum*	GH11-CBM6-CE4	3.2.1.8 and 3.1.1.72	4,5-8,0	65	0,75
CZ0107	Xylanase 11A	*Bacillus subtilis*	GH11	3.2.1.8	6,0	40	1
CZ0185	Xylanase 10D	*Clostridium thermocellum*	GH10	3.2.1.8	6,0-9,0	60	1
CZ0204	Xylanase 10D	*Cellvibrio japonicus*	GH10	3.2.1.8	5,0-8,0	50	1
CZ0275	Xylanase 10A	*Thermobifida fusca*	GH10	3.2.1.8	5,0-8,0	50	1
CZ0276	Xylanase 11A	*Thermobifida fusca*	GH11	3.2.1.8	5,0-8,0	50	1
CZ0290	Xylanase 11A	*Podospora anserina*	GH11-CBM1	3.2.1.8	5,0-7,0	50	0,5
CZ0325	Xylanase 11A	*Ruminococcus flavefaciens*	GH11	3.2.1.8	6,5	37	1
CZ0382	Xylanase 10A	*Caldicellulosiruptor saccharolyticus*	GH10	3.2.1.8	5,5-6,0	70	1
CZ0383	Xylanase 10B	*Caldicellulosiruptor saccharolyticus*	GH10	3.2.1.8	7,5	70-85	1

XYLANASES (CONT.)

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0401	Xylanase 10A	*Bacillus halodurans*	GH10	3.2.1.8	9,0-10,0	65-75	1
CZ0433	Xylanase 11B	*Ruminococcus flavefaciens*	GH11	3.2.1.8	6,5	37	1
CZ0491	Xylanase 98A	*Bacteroides ovatus*	GH98-CBM35	3.2.1.8	7,2	25	0,5
CZ0495	Xylanase 10A	*Bacteroides ovatus*	GH10	3.2.1.8	7,2	25	1
CZ0563	Xylanase 10A	*Thermotoga maritima*	GH10	3.2.1.8	5,8	90	0,5
CZ0716	Xylanase 10B	*Bacteroides ovatus*	GH10-CBM22-GH10	3.2.1.8	7,2	37	0,25
CZ0718	Xylanase 11A	*Cellvibrio japonicus*	GH11	3.2.1.8	7,0	37	0,25
CZ0746	Xylanase 5A	*Bacteroides eggerthii*	GH5	3.2.1.8	6,0	37	1
CZ0900	Xylanase 10A	*Ruminococcus champanellensis*	CBM22-GH10	3.2.1.8	6,0	37	1
CZ0911	Xylanase 10A	*Thermobifida fusca*	GH10-CBM2	3.2.1.8	5,5-6,0	55-60	1
CZ0912	Xylanase 11A	*Thermobifida fusca*	GH11-CBM2	3.2.1.8	5,0-8,0	50	0,5
CZ0915	Xylanase 8A	*Clostridium papyrosolvens*	GH8-doc-doc	3.2.1.8	6,0	37	1
CZ0918	Xylanase 10A	*Geobacillus stearothermophilus*	GH10-doc	3.2.1.8	6,5	65	1
CZ0945	Xylanase 98A	*Ruminococcus champanellensis*	GH98-CBM35	3.2.1.8	6,0	37	0,5
CZ0975	Xylanase 10A	*Alicyclobacillus acidocaldarius*	GH10	3.2.1.8	6,0-8,0	75	1
CZ0987	Xylanase 10A	*Ruminococcus flavefaciens*	CBM22-GH10-Doc	3.2.1.8	6,5-7,5	37	1
CZ0988	Xylanase 10B	*Ruminococcus flavefaciens*	CBM22-GH10-CBM22-Doc	3.2.1.8	6,5-7,5	37	0,5
CZ0995	Xylanase 10BA & Arabinofuranosidase 43B	*Ruminococcus champanellensis*	CBM22-GH10-CBM22-GH43-CBM6	3.2.1.8 and 3.2.1.55	5,0-6,0	37	0,5
CZ0996	Xylanase 11A	*Ruminococcus champanellensis*	GH11-CBM22-doc-CBM22-CE4	3.2.1.8	5,0-6,0	37	0,5
CZ1000	Xylanase 10A	*Clostridium papyrosolvens*	GH10	3.2.1.8	6,5-7,5	37	1
CZ1028	Xylanase 30A	*Ruminococcus champanellensis*	GH30	3.2.1.8	6,0	37	1
CZ1030	Xylanase 30B	*Ruminococcus champanellensis*	GH30-CBM22	3.2.1.8	6,0	37	1
CZ1051	Xylanase 10B	*Thermotoga maritima*	GH10	3.2.1.8	6,2	75	1
CZ1063	Xylanase 10A	*Zobellia galactanivorans*	GH10	3.2.1.8	6,5-7,5	37	0,5
CZ1079	Xylanase 10A	*Rhodopirellula baltica*	GH10	3.2.1.8	6,5-7,5	37	0,25

XYLOGLUCANASES

Xyloglucanases are enzymes that cleave the 1,4-β-glucan backbone of xyloglucan but do not attack cellulosic substrates. The majority of 1,4-β-glucan active enzymes may non-specifically cleave xyloglucan.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0021	Xyloglucanase 74A	*Clostridium thermocellum*	GH74	3.2.1.151	6,0-8,0	60	1,75
CZ0522	Xyloglucanase 5A	*Paenibacillus pabuli*	GH5	3.2.1.151	5,5	30	1
CZ0535	Xyloglucanase 74A	*Acidothermus cellulolyticus*	GH74	3.2.1.-	4,0-5,0	75-83	0,5
CZ0866	Xyloglucanase 9A	*Clostridium cellulolyticum*	CBM30-GH9-doc-doc	3.2.1.151	6,0	37	0,5
CZ0888	Xyloglucanase 74A	*Clostridium cellulolyticum*	GH74-doc-doc	3.2.1.151	6,5-7,5	37	0,5
CZ0944	Xyloglucanase 74A	*Ruminococcus champanellensis*	GH74	3.2.1.151	6,0	37	1
CZ0998	Xyloglucanase 44A	*Ruminococcus champanellensis*	GH44-CBM76	3.2.1.151	5,0-6,0	37	0,5

XYLOSIDASES

Xylosidases are exo-acting enzymes that act on poly or oligosaccharides to remove successive D-xylose residues from the reducing or non-reducing termini of the carbohydrate.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0206	Xylosidase 43A	*Cellvibrio japonicus*	GH43	3.2.1.37	7,0	25	1
CZ0207	Xylosidase 43B	*Cellvibrio japonicus*	GH43	3.2.1.37 and 3.2.1.55	7,0	37	1
CZ0310	Xylosidase 43A	*Bacteroides ovatus*	GH43	3.2.1.37	6,8	37	1
CZ0389	Xylosidase 43A	*Bifidobacterium adolescentis*	GH43	3.2.1.37	6,0	55	1
CZ0462	Xylosidase 120B	*Bifidobacterium adolescentis*	GH120	3.2.1.37	6,0	45	0,25
CZ0486	Xylosidase 3A	*Bacteroides ovatus*	GH3	3.2.1.37	7,2	25	0,5
CZ0488	α-Xylosidase 31A	*Bacteroides ovatus*	GH31	3.2.1.177	7,2	25	0,5
CZ0536	Xylosidase 120A	*Thermoanaerobacterium saccharolyticum*	GH120	3.2.1.37	6,0	65	1
CZ0706	Xylosidase 3A	*Thermotoga maritima*	GH3	3.2.1.37	7,5	100	0,5
CZ0715	β-Xylosidase 43B	*Bacteroides ovatus*	GH43	3.2.1.37	7,2	37	1
CZ0776	Xylosidase 3A	*Pseudothermotoga thermarum*	GH3	3.2.1.37	5,0-7,0	75-85	0,5
CZ0789	Xylosidase 39A	*Clostridium stercorarium*	GH39	3.2.1.37	5,5-6,5	60	0,25
CZ0910	Xylosidase 43A	*Thermobifida fusca*	GH43	3.2.1.37	5,5-6,0	55-60	0,5
CZ0957	Xylosidase 43A	*Clostridium stercorarium*	GH43	3.2.1.37	3,5	80	0,25
CZ0971	Xylosidase 3A	*Prevotella bryantii*	GH3	3.2.1.37	5,5	37	1
CZ1010	Xylosidase 3A	*Sulfolobus solfataricus*	GH3	3.2.1.37 and 3.2.1.56	6,5	75	0,25
CZ1062	Xylosidase 43A	*Zobellia galactanivorans*	GH43	3.2.1.37	6,5-7,5	37	0,5

OTHER ACTIVITIES

Below are a range of enzymes that are not in sufficient number to be classified as a separate group.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0388	Sucrose phosphorylase 13 A	*Bifidobacterium adolescentis*	GH13	2.4.1.7	6,5-7,0	30	1
CZ0402	Glucan 1,4-α-maltohexaosidase 13A	*Bacillus halodurans*	GH13	3.2.1.98	7,0	25	1
CZ0518	1,3-β-Glucanosyltransglucosidase 17A	*Pseudomonas putida*	GH17	2.4.1.-	6,5	22	1
CZ0521	Endoglycosylceramidase 5A	*Rhodococcus sp.*	GH5	3.2.1.123	5,0	37	0,25
CZ0531	Sucrose glucosylmutase 13A	*Erwinia rhapontici*	GH13	5.4.99.11	5,0	30	1
CZ0787	Oligosaccharide 4-α-D-glucosyl-transferase 31A	*Cellvibrio japonicus*	GH31	2.4.1.161	6,5	25	1
CZ0796	Sulfoquinovosidase 31A	*Escherichia coli*	GH31	3.2.1.-	6,0	37	1
CZ0800	Inulosucrase 68A	*Lactobacillus gasseri*	GH68	2.4.1.9	4,5-6,0	50	0,5
CZ0802	β-Mannooligosaccharide phosphorylase 130A	*Ruminococcus albus*	GH130	2.4.1.319	6,5	30	1
CZ0803	Aceric acid hydrolase 127A	*Bacteroides thetaiotaomicron*	GH127	3.2.1.-	6,5-7,5	37	1
CZ0809	Endo-apiosidase 140A	*Bacteroides thetaiotaomicron*	GH140	3.2.1.-	6,5-7,5	37	1
CZ0815	α-1,4-Glucan branching enzyme 13A	*Escherichia coli*	CBM48-GH13	2.4.1.18	6,5-7,5	37	0,25
CZ0819	Dha hydrolase 143A & β-L-Arabino-furanosidase 142A	*Bacteroides thetaiotaomicron*	GH143-GH142	3.2.1.- and 3.2.1.185	6,5-7,5	37	1
CZ0820	Mannosylglycerate hydrolase 63A	*Rubrobacter radiotolerans*	GH63	3.2.1.170	4,0	55	0,25
CZ0848	Rhamnogalacturonan rhamnohy-drolase 106A	*Bacteroides thetaiotaomicron*	GH106	3.2.1.174	6,5-7,5	37	1
CZ0872	Cyclomaltodextrinase 13A	*Paenibacillus sp.*	CBM34-GH13	3.2.1.54	7,0	40	0,25
CZ0884	α-Rhamnosidase 78B & Kdo hydrolase 33A	*Bacteroides thetaiotaomicron*	CBM67-GH78-GH33	3.2.1.40 and 3.2.1.-	6,5-7,5	37	1
CZ0929	Cyclodextrin glucanotransferase 13A	*Bacillus sp.*	GH13-CBM20	2.4.1.19	9,0	40	0,25
CZ0930	β-L-Arabinosidase 27A	*Geobacillus stearothermophilus*	GH27	3.2.1.88	5,0-6,0	50	1
CZ0932	Amylosucrase 13A	*Neisseria polysaccharea*	GH13	2.4.1.4	7,0	30	0,5
CZ0941	Glucosylceramidase 3A	*Paenibacillus sp.*	GH3	3.2.1.45	6,5	37	1
CZ0956	Nigerose phosphorylase 65A	*Clostridium phytofermentans*	GH65	2.4.1.279	7,0	40	0,25
CZ0964	Cellodextrin phosphorylase 94A	*Ruminococcus albus*	GH94	2.4.1.49	6,0	37	1
CZ0979	3-O-α-D-Glucosyl-L-rhamnose phosphorylase 65A	*Clostridium phytofermentans*	GH65	2.4.1.282	6,5	30	1
CZ1003	Aceric acid hydrolase 127B	*Bacteroides thetaiotaomicron*	GH127	3.2.1.-	6,5-7,5	37	1
CZ1025	Dha hydrolase 143A	*Bacteroides thetaiotaomicron*	GH143	3.2.1.-	6,5-7,5	37	1

carbohydrate esterases

ACETYL XYLAN ESTERASES

ACETYLGLUCOSAMINE DEACETYLASES

DIACETYLCHITOBIOSE DEACETYLASES

FERULOYL ESTERASES

GLUCURONYL ESTERASES

PECTIN ACETYL ESTERASES

PECTIN METHYLESTERASES

* Structure of Feruloyl esterase 1A from *Clostridium thermocellum* (PDB 1GKL), #CZ0031, pg 41

ACETYL XYLAN ESTERASES

Acety xylan esterases hydrolyze the ester linkages of the acetyl groups in position 2 and/or 3 of the xylose moieties of natural acetylated xylan and xylo-oligosaccharides.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0010	Cellulase 5C & Acetyl xylan esterase 2A	*Clostridium thermocellum*	GH5-CE2	3.2.1.4 and 3.1.1.72	6,5-8,0	60	1
CZ0032	Acetyl xylan esterase 2A	*Clostridium thermocellum*	CE2	3.1.1.72	6,5-8,0	50	2
CZ0033	Acetyl xylan esterase 3A	*Clostridium thermocellum*	CE3	3.1.1.72	6,0-8,0	50	2,5
CZ0034	Acetyl xylan esterase 4A	*Clostridium thermocellum*	CE4	3.1.1.72	5,0-7,5	65	4
CZ0051	Xylanase 11A & Acetyl xylan esterase 4A	*Clostridium thermocellum*	GH11-CBM6-CE4	3.2.1.8 and 3.1.1.72	4,5-8,0	65	0,75
CZ0052	Acetyl xylan esterase 4A	*Clostridium thermocellum*	CBM6-CE4	3.1.1.72	4,5-8,0	65	1,5
CZ0132	Acetyl xylan esterase 7A	*Bacillus subtilis*	CE7	3.1.1.72 and 3.1.1.41	6,5	37	1
CZ0134	Acetyl xylan esterase 12A	*Bacillus subtilis*	CE12	3.1.1.72	8,5	35	1
CZ0210	Acetyl xylan esterase 2C	*Cellvibrio japonicus*	CE2	3.1.1.72	6,0	40	0,25
CZ0241	Acetyl xylan esterase 7A	*Thermotoga maritima*	CE7	3.1.1.72	7,5	100	1
CZ0242	Acetyl xylan esterase 4A	*Cellvibrio japonicus*	CE4	3.1.1.72	7,0	37	0,25
CZ0327	Acetyl xylan esterase 15A	*Ruminococcus flavefaciens*	CE15	3.1.1.72	7,5	37	1
CZ0435	Acetyl xylan esterase 3A	*Ruminococcus flavefaciens*	CE3	3.1.1.72	6,8	35	1
CZ0436	Acetyl xylan esterase 3B	*Ruminococcus flavefaciens*	CE3	3.1.1.72	6,8	37	1
CZ0682	Acetyl xylan esterase 6A	*Fibrobacter succinogenes*	CE6	3.1.1.72	7,0	45	1
CZ0685	Acetyl xylan esterase 6B	*Fibrobacter succinogenes*	CE6	3.1.1.72	7,0	37	1
CZ0785	Acetyl xylan esterase 2B	*Cellvibrio japonicus*	CE2	3.1.1.72	6,0	40	1
CZ0949	Acetyl xylan esterase 12A	*Bacillus halodurans*	CE12	3.1.1.72	7,3	37	1

ACETYLGLUCOSAMINE DEACETYLASES

Acetylglucosamine deacetylases are enzymes that deacetylate carbohydrates containing N-acetyl-D-glucosamine.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0133	N-acetylglucosamine 6-phosphate deacetylase 9A	*Bacillus subtilis*	CE9	3.5.1.25	8,0	37	1
CZ0170	N-acetylglucosamine 6-phosphate deacetylase 9B	*Escherichia coli*	CE9	3.5.1.25	7,5	30	1
CZ0190	UDP-acetylglucosamine deacetylase 11A	*Escherichia coli*	CE11	3.5.1.-	7,5	30	1
CZ0224	Peptidoglycan N-acetylglucosamine deacetylase 4A	*Streptococcus pneumoniae*	CE4	3.5.1.-	7,0	37	1
CZ0429	UDP-acetylglucosamine deacetylase 11A	*Pseudomonas aeruginosa*	CE11	3.5.1.-	7,5	30	1
CZ0520	N-Acetylglucosaminylphosphatidylinositol deacetylase 14A	*Mycobacterium tuberculosis*	CE14	3.5.1.89	7,5	37	0,5
CZ0683	N-Acetylglucosaminylphosphatidylinositol deacetylase 14A	*Mycobacterium smegmatis*	CE14	3.5.1.89	8,0	37	1
CZ0699	Peptidoglycan N-Acetylglucosamine deacetylase 4A	*Bacillus subtilis*	CE4	3.5.1.-	7,0	37	0,25

DIACETYLCHITOBIOSE DEACETYLASES

Diacetylchitobiose deacetylases are enzymes that deacetylate diacetylchitobiose.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0439	Diacetylchitobiose deacetylase 14A	*Bacillus cereus*	CE14	3.5.1.-	8,0	37	1

FERULOYL ESTERASES

Feruloyl esterases catalyze the hydrolysis of the 4-hydroxy-3-methoxycinnamoyl (feruloyl) group from an esterified sugar, which is usually arabinose in "natural" substrates. These enzymes have the ability not only to deconstruct plant biomass, through the release of lignin from carbohydrates, but also to synthesize a broad range of novel bioactive components for use in food, cosmetic and pharmaceutical industries.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0031	Feruloyl esterase 1A	*Clostridium thermocellum*	CE1	3.1.1.73	4,0-7,0	60	2
CZ0143	Feruloyl esterase 1B	*Clostridium thermocellum*	CE1	3.1.1.73	4,0-7,0	60	1
CZ0405	Feruloyl esterase 1A	*Ruminococcus albus*	CE1	3.1.1.73	7,0	37	1
CZ0580	Feruloyl esterase 1A	*Clostridium cellulovorans*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0581	Feruloyl esterase 1A	*Clostridium saccharoperbutylacetonicum*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0582	Feruloyl esterase 1A	*Clostridium stercorarium*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0583	Feruloyl esterase 1A	*Melioribacter roseus*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0584	Feruloyl esterase 1A	*Streptococcus pneumoniae*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0585	Feruloyl esterase 1A	*Streptococcus pyogenes*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0586	Feruloyl esterase 1A	*Zunongwangia profunda*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0587	Feruloyl esterase 1A	*Sphingomonas wittichii*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0588	Feruloyl esterase 1A	*Dickeya dadantii*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0589	Feruloyl esterase 1A	*Lactobacillus fabifermentans*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0590	Feruloyl esterase 1A	*Opitutus terrae*	CE1	3.1.1.73	7,0-9,0	37	0,25
CZ0591	Feruloyl esterase 1A	*Lactobacillus buchneri*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0592	Feruloyl esterase 1A	*Lactobacillus johnsonii*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0593	Feruloyl esterase 1B	*Lactobacillus johnsonii*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0594	Feruloyl esterase 1A	*Uncultured rumen bacterium*	CE1	3.1.1.73	7,0-9,0	37	0,25
CZ0595	Feruloyl esterase 1B	*Uncultured soil bacterium*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0596	Feruloyl esterase 1C	*Butyrivibrio fibrisolvens*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0597	Feruloyl esterase 1A	*Acetivibrio cellulolyticus*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0598	Feruloyl esterase 1A	*Lactobacillus reuteril*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0599	Feruloyl esterase 1A	*Paenibacillus mucilaginosus*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0600	Feruloyl esterase 1B	*Clostridium saccharoperbutylacetonicum*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0601	Feruloyl esterase 1B	*Mycobacterium avium*	CE1	3.1.1.73	7,0-9,0	37	0,5

FERULOYL ESTERASES (CONT.)

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0602	Feruloyl esterase 1A	*Mycobacterium mageritense*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0603	Feruloyl esterase 1A	*Butyrivibrio proteoclasticus*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0604	Feruloyl esterase 1A	*Cellulosilyticum ruminicola*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0605	Feruloyl esterase 1A	*Thermobacillus xylanilyticus*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0606	Feruloyl esterase 1B	*Bacteroides cellulosilyticus*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0607	Feruloyl esterase 1A	*Butyrivibrio fibrisolvens*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0608	Feruloyl esterase 1B	*Butyrivibrio fibrisolvens*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0609	Feruloyl esterase 1A	*Paenibacillus polymyxa*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0610	Feruloyl esterase 1A	*Paenibacillus terrae*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0611	Feruloyl esterase 1A	*Amycolatopsis mediterranei*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0612	Feruloyl esterase 1A	*Mycobacterium smegmatis*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0613	Feruloyl esterase 1A	*Klebsiella oxytoca*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0614	Feruloyl esterase 1B	*Mycobacterium mageritense*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0615	Feruloyl esterase 1A	*Klebsiella pneumoniae*	CE1	3.1.1.73	7,0-9,0	37	0,25
CZ0616	Feruloyl esterase 1A	*Mycobacterium kansasii*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0617	Feruloyl esterase 1A	*Rhodococcus jostii*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0618	Feruloyl esterase 1A	*Actinomyces sp.*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0619	Feruloyl esterase 1B	*Klebsiella pneumoniae*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0620	Feruloyl esterase 1B	*Butyrivibrio proteoclasticus*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0621	Feruloyl esterase 1B	*Ruminococcu salbus*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0622	Feruloyl esterase 1A	*Deinococcus gobiensis*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0623	Feruloyl esterase 1A	*Lactobacillus amylovorus*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0624	Feruloyl esterase 1A	*Lactobacillus kefiranofaciens*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0625	Feruloyl esterase 1B	*Paenibacillus terrae*	CE1	3.1.1.73	7,0-9,0	37	0,25
CZ0626	Feruloyl esterase 1A	*Butyrivibrio sp.*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0627	Feruloyl esterase 1A	*Mycobacterium tuberculosis*	CE1	3.1.1.73	7,0-9,0	37	0,25
CZ0628	Feruloyl esterase 1A	*Lactobacillus helveticus*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0629	Feruloyl esterase 1A	*Shigella boydii*	CE1	3.1.1.73	7,0-9,0	37	0,25
CZ0630	Feruloyl esterase 1C	*Clostridium saccharoperbutylace-tonicum*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0631	Feruloyl esterase 1A	*Streptococcus downei*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0632	Feruloyl esterase 1A	*Streptococcus sobrinus*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0633	Feruloyl esterase 1B	*Butyrivibrio sp.*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0634	Feruloyl esterase 1A	*Thioalkalivibrio sp.*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0635	Feruloyl esterase 1A	*Legionella pneumophila*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0636	Feruloyl esterase 1C	*Uncultured bacterium*	CE1	3.1.1.73	7,0-9,0	37	1

FERULOYL ESTERASES (CONT.)

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0637	Feruloyl esterase 1A	*Thermoanaerobacter mathranii*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0638	Feruloyl esterase 1D	*Uncultured bacterium*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0639	Feruloyl esterase 1A	*Olsenella uli*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0640	Feruloyl esterase 1A	*Ruminococcus callidus*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0641	Feruloyl esterase 1A	*Lactobacillus crispatus*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0642	Feruloyl esterase 1A	*Streptococcus criceti*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0643	Feruloyl esterase 1C	*Paenibacillus terrae*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0644	Feruloyl esterase 1A	*Eubacterium rectale*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0645	Feruloyl esterase 1A	*Acinetobacter baumannii*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0646	Feruloyl esterase 1C	*Butyrivibrio sp.*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0647	Feruloyl esterase 1A	*Bacteroide reticulotermitis*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0648	Feruloyl esterase 1A	*Leuconostoc citreum*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0649	Feruloyl esterase 1A	*Bacteroides plebeius*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0650	Feruloyl esterase 1A	*Bacillus licheniformis*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0651	Feruloyl esterase 1B	*Lactobacillus kefiranofaciens*	CE1	3.1.1.73	7,0-9,0	37	0,25
CZ0652	Feruloyl esterase 1A	*Lactobacillus acidophilus*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0653	Feruloyl esterase 1A	*Variovorax paradoxus*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0654	Feruloyl esterase 1B	*Lactobacillus crispatus*	CE1	3.1.1.73	7,0-9,0	37	0,25
CZ0655	Feruloyl esterase 1A	*Lactobacillus delbrueckii*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0656	Feruloyl esterase 1A	*Bifidobacterium bifidum*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0657	Feruloyl esterase 1A	*Streptococcus sanguinis*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0658	Feruloyl esterase 1A	*Mycobacterium vanbaalenii*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0659	Feruloyl esterase 1A	*Bifidobacterium longum*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0660	Feruloyl esterase 1A	*Bifidobacterium breve*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0661	Feruloyl esterase 1A	*Segniliparus rotundus*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0662	Feruloyl esterase 1A	*Pelagibacter halotolerans*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0663	Feruloyl esterase 1B	*Bifidobacterium longum*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0664	Feruloyl esterase 1A	*Frankia sp.*	CE1	3.1.1.73	7,0-9,0	37	0,25
CZ0665	Feruloyl esterase 1B	*Mycobacterium tuberculosis*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0666	Feruloyl esterase 1A	*Mycobacterium tuberculosis*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0667	Feruloyl esterase 1C	*Mycobacterium tuberculosis*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0668	Feruloyl esterase 1A	*Spiribacter salinus*	CE1	3.1.1.73	7,0-9,0	37	1
CZ0669	Feruloyl esterase 1A	*Ruegeria pomeroyi*	CE1	3.1.1.73	7,0-9,0	37	0,25
CZ0670	Feruloyl esterase 1A	*Lysinibacillus sphaericus*	CE1	3.1.1.73	7,0-9,0	37	0,25
CZ0671	Feruloyl esterase 1B	*Dickeya dadantii*	CE1	3.1.1.73	7,0-9,0	37	1

FERULOYL ESTERASES (CONT.)

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0672	Feruloyl esterase 1B	*Frankia sp.*	CE1	3.1.1.73	7,0-9,0	37	0,5
CZ0727	Feruloyl esterase 1B	*Anaeromyces mucronatus*	CE1	3.1.1.73	7,2	37	0,5

GLUCURONYL ESTERASES

Glucuronyl esterases participate in the hydrolysis of the ester bond between 4-O-methyl-D-glucuronic acid residues of glucuronoxylans and aromatic alcohols of lignin.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0573	Glucuronyl esterase 15B	*Teredinibacter turnerae*	CE15	3.1.1.-	6,0	37	0,5
CZ0574	Glucuronyl esterase 15A	*Clostridium cellobioparum*	CE15	3.1.1.-	6,0	37	1
CZ0575	Glucuronyl esterase 15A	*Teredinibacter turnerae*	CE15	3.1.1.-	6,0	37	1
CZ0576	Glucuronyl esterase 15A	*Zobellia galactanivorans*	CE15	3.1.1.-	6,0	37	0,5
CZ0577	Glucuronyl esterase 15B	*Opitutus terrae*	CE15	3.1.1.-	6,0	37	1
CZ0578	Glucuronyl esterase 15A	*Caldicellulosiruptor kristjanssonii*	CE15	3.1.1.-	6,0	37	0,5
CZ0579	Glucuronyl esterase 15A	*Prevotella ruminicola*	CE15	3.1.1.-	6,0	37	1

PECTIN ACETYL ESTERASES

Pectin acetyl esterases are enzymes that participate in the removal of the acetyl side chains of pectin.

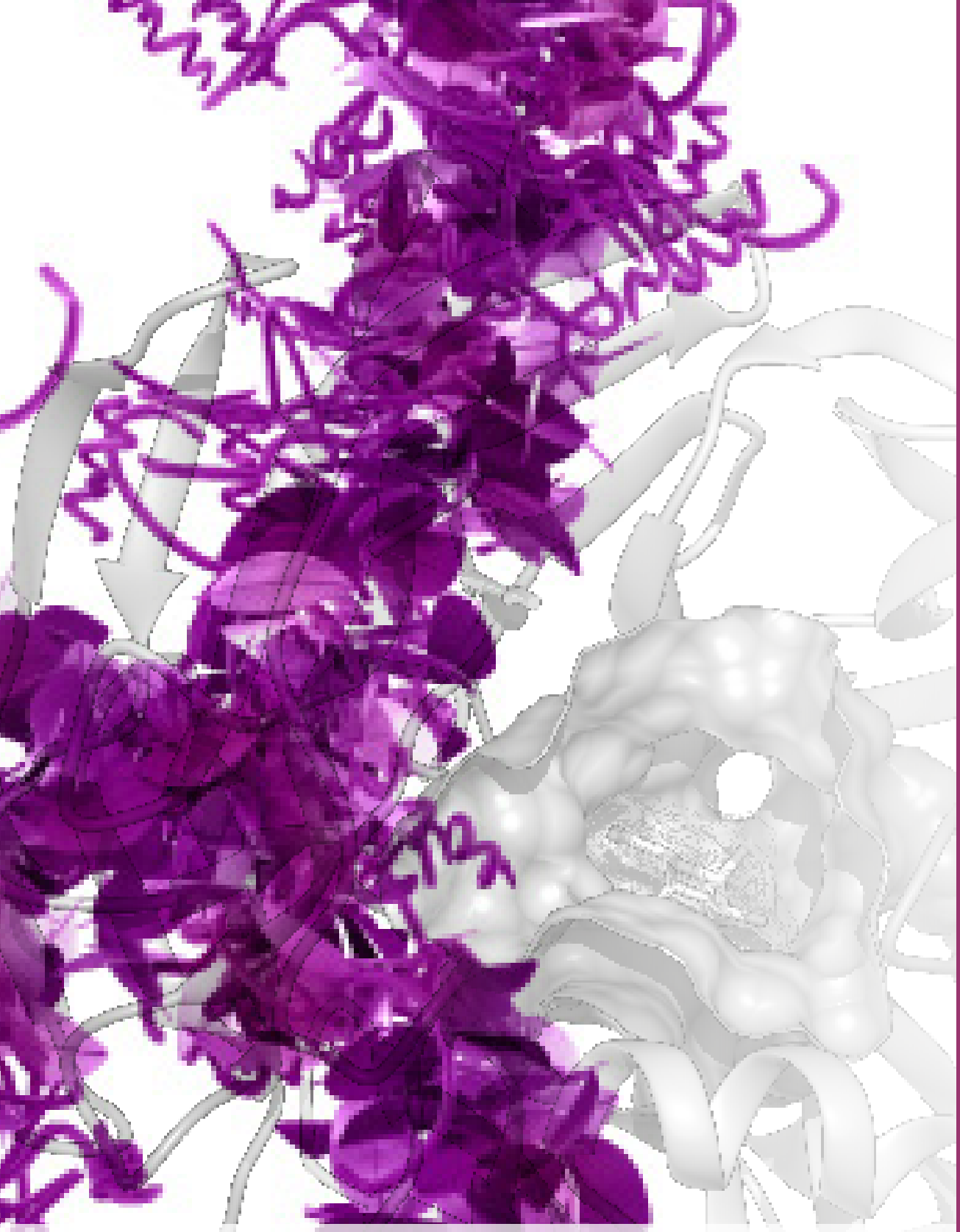
Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0036	Pectin acetyl esterase 12A	*Clostridium thermocellum*	CE12	3.1.1.-	6,0-8,5	65	2
CZ0037	Pectin acetyl esterase 12B	*Clostridium thermocellum*	CE12	3.1.1.-	6,0-8,5	65	1,5
CZ0814	Pectin acetyl Esterase 12A	*Dickeya dadantii*	CE12	3.1.1.-	8,0	30	1
CZ1013	RGI acetyl esterase NC	*Bacteroides thetaiotaomicron*	CE NC	3.1.1.-	6,5-7,5	37	0,25

PECTIN METHYLESTERASES

Pectin methylesterases are enzymes that participate in the removal of the methyl side chains of pectin.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0216	Pectin methylesterase 8A	*Dickeya dadantii*	CE8	3.1.1.11	8,0-9,0	50	1
CZ0721	Pectin methylesterase 8A	*Ruminiclostridium thermocellum*	CE8	3.1.1.11	8,0-9,0	45-70	0,25
CZ0791	Pectin methylesterase 8A	*Dickeya chrysanthemi*	CE8	3.1.1.11	7,5	40	1
CZ0813	Pectin methylesterase NC	*Bacteroides thetaiotaomicron*	CE NC	3.1.1.11	8,0-9,0	37	1

polysaccharide lyases



ALGINATE LYASES

CHONDROITIN LYASES

HEPARIN LYASES

HYALURONATE LYASES

OLIGOGALACTURONATE LYASES

PECTATE LYASES

PECTIN LYASES

POLY-α-GULURONATE LYASES

RHAMNOGALACTURONAN LYASES

ULVAN LYASES

XANTHAN LYASES

* Structure of Oligogalacturonate lyase 22A from *Yersinia enterocolitica* (PDB 3PE7), #CZ0726, pg 47

ALGINATE LYASES

Alginate lyases are enzymes that catalyze the degradation of alginate by a β-elimination mechanism. Alginate is an anionic polysaccharide distributed widely in the cell walls of brown algae, where through binding with water it forms a viscous gum.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0312	Oligoalginate lyase 17A	*Saccharophagus degradans*	PL17	4.2.2.-	7,5	30	1
CZ0431	Alginate lyase 7A	*Saccharophagus degradans*	PL7	4.2.2.3	7,0	50	1
CZ0432	Oligoalginate lyase 7A	*Pseudomonas aeruginosa*	PL7	4.2.2.-	8,5	40	1
CZ0529	Alginate lyase 7A	*Agarivorans sp.*	PL7	4.2.2.-	9,0-10,0	30	1
CZ0540	Alginate lyase 5A	*Sphingomonas sp.*	PL5	4.2.2.3	8,0	30	1
CZ0756	Alginate lyase 7A	*Zobellia galactanivorans*	PL7	4.2.2.-	7,0	30	1
CZ0937	Alginate lyase 15A	*Agrobacterium fabrum*	PL15	4.2.2.-	7,5	30	1
CZ0938	Oligoalginate lyase 15A	*Sphingomonas sp.*	PL15	4.2.2.-	7,5-8,5	37	0,5
CZ0940	Alginate lyase 7A	*Vibrio sp.*	PL7	4.2.2.3	7,6-9,0	30	0,5
CZ1078	Alginate lyase 7A	*Rhodopirellula baltica*	PL7	4.2.2.-	6,5-7,5	37	1
CZ1081	Alginate lyase 7A	*Photobacterium sp.*	PL7	4.2.2.-	6,5-7,5	37	1
CZ1084	Alginate lyase 7B	*Agarivorans sp*	PL7	4.2.2.-	6,5-7,5	37	1
CZ1085	Alginate lyase 7A	*Klebsiella pneumoniae*	PL7	4.2.2.-	6,5-7,5	37	1
CZ1086	Alginate lyase 14A	*Zobellia galactanivorans*	PL14	4.2.2.-	6,5-7,5	37	0,5

CHONDROITIN LYASES

Chondroitin lyases are enzymes that catalyze the degradation of chondroitin by a β-elimination mechanism. Chondroitin sulfate is a sulfated glycosaminoglycan (GAG) composed of a chain of alternating sugars (N-acetylgalactosamine and glucuronic acid). It is usually found attached to proteins as part of a proteoglycan.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0157	Chondroitin ABC lyase 8B	*Bacteroides thetaiotaomicron*	PL8	4.2.2.20	7,6	37	0,5
CZ0722	Chondroitin AC lyase 8A	*Pseudopedobacter saltans*	PL8	4.2.2.5	7,2	39	0,5
CZ0817	Chondroitin AC lyase 8A	*Pedobacter heparinus*	PL8	4.2.2.5	6,5-7,5	40	0,5
CZ0935	Chondroitin AC lyase 8A	*Bacteroides stercoris*	PL8	4.2.2.5	5,5-6,5	45	0,25

HEPARIN LYASES

Heparin lyases are enzymes that participate in the eliminative cleavage of polysaccharides containing 1,4-linked D-glucuronate or L-iduronate residues and 1,4-α-linked 2-sulfoamino-2- deoxy-6-sulfo-D-glucose residues to give oligosaccharides with terminal 4-deoxy-α-D-gluc-4-enuronosyl groups at their non-reducing ends.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0158	Heparin-sulfate lyase 12A	*Bacteroides thetaiotaomicron*	PL12	4.2.2.8	7,0	37	1
CZ0159	Heparin lyase 13A	*Bacteroides thetaiotaomicron*	PL13	4.2.2.7	6,7-7,3	37	1
CZ0766	Heparin-sulfate lyase 12B	*Bacteroides thetaiotaomicron*	PL12	4.2.2.8	6,0-7,5	25-37	1
CZ0801	Heparin-sulfate lyase 12A	*Pedobacter heparinus*	PL12	4.2.2.8	7,0-8,0	35	0,5
CZ0857	Heparin lyase 15A	*Bacteroides thetaiotaomicron*	PL15	4.2.2.-	6,5	37	1
CZ0934	Heparin lyase 21A	*Bacteroides stercoris*	PL21	4.2.2.8 and 4.2.2.7	7,4	32	1

HYALURONATE LYASES

Hyaluronate lyases are enzymes that cleave hyaluronate chains at a β-D-GalNAc-1,4-β-D-GlcA bond, ultimately breaking the polysaccharide down to 3-(4-deoxy-β-D-gluc-4-enuronosyl)-N-acetyl-D-glucosamine.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0981	Hyaluronate lyase 8A	*Streptococcus pneumoniae*	PL8	4.2.2.1	6,0	30	1

OLIGOGALACTURONATE LYASES

Oligogalacturonate lyases are enzymes that participate in the eliminative cleavage of 4-(4-deoxy-β-D-gluc-4-enuronosyl)-D-galacturonate.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0251	Oligogalacturonate lyase 22A	*Dickeya dadantii*	PL22	4.2.2.6	7,2	30	1
CZ0726	Oligogalacturonate lyase 22A	*Yersinia enterocolitica*	PL22-PL22	4.2.2.6	7,0	37	1

PECTATE LYASES

Pectate lyases are enzymes involved in the maceration and soft rotting of plant tissue. Pectate lyases are responsible for the eliminative cleavage of pectate, yielding oligosaccharides with 4-deoxy-α-D-mann-4-enuronosyl groups at their non-reducing ends.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0038	Pectate lyase 1A	*Clostridium thermocellum*	PL1	4.2.2.2	7,0-10,4	55	1
CZ0039	Pectate lyase 9A	*Clostridium thermocellum*	PL9	4.2.2.2	7,0-9,0	60	1
CZ0130	Pectate lyase 1A	*Bacillus subtilis*	PL1	4.2.2.2	8,5	55	1
CZ0131	Pectate lyase 3C	*Bacillus subtilis*	PL3	4.2.2.2	10,5	40-45	1
CZ0208	Pectate lyase 10A	*Cellvibrio japonicus*	PL10	4.2.2.2	9,5-10,5	62	1
CZ0240	Pectate lyase 1A	*Thermotoga maritima*	PL1	4.2.2.2	8,5	37	1
CZ0247	Pectate lyase 1A	*Dickeya dadantii*	PL1	4.2.2.2	8,5	37	1
CZ0248	Exo-pectate lyase 2A	*Dickeya dadantii*	PL2	4.2.2.9	8,5	37	0,25
CZ0250	Pectate lyase 9A	*Dickeya dadantii*	PL9	4.2.2.2	8,0	37	1

PECTATE LYASES (CONT.)

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0303	Pectate lyase 1A	*Erwinia chrysanthemi*	PL1	4.2.2.2	8,5	55	1
CZ0304	Pectate lyase 1B	*Erwinia chrysanthemi*	PL1	4.2.2.2	8,0-8,8	50	1
CZ0309	Pectate lyase 9A	*Clostridium cellulovorans*	PL9	4.2.2.2	9,0	37	1
CZ0398	Pectate lyase 2A	*Pectobacterium carotovorum*	PL2	4.2.2.2	8,5	37	1
CZ0417	Exo-pectate lyase 9A	*Erwinia chrysanthemi*	PL9	4.2.2.9	7,0-9,0	37	1
CZ0460	Pectate lyase 1A	*Bacillus halodurans*	PL1	4.2.2.2	9,0	50	0,25
CZ0513	Pectate lyase 1B	*Dickeya dadantii*	PL1	4.2.2.2	9,0-10,0	55	1
CZ0530	Pectate lyase 10A	*Xanthomonas campestris*	PL10	4.2.2.2	9,0	30	0,25
CZ0539	Pectate lyase 2A	*Klebsiella sp.*	PL2	4.2.2.2	9,0	30-50	1
CZ0558	Pectate lyase 1A	*Bacillus licheniformis*	PL1	4.2.2.2	11,0	50	1
CZ0728	Exo-pectate lyase 2B	*Yersinia enterocolitica*	PL2	4.2.2.9	8,6	37	0,5
CZ0834	Pectate lyase 2A	*Yersinia enterocolitica*	PL2	4.2.2.2	8,6	37	0,5
CZ0836	Pectate lyase 1A	*Bacteroides thetaiotaomicron*	PL1	4.2.2.2	6,5-7,5	37	0,25
CZ0846	Pectate lyase 1B	*Bacteroides thetaiotaomicron*	PL1	4.2.2.2	6,5-7,5	37	1
CZ0885	Pectate lyase 1C	*Bacteroides thetaiotaomicron*	PL1	4.2.2.2	6,5-7,5	37	1
CZ0886	Pectate lyase 1D	*Bacteroides thetaiotaomicron*	PL1	4.2.2.2	6,5-7,5	37	0,5
CZ1077	Pectate lyase 10A	*Rhodopirellula baltica*	PL10	4.2.2.2	6,5-7,5	37	1
CZ1090	Pectate lyase 1A	*Rhodopirellula baltica*	PL1	4.2.2.2	6,5-7,5	37	0,5
CZ1091	Pectate lyase 1B	*Rhodopirellula baltica*	PL1	4.2.2.2	6,5-7,5	37	0,25

PECTIN LYASES

Pectin lyases promote the eliminative cleavage of 1,4-α-D-galacturonan methyl ester to give oligosaccharides with 4-deoxy-6-O-methyl-α-D-galact-4-enuronosyl groups at their non-reducing ends.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0528	Pectin lyase 1A	*Pseudomonas marginalis*	PL1	4.2.2.10	6,6	30-37	0,5
CZ0697	Pectin lyase 1A	*Bacillus subtilis*	PL1	4.2.2.10	8,0	60	0,25

POLY-α-GULURONATE LYASES

Poly-α-guluronate lyases are enzymes that participate in the eliminative cleavage of polysaccharides containing a terminal α-L-guluronate group, to give oligosaccharides with 4-deoxy-α-L-erythro-hex- 4-enuronosyl groups at their non-reducing ends.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0408	Poly α-guluronate lyase 7A	*Zobellia galactanivorans*	PL7	4.2.2.11	7,5	30	1
CZ0755	Poly α-guluronate lyase 7A	*Zobellia galactanivorans*	CBM32-PL7	4.2.2.11	7,0	30	0,5

RHAMNOGALACTURONAN LYASES

Rhamnogalacturonan lyases are endo-enzymes that participate in the eliminative cleavage of L-α- rhamnopyranosyl-1,4-α-D-galactopyranosyluronic acid bonds of rhamnogalacturonan I domains in ramified hairy regions of pectin leaving L-rhamnopyranose at the reducing end and 4-deoxy-4,5- unsaturated D-galactopyranosyluronic acid at the non-reducing end.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0040	Rhamnogalacturonan Lyase 11A	*Clostridium thermocellum*	PL11	4.2.2.-	8,0-10,0	65	0,25
CZ0067	Rhamnogalacturonan Lyase 11A	*Cellvibrio japonicus*	PL11	4.2.2.-	9,0-10,0	45	0,25
CZ0186	Rhamnogalacturonan endolyase 9B	*Bacteroides thetaiotaomicron*	PL9	4.2.2.23	9,0	37	1
CZ0693	Rhamnogalacturonan lyase 4A	*Dickeya dadantii*	PL4	4.2.2.-	6,0	37	0,25
CZ0704	Rhamnogalacturonan endolyase 11A	*Bacteroides thetaiotaomicron*	PL11	4.2.2.23	8,0	37	0,25
CZ0725	L-Rhamnose-1,4-α-D-glucuronate lyase 27A	*Bacteroides cellulosilyticus*	PL27	4.2.2.-	7,0	37	1
CZ0744	Rhamnogalacturonan endolyase 9A	*Bacteroides thetaiotaomicron*	PL9	4.2.2.23	6,5-7,5	37	0,5
CZ0881	Rhamnogalacturonan exolyase 26A	*Bacteroides thetaiotaomicron*	CBM66-PL26	4.2.2.24	6,5-7,5	37	0,5

ULVAN LYASES

Enzymes that catalyze the β-eliminative cleavage of the glycosidic bond between the sulfated rhamnose and the glucuronic or iduronic acid residues in Ulvan.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0740	Ulvan lyase 24A	*Pseudoalteromonas sp.*	PL24	4.2.2.-	8,0	50	1
CZ1069	Ulvan lyase 25A	*Pseudoalteromonas sp.*	PL25	4.2.2.-	6,5-7,5	37	0,25
CZ1070	Ulvan lyase 25A	*Nonlabens ulvanivorans*	PL25	4.2.2.-	6,5-7,5	37	0,5
CZ1072	Ulvan lyase 25A	*Algibacter pectinivorans*	PL25	4.2.2.-	6,5-7,5	37	1
CZ1073	Ulvan lyase 25A	*Arenitalea lutea*	PL25	4.2.2.-	6,5-7,5	37	1
CZ1074	Ulvan lyase 25A	*Catenovulum agarivorans*	PL25	4.2.2.-	6,5-7,5	37	1
CZ1080	Ulvan lyase 25A	*Vibrio celticus*	PL25	4.2.2.-	6,5-7,5	37	1
CZ1083	Ulvan lyase 25B	*Catenovulum agarivorans*	PL25	4.2.2.-	6,5-7,5	37	0,25

XANTHAN LYASES

Enzymes that catalyse the β-eliminative cleavage of the glycosidic bond between the sulfated rhamnose and the glucuronic or iduronic acid residues in Xanthan.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0527	Xanthan lyase 8A	*Paenibacillus alginolyticus*	PL8	4.2.2.12	6,0	45-55	0,5

RHAMNOGLUCURONATE LYASES

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ1092	L-Rhamnose-α1,4-D-glucuronate lyase 42A	*Bacteroides thetaiotaomicron*	PL42	4.2.2.-	7	37	1

auxiliar activities

LACCASES
LYTIC POLYSACCHARIDE MONOOXYGENASES

* Structure of Cellulase 5B from *Bacillus halodurans* (PDB 4V2X), #CZ0476, pg 17

LACCASES

Laccases are copper-containing oxidase enzymes that are found in many plants, fungi and microorganisms. Laccases act on phenols and similar molecules, performing a one-electron oxidation of substrate with the four-electron reduction of molecular oxygen to water. It is proposed that laccases play a role in the formation of lignin by promoting the oxidative coupling of monolignols, a family of naturally occurring phenols.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0120	Laccase A	*Bacillus subtilis*	AA NC	1.3.3.5	3,0	50-60	1
CZ0162	Laccase A	*Escherichia coli*	AA NC	1.10.3.-	6,5	55	1
CZ0541	Laccase 1A	*uncultured bacterium*	AA1	1.10.3.2	7,5	45	1

LYTIC POLYSACCHARIDE MONOOXYGENASES

Lytic polysaccharide monooxygenases (LPMOs) are a recently discovered class of enzymes capable of oxidizing recalcitrant polysaccharides, such as cellulose and chitin. Members of the previously described families CBM33 and family GH61 are in fact LPMOs. These enzymes are attracting considerable attention owing to their potential use in biomass conversion, notably in the production of biofuels.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0274	Lytic cellulose monooxygenase 10A	*Thermobifida fusca*	AA10	1.-.-.-	8,0	50	0,25
CZ0300	Lytic chitin monooxygenase 10A	*Bacillus licheniformis*	AA10	1.-.-.-	6,0-7,0	20-60	1
CZ0463	Lytic chitin monooxygenase 10A	*Lactococcus lactis*	AA10	1.-.-.-	3,8	37	0,25
CZ0512	Lytic cellulose monooxygenase 10A	*Enterococcus faecalis*	AA10	1.-.-.-	6,0	25	0,5
CZ0959	Lytic cellulose monooxygenase 9B	*Geotrichum candidum*	AA9	1.-.-.-	5,0	40	1

carbohydrate-binding modules

CBMs
GFP-CBM
ZZ-CBM

* Structure of Carbohydrate Binding Module 42A from *Clostridium thermocellum* (PDB 3KMV), #CZ0047, pg 53

CBMs

Carbohydrate-binding modules (CBMs) are protein domains found in carbohydrate-active enzymes (CAZymes), for example glycoside hydrolases. The majority of these domains have carbohydrate-binding activity. Some of these domains are found on cellulosomal scaffoldin proteins. CBMs were previously known as cellulose-binding domains. CBMs can recognize both crystalline and amorphous cellulose forms and different hemicelluloses and pectin. CBMs are the most common non-catalytic modules associated with enzymes active in plant cell-wall hydrolysis. CBMs are classified into numerous families, based on amino acid sequence similarity in the CAZy database (www.cazy.org).

Catalogue Number	CBM name	Source Organism	CAZy Architecture	Carbohydrate Ligands	mg/vial
CZ0035	Carbohydrate Binding Module 35A	*Clostridium thermocellum*	CBM35	fj-4,5-anhydro-galacturonic acid	1
CZ0041	Carbohydrate Binding Module 3A	*Clostridium thermocellum*	CBM3	crystalline forms of cellulose	3
CZ0042	Carbohydrate Binding Module 6A	*Celvibrio mixtus*	CBM6	1,3-1,4-β-glucans, 1,3-β-glucans and soluble 1,4-β-glucans	2
CZ0043	Carbohydrate Binding Module 6A	*Clostridium thermocellum*	CBM6	arabinoxylans and arabinogalactans	1,3
CZ0044	Carbohydrate Binding Module 11A	*Clostridium thermocellum*	CBM11	1,3-1,4-β-glucans and soluble 1,4-β-glucans	0,5
CZ0045	Carbohydrate Binding Module 22A	*Clostridium thermocellum*	CBM22	decorated and undecorated 1,4-β-xylans. CBM22 also binds to 1,3-1,4-β-glucans	0,5
CZ0046	Carbohydrate Binding Module 35B	*Clostridium thermocellum*	CBM35	specifically recognizes the galactose side-chains of galactomannan	0,5
CZ0047	Carbohydrate Binding Module 42A	*Clostridium thermocellum*	CBM42	specifically recognizes the arabinose side-chains of arabinoxylan	0,5
CZ0048	Carbohydrate Binding Module 30A	*Clostridium thermocellum*	CBM30	1,3-1,4-β-glucans and soluble undecorated (cellulose) and decorated (xyloglucan) 1,4-β-glucans	3
CZ0049	Carbohydrate Binding Module 44A	*Clostridium thermocellum*	CBM44	1,3-1,4-β-glucans and soluble undecorated (cellulose) and decorated (xyloglucan) 1,4-β-glucans	2
CZ0050	Carbohydrate Binding Module 62A	*Clostridium thermocellum*	CBM62	specifically recognizes the galactose side-chains of xyloglucan and galactomannan	3
CZ0243	Carbohydrate Binding Module 13C	*Ruminococcus flavefaciens*	CBM13	pectins	1
CZ0280	Carbohydrate Binding Module 77	*Ruminococcus flavefaciens*	CBM77	pectins	1
CZ0282	Carbohydrate Binding Module 60A	*Uncultured bacterium*	CBM60	1,4-β-xylans	1
CZ0283	Carbohydrate Binding Module 15A	*Cellvibrio japonicus*	CBM15	xylans	1
CZ0284	Carbohydrate Binding Module 13A	*Clostridium thermocellum*	CBM13	xyloglucan	1
CZ0285	Carbohydrate Binding Module 3D	*Clostridium thermocellum*	CBM3	crystalline forms of cellulose	1
CZ0287	Carbohydrate Binding Module 3E	*Clostridium thermocellum*	CBM3	crystalline forms of cellulose	1
CZ0336	Carbohydrate Binding Module 35C	*Ruminococcus flavefaciens*	CBM35	galactomannans	1
CZ0337	Carbohydrate Binding Module 32A	*Clostridium thermocellum*	CBM32	nonreducing ends of mannooligosaccharides	1
CZ0338	Carbohydrate Binding Module 42B	*Clostridium thermocellum*	CBM42	1,4-β-xylan, xyloglucan and galactomannan	1
CZ0339	Carbohydrate Binding Module 6B	*Clostridium thermocellum*	CBM6	arabinoxylans and arabinogalactans	1
CZ0340	Carbohydrate Binding Module 4A	*Clostridium thermocellum*	CBM4	arabinogalactans and weakly to both decorated and undecorated 1,4-β-xylans	1
CZ0341	Carbohydrate Binding Module 22B	*Clostridium thermocellum*	CBM22	arabinoxylans and arabinogalactans	1
CZ0343	Carbohydrate Binding Module 6C	*Clostridium thermocellum*	CBM6	arabinoxylans and arabinogalactans	1
CZ0344	Carbohydrate Binding Module 42C	*Clostridium thermocellum*	CBM42	decorated and undecorated 1,4-β-xylans and arabinogalactans	1
CZ0345	Carbohydrate Binding Module 42D	*Clostridium thermocellum*	CBM42	decorated and undecorated 1,4-β-xylans and arabinogalactans	1
CZ0347	Carbohydrate Binding Module 6D	*Clostridium thermocellum*	CBM6	arabinoxylans and arabinogalactans	1
CZ0348	Carbohydrate Binding Module 6E	*Clostridium thermocellum*	CBM6	arabinoxylans and arabinogalactans	1

CBMs (CONT.)

Catalogue Number	CBM name	Source Organism	CAZy Architecture	Carbohydrate Ligands	mg/vial
CZ0349	Carbohydrate Binding Module 6F	*Clostridium thermocellum*	CBM6	arabinoxylans and arabinogalactans	1
CZ0350	Carbohydrate Binding Module 22C	*Clostridium thermocellum*	CBM22	arabinoxylans and arabinogalactans	1
CZ0351	Carbohydrate Binding Module 4B	*Clostridium thermocellum*	CBM4	linear 1,3-β-glucans with occasional decorations of 1,6-β-glucose side-chains	1
CZ0352	Carbohydrate Binding Module 4B	*Clostridium thermocellum*	CBM4	1,3-1,4-β-glucans	1
CZ0353	Carbohydrate Binding Module 6G	*Clostridium thermocellum*	CBM6	arabinoxylans and arabinogalactans	1
CZ0355	Carbohydrate Binding Module 50A	*Clostridium thermocellum*	CBM50	linear 1,3-β-glucans with occasional decorations of 1,6-β-glucose side-chains	1
CZ0357	Carbohydrate Binding Module 50C	*Clostridium thermocellum*	CBM50	linear 1,3-β-glucans with occasional decorations of 1,6-β-glucose side-chains	1
CZ0358	Carbohydrate Binding Module 25A	*Clostridium thermocellum*	CBM25	1,4-1,6-α-glucans, such as pullulan, and α-manno-se polysaccharides	1
CZ0359	Carbohydrate Binding Module 22A	*Ruminococcus flavefaciens*	CBM22	arabinoxylans and arabinogalactans	0,25
CZ0360	Carbohydrate Binding Module 22A	*Ruminococcus flavefaciens*	CBM22	arabinoxylans and arabinogalactans	0,25
CZ0361	Carbohydrate Binding Module 62A	*Ruminococcus flavefaciens*	CBM62	pectins	1
CZ0362	Carbohydrate Binding Module 22B	*Ruminococcus flavefaciens*	CBM22	arabinoxylans and arabinogalactans	1
CZ0363	Carbohydrate Binding Module 35A	*Ruminococcus flavefaciens*	CBM35	galactomannans	0,5
CZ0364	Carbohydrate Binding Module 13A	*Ruminococcus flavefaciens*	CBM13	arabinoxylan	1
CZ0365	Carbohydrate Binding Module 22C	*Ruminococcus flavefaciens*	CBM22	arabinoxylans and arabinogalactans	1
CZ0366	Carbohydrate Binding Module 22D	*Ruminococcus flavefaciens*	CBM22	arabinoxylans and arabinogalactans	1
CZ0368	Carbohydrate Binding Module 22E	*Ruminococcus flavefaciens*	CBM22	arabinoxylans and arabinogalactans	1
CZ0369	Carbohydrate Binding Module 4B	*Ruminococcus flavefaciens*	CBM4	1,3-1,4-β-glucans	1
CZ0370	Carbohydrate Binding Module 22F	*Ruminococcus flavefaciens*	CBM22	arabinoxylans and arabinogalactans	1
CZ0371	Carbohydrate Binding Module 35B	*Ruminococcus flavefaciens*	CBM35	galactomannans	0,5
CZ0372	Carbohydrate Binding Module 22G	*Ruminococcus flavefaciens*	CBM22	arabinoxylans and arabinogalactans	1
CZ0373	Carbohydrate Binding Module 22H	*Ruminococcus flavefaciens*	CBM22	arabinoxylans and arabinogalactans	1
CZ0374	Carbohydrate Binding Module 22I	*Ruminococcus flavefaciens*	CBM22	both decorated and undecorated 1,4-β-xylans and arabinogalactans	0,5
CZ0375	Carbohydrate Binding Module 4C	*Ruminococcus flavefaciens*	CBM4	1,3-1,4-β-glucans	1
CZ0376	Carbohydrate Binding Module 13B	*Ruminococcus flavefaciens*	CBM13	arabinan an pectins	1
CZ0377	Carbohydrate Binding Module 4D	*Ruminococcus flavefaciens*	CBM4	undecorated linear 1,3-β-glucans or decorated with 1,6-β-glucose side-chains	1
CZ0378	Carbohydrate Binding Module 22J	*Ruminococcus flavefaciens*	CBM22	arabinoxylans and arabinogalactans	1
CZ0379	Carbohydrate Binding Module 6A	*Ruminococcus flavefaciens*	CBM6	arabinoxylan and weakly to arabinogalactan	1
CZ0380	Carbohydrate Binding Module 22K	*Ruminococcus flavefaciens*	CBM22	arabinoxylans and arabinogalactans	1
CZ0448	Carbohydrate Binding Module 9A	*Thermotoga maritima*	CBM9_1-CBM9_2	non-reducing ends of cellulose	1
CZ0465	Carbohydrate Binding Module 65A	*Eubacterium cellulosolvens*	CBM65_1	1,4-β-glucans and 1,3-1,4-β-glucans but displays a preference for decorated 1,4-β-glucans (xyloglucan)	0,5

CBMs (CONT.)

Catalogue Number	CBM name	Source Organism	CAZy Architecture	Carbohydrate Ligands	mg/vial
CZ0466	Carbohydrate Binding Module 65A	*Eubacterium cellulosolvens*	CBM65_2	1,4-β-glucans and 1,3-1,4-β-glucans but displays a preference for decorated 1,4-β-glucans (xyloglucan)	0,5
CZ0467	Carbohydrate Binding Module 78A	*Ruminococcus flavefaciens*	CBM78	1,3-1,4-β-glucans, soluble 1,4-β-glucans, xyloglucan and galactomannans	0,5
CZ0468	Carbohydrate Binding Module 80A	*Ruminococcus flavefaciens*	CBM80	1,3-1,4-β-glucans, soluble 1,4-β-glucans, xyloglucan and galactomannans	0,5
CZ0469	Carbohydrate Binding Module 79A	*Ruminococcus flavefaciens*	CBM79	1,3-1,4-β-glucans, soluble 1,4-β-glucans and xyloglucan	0,5
CZ0470	Carbohydrate Binding Module Rf999	*Ruminococcus flavefaciens*	CBM Rf999	linear arabinans	0,5
CZ0471	Carbohydrate Binding Module 2b	*Cellulomonas fimi*	CBM2b	1,4-β-xylans	0,5
CZ0472	Carbohydrate Binding Module 6A	*Bacillus halodurans*	CBM6	1,3-β-glucans	0,5
CZ0473	Carbohydrate Binding Module 4A	*Cellulomonas fimi*	CBM4	1,3-β-glucans	0,5
CZ0474	Carbohydrate Binding Module 61A	*Thermotoga maritima*	CBM61	1,4-β-galactans	0,5
CZ0475	Carbohydrate Binding Module 27A	*Thermotoga maritima*	CBM27	1,4-β-mannans	0,5
CZ0482	Carbohydrate Binding Module 2D	*Thermobifida fusca*	CBM2	crystalline forms of cellulose	0,5
CZ0483	Carbohydrate Binding Module 2F	*Thermobifida fusca*	CBM2	crystalline forms of cellulose	0,25
CZ0484	Carbohydrate Binding Module 64A	*Spirochaeta thermophila*	CBM64	crystalline forms of cellulose	0,5
CZ0500	Carbohydrate Binding Module 2b-1	*Cellulomonas fimi*	CBM2b-1	1,4-β-xylans	0,5
CZ0501	Carbohydrate Binding Module 2b-2	*Cellulomonas fimi*	CBM2b-2	1,4-β-xylans	0,5
CZ0504	Carbohydrate Binding Module 75A	*Ruminococcus flavefaciens*	CBM75	xyloglucan	1
CZ0505	Carbohydrate Binding Module 76A	*Ruminococcus flavefaciens*	CBM76	1,4-β-glucans	1
CZ0506	Carbohydrate Binding Module 56A	*Bacillus circulans*	CBM56	1,3-β-glucans such as laminarin and curdlan	1
CZ0507	Carbohydrate Binding Module 66A	*Bacillus subtilis*	CBM66	fructans	0,5
CZ0752	Carbohydrate Binding Module 57A	*Bacteroides thetaiotaomicron*	CBM57	xylans and arabinoxylans	0,25
CZ0859	Carbohydrate Binding Module 56A	*Paenibacillus sp.*	CBM56	1,3-β-glucans such as laminarin and curdlan	1
CZ0862	Carbohydrate Binding Module 56B	*Paenibacillus sp.*	CBM56	1,3-β-glucans such as laminarin and curdlan	1
CZ0873	Carbohydrate Binding Module 17A	*Clostridium cellulovorans*	CBM17	non-crystalline cellulose and soluble 1,4-β-glucans	0,5
CZ0874	Carbohydrate Binding Module 21A	*Homo sapiens*	CBM21	1,4-α-glucans	1
CZ0875	Carbohydrate Binding Module 26A	*Bacillus halodurans*	CBM26	α-glucooligosaccharides, particularlythose containing α-1,6 linkages	0,5
CZ0876	Carbohydrate Binding Module 28A	*Clostridium josui*	CBM28	cellooligosaccharide ligands	1
CZ0877	Carbohydrate Binding Module 41A	*Thermotoga maritima*	CBM41	1,4-α-glucans	0,5
CZ0878	Carbohydrate Binding Module 51A	*Clostridium perfringens*	CBM51	galactose residues in oligosaccharides	1
CZ0889	Carbohydrate Binding Module 47A	*Streptococcus mitis*	CBM47	fucose containing oligosaccharides	1
CZ0890	Carbohydrate Binding Module 16A	*Caldanaerobius polysaccharolyticus*	CBM16	glucose-, mannose-, and glucose/mannose-configured substrates	1
CZ0983	Carbohydrate Binding Module 5A	*Pyrococcus furiosus*	CBM5	chitin	1
CZ1014	Carbohydrate Binding Module 63A	*Bacillus subtilis*	CBM63	crystalline forms of cellulose. The protein is a bacterial expansin that promotes root colonization	1

CBMs (CONT.)

Catalogue Number	CBM name	Source Organism	CAZy Architecture	Carbohydrate Ligands	mg/vial
CZ1015	Carbohydrate Binding Module 32A	*Clostridium perfringens*	CBM32	LacNAc (β-D-galactosyl-1,4-β-D-N-acetylglucosamine)	1
CZ1016	Carbohydrate Binding Module 66A	*Streptococcus mutans*	CBM66	terminal fructoside residue of fructans	1
CZ1017	Carbohydrate Binding Module 32B	*Clostridium perfringens*	CBM32-CBM32	galactose residues in oligosaccharides	0,5
CZ1018	Carbohydrate Binding Module 32A	*Zobellia galactanivorans*	CBM32	alginate	0,5
CZ1019	Carbohydrate Binding Module 44A	*Clostridium cellulolyticum*	PKD-CBM44	cellulose and xyloglucan	1
CZ1020	Carbohydrate Binding Module 34A	*Geobacillus stearothermo-philus*	CBM34	pullulan	1
CZ1021	Carbohydrate Binding Module 20A	*Bacillus sp.*	CBM20	cyclodextrins	1
CZ1022	Carbohydrate Binding Module 28A	*Caldicellulosiruptor bescii*	CBM28	cellooligosaccharide ligands	1
CZ1026	Carbohydrate Binding Module 67A	*Bacteroides thetaiotaomicron*	CBM67	L-rhamnose	1
CZ1029	Carbohydrate Binding Module 22A	*Ruminococcus champanel-lensis*	CBM22	xylans	1
CZ1048	Carbohydrate Binding Module 48A	*Rhizobium sp.*	CBM48	glycogen	1

GFP-CBM

NZYTech has developed a series of CBMs fused with the green fluorescent protein (GFP). GFP is a protein composed of 238 amino acid residues (26.9 kDa) that exhibits bright green fluorescence when exposed to light in the blue to ultraviolet range. GFP fused CBMs are excellent tools for cell signalling studies.

Catalogue Number	CBM name	Source Organism	CAZy Architecture	Carbohydrate Ligands	mg/vial
CZ0057	Carbohydrate Binding Module 3A	*Clostridium thermocellum*	GFP-CBM3	crystalline forms of cellulose	5
CZ0058	Carbohydrate Binding Module 9A	*Thermotoga maritima*	GFP-CBM9	the reducing ends of 1,3-1,4-β-glu-cans, 1,4-β-glucans and 1,4-β-xylans	1
CZ0059	Carbohydrate Binding Module 9A	*Thermotoga maritima*	GFP-CBM9_1-CBM9_2	the reducing ends of 1,3-1,4-β-glu-cans, 1,4-β-glucans and 1,4-β-xylans	1
CZ0069	Carbohydrate Binding Module 3A	*Bacteroides cellulosolvens*	GFP-CBM3	crystalline forms of cellulose	1
CZ0070	Carbohydrate Binding Module 3A	*Acidothermus cellulolyticus*	GFP-CBM3	crystalline forms of cellulose	1
CZ0071	Carbohydrate Binding Module 3A	*Acetivibrio cellulolyticus*	GFP-CBM3	crystalline forms of cellulose	0,5
CZ0072	Carbohydrate Binding Module 3B	*Clostridium stercorarium*	GFP-CBM3	crystalline forms of cellulose	1
CZ0073	Carbohydrate Binding Module 3A	*Bacillus subtilis*	GFP-CBM3	crystalline forms of cellulose	1
CZ0074	Carbohydrate Binding Module 2A	*Ampullaria crossean*	GFP-CBM2	crystalline forms of cellulose	0,5
CZ0075	Carbohydrate Binding Module 3A	*Caldicellulosiruptor bescii*	GFP-CBM3	crystalline forms of cellulose	0,5
CZ0076	Carbohydrate Binding Module 3A	*Paenibacillus barcinonensis*	GFP-CBM3	crystalline forms of cellulose	1
CZ0077	Carbohydrate Binding Module 2A	*Pyrococcus furiosus*	GFP-CBM2	crystalline forms of chitin	1
CZ0078	Carbohydrate Binding Module 2A	*Thermobifida fusca*	GFP-CBM2	crystalline forms of cellulose	1
CZ0079	Carbohydrate Binding Module 2B	*Thermobifida fusca*	GFP-CBM2	crystalline forms of cellulose	0,5
CZ0080	Carbohydrate Binding Module 2C	*Thermobifida fusca*	GFP-CBM2	crystalline forms of cellulose	0,5
CZ0081	Carbohydrate Binding Module 3A	*Clostridium clariflavum*	GFP-CBM3	crystalline forms of cellulose	1
CZ0082	Carbohydrate Binding Module 10A	*Teredinibacter turnerae*	GFP-CBM10	crystalline forms of chitin	1
CZ0083	Carbohydrate Binding Module 10A	*Cellvibrio japonicus*	GFP-CBM10	crystalline forms of cellulose	1

GFP-CBM (CONT.)

Catalogue Number	CBM name	Source Organism	CAZy Architecture	Carbohydrate Ligands	mg/vial
CZ0084	Carbohydrate Binding Module 3A	*Clostridium acetobutylicum*	GFP-CBM3	crystalline forms of cellulose	1
CZ0085	Carbohydrate Binding Module 2A	*Butyrivibrio fibrisolvens*	GFP-CBM2	crystalline forms of cellulose	0,5
CZ0086	Carbohydrate Binding Module 1A	*Trichoderma reesei*	GFP-CBM1	crystalline forms of cellulose	1
CZ0087	Carbohydrate Binding Module 1A	*Neocallimastix patriciarum*	GFP-CBM1	crystalline forms of cellulose	0,5
CZ0088	Carbohydrate Binding Module 2E	*Thermobifida fusca*	GFP-CBM2	crystalline forms of cellulose	0,5
CZ0089	Carbohydrate Binding Module 63A	*Bacillus subtilis*	GFP-CBM63	crystalline forms of cellulose; the protein is a bacterial expansin that promotes root colonization	1
CZ0090	Carbohydrate Binding Module 2F	*Thermobifida fusca*	GFP-CBM2	crystalline forms of cellulose	0,5
CZ0091	Carbohydrate Binding Module 2G	*Thermobifida fusca*	GFP-CBM2	crystalline forms of cellulose	1
CZ0092	Carbohydrate Binding Module 64A	*Spirochaeta thermophila*	GFP-CBM64	crystalline forms of cellulose	1
CZ0093	Carbohydrate Binding Module 2D	*Thermobifida fusca*	GFP-CBM2	crystalline forms of cellulose	1
CZ0094	Carbohydrate Binding Module 3A	*Clostridium cellulolyticum*	GFP-CBM3	crystalline forms of cellulose	1
CZ0095	Carbohydrate Binding Module 3C	*Clostridium thermocellum*	GFP-CBM3	crystalline forms of cellulose	1
CZ0096	Carbohydrate Binding Module 3A	*Clostridium stercorarium*	GFP-CBM3	crystalline forms of cellulose	1
CZ0142	Carbohydrate Binding Module 61A	*Thermotoga maritima*	GFP-CBM61	1,4-β-galactans	0,5
CZ0177	Carbohydrate Binding Module 27A	*Thermotoga maritima*	GFP-CBM27	1,4-β-mannans	0,5
CZ0286	Carbohydrate Binding Module 30B	*Clostridium thermocellum*	GFP-CBM30	1,3-1,4-β-glucans and soluble undecorated (cellulose) and decorated (xyloglucan) 1,4-β-glucans	1
CZ0335	Carbohydrate Binding Module 22A	*Clostridium thermocellum*	GFP-CBM22	decorated and undecorated 1,4-β-xylans; it also binds to 1,3-1,4-β-glucans	1
CZ0342	Carbohydrate Binding Module 11A	*Clostridium thermocellum*	GFP-CBM11	1,3-1,4-β-glucans and 1,4-β-glucans	1
CZ0346	Carbohydrate Binding Module 62A	*Clostridium thermocellum*	GFP-CBM62	xyloglucan and galactomannan; it specifically recognizes the galactose side-chains of these polysaccharides	1
CZ0354	Carbohydrate Binding Module 6A	*Clostridium thermocellum*	GFP-CBM6	arabinoxylans and arabinogalactans	0,25
CZ0496	Carbohydrate Binding Module 4A	*Cellulomonas fimi*	GFP-CBM4	1,3-β-glucans	1
CZ0497	Carbohydrate Binding Module 6A	*Bacillus halodurans*	GFP-CBM6	1,3-β-glucans	1
CZ0502	Carbohydrate Binding Module 2b-1	*Cellulomonas fimi*	GFP-CBM2b-1	1,4-β-xylans	1
CZ0503	Carbohydrate Binding Module 2b-2	*Cellulomonas fimi*	GFP-CBM2b-2	1,4-β-xylans	1
CZ1031	Carbohydrate Binding Module 32A	*Clostridium perfringens*	GFP-CBM32	LacNAc (β-D-galactosyl-1,4-β-D-N--acetylglucosamine)	1
CZ1032	Carbohydrate Binding Module 66A	*Streptococcus mutans*	GFP-CBM66	terminal fructoside residue of fructans	1
CZ1033	Carbohydrate Binding Module 32A	*Zobellia galactanivorans*	GFP-CBM32	alginate	0,5
CZ1034	Carbohydrate Binding Module 48A	*Escherichia coli*	GFP-CBM48	glycogen	0,5
CZ1035	Carbohydrate Binding Module 44A	*Clostridium cellulolyticum*	GFP-PKD-CBM44	cellulose and xyloglucan	1
CZ1036	Carbohydrate Binding Module 34A	*Geobacillus stearothermophilus*	GFP-CBM34	pullulan	0,5
CZ1037	Carbohydrate Binding Module 48A	*Nostoc punctiforme*	GFP-CBM48	glycogen	0,5
CZ1038	Carbohydrate Binding Module 20A	*Bacillus sp.*	GFP-CBM20	cyclodextrins	1

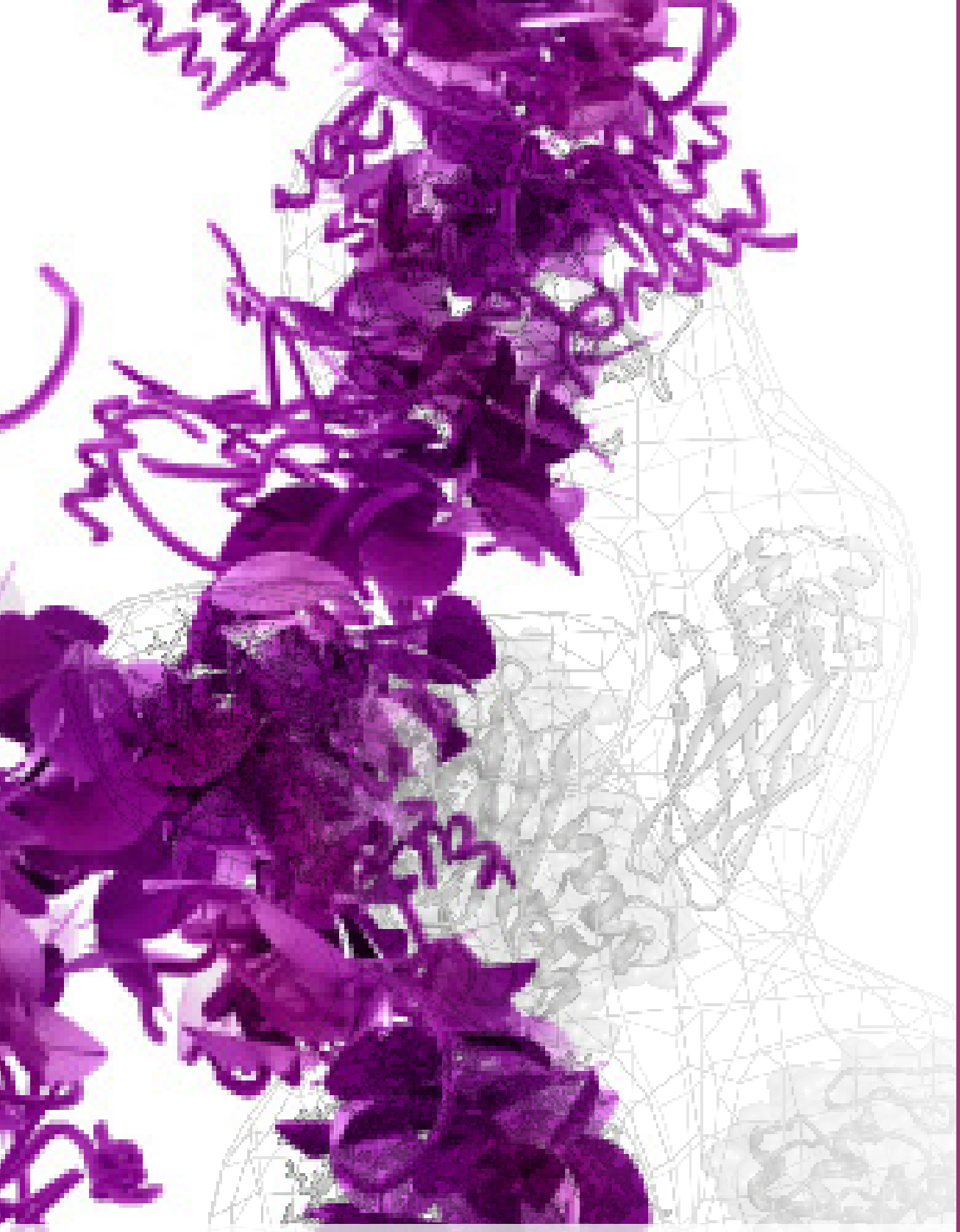
GFP-CBM (CONT.)

Catalogue Number	CBM name	Source Organism	CAZy Architecture	Carbohydrate Ligands	mg/vial
CZ1039	Carbohydrate Binding Module 28A	*Caldicellulosiruptor bescii*	GFP-CBM28	cellooligosaccharide ligands	1
CZ1040	Carbohydrate Binding Module 57A	*Bacteroides thetaiotaomicron*	GFP-CBM57	xylans and arabinoxylans	1
CZ1041	Carbohydrate Binding Module 22A	*Ruminococcus champanellensis*	GFP-CBM22	xylans	1
CZ1043	Carbohydrate Binding Module 32B	*Clostridium perfringens*	GFP-CBM32-CBM32	galactose residues in oligosaccharides	0,5
CZ1045	Carbohydrate Binding Module 34A	*Escherichia coli*	GFP-CBM34	starch	1
CZ1046	Carbohydrate Binding Module 67A	*Bacteroides thetaiotaomicron*	GFP-CBM67	L-rhamnose	1
CZ1047	Carbohydrate Binding Module 48A	*Rhizobium sp.*	GFP-CBM48	glycogen	1

ZZ-CBM

ZZ-CBMs are modular proteins where different CBMs are fused to the immunoglobulin G (IgG) binding ZZ domain of protein A from *Staphylococcus aureus*. This ZZ domain protein derivative is particularly recommended to mediate the anchorage of antibodies to cellulosic supports.

Catalogue Number	CBM name	Source Organism	CAZy Architecture	Carbohydrate Ligands	mg/vial
CZ0498	Carbohydrate Binding Module 3A	*Clostridium thermocellum*	ZZ-CBM3	crystalline forms of cellulose	1
CZ0499	Carbohydrate Binding Module 64A	*Spirochaeta thermophila*	ZZ-CBM64	crystalline forms of cellulose	1



mini-cellulosomes & other enzymes

MINI-CELLULOSOMES

CELLOBIOSE DEHYDROGENASE

XYLOSE ISOMERASE

* Structure of *Clostridium thermocellum* Mini-Cellulosome (PDB EMD-1823), #CZ0065, pg 60

MINI-CELLULOSOMES

It is well established that cellulosomes are elaborate "Lego"-like structures that perform the efficient hydrolysis of plant cell wall recalcitrant polysaccharides. Previous research on designer cellulosomes has shown that cellulosomal cellulases act together in an enhanced synergistic manner in the degradation of cellulosic substrates. At NZYTech, we can integrate our current knowledge on the mechanisms of cellulosome assembly and protein function to produce highly efficient multi-enzyme complexes for all biological processes that might benefit from enzyme proximity. In this catalogue, NZYTech has made available three novel mini-cellulosome combinations but can cooperate with different partners to produce tailor made novel mini-cellulosomes combinations.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0065	Cellulase 8A, Mini-Cellulosome	*Clostridium thermocellum*	3×GH8 + Coh-Coh-Coh	3.2.1.4	5.0-7.5	60	1
CZ0066	Cellulase 8A, Mini-Cellulosome	*Clostridium thermocellum*	3×GH8 + Coh-CBM3-Coh-Coh	3.2.1.4	5.0-7.5	60	0,5
CZ0068	Lichenase 26A, Mini-Cellulosome	*Clostridium thermocellum*	3×GH16 + Coh-Coh-Coh	3.2.1.73	5.5-7.0	65	0,5

CELLOBIOSE DEHYDROGENASE

Cellobiose dehydrogenases (CDH) are extracellular enzymes produced by various lignocellulose-degrading microbes. They oxidize soluble cellodextrins efficiently to their corresponding lactones by a ping-pong mechanism using a wide spectrum of electron acceptors including quinones, phenoxyradicals, Fe^{3+}, Cu^{2+} and triiodide ion.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0960	Cellobiose dehydrogenase	*Podospora anserina*	CDH	1.1.99.18	5,0	30	0,25

XYLOSE ISOMERASE

Xylose isomerases are enzymes that catalyze the interconversion of D-xylose and D-xylulose. These enzymes belong to the family of isomerases, specifically those intramolecular oxidoreductases interconverting aldoses and ketoses.

Catalogue Number	Enzyme	Source Organism	CAZy Architecture	EC	Optimum pH	Optimum Temperature (°C)	mg/ vial
CZ0887	Xylose isomerase A	*Bacteroides thetaiotaomicron*	N/A	5.3.1.5	6.5-7.5	37	1

TERMS & CONDITIONS

By placing an order, CUSTOMERS accept all terms and conditions of this agreement.

CUSTOMERS that do not agree to the full terms and conditions of this agreement should not place an order. Once a customer accepts these terms and conditions the CUSTOMER cannot subsequently decline or modify any term or condition without the prior written consent of NZYTech.

Use of Products

NZYTech products, services, kits and reagents are for laboratory research and *in vitro* use only. CUSTOMERS must read all relevant information about the product before starting the work. Please visit our website to find out more details about the Products, Product Brochures and Material Safety Data Sheets (MSDS) available for download. NZYTech Products should NOT be used as Agricultural or Pesticide Products, Cosmetics, Drugs, Food Additives or Household Chemicals. NZYTech products may not be reformulated, repacked or resold by CUSTOMER in any form without consent.

Warranty

NZYTech warrants that its products comply with the specifications indicated in the accompanying technical brochure as long as the product itself has a valid Certificate of Analysis (CoA). If a product fails to comply with its specifications, NZYTech should be informed as it may choose to replace it free of charge or refund the purchase price. This warranty applies only to products that have been handled and stored in accordance with NZYT recommendations/specifications.

Complaints

Complaints regarding product quality will only be accepted as long as the relevant product has a valid certificate of analysis (CoA). NZYTech will require the CUSTOMER to provide all the necessary information in order to process the complaint accordingly, i.e., include invoice number or Purchase Order number, batch number, problem description and evidence to sustain the complaint.

Pricing

Prices are shown in Euro (€). Prices may be subjected to change without prior notice. NZYTech, at its own discretion, may require pre-payment of any order. Specific written quotations are valid for 90 days, excluding promotions, for which quotations are valid for 30 days.

Orders

If applicable, when placing your order please refer the quote or pro-forma invoice number. NZYTech may not initiate the invoicing process without a Purchase Order. NZYTech will not accept orders by phone. Orders are only accepted via website (online store), e-mail or fax. If you order via our website (online store), we will guarantee the price shown at the website at that time. Prices shown in catalogue and NZYTech website exclude VAT, which might be applied when the invoice is issued. At NZYTech sole discretion, shipment will be made promptly if orders have been fully paid.

Payment Terms

For international sales, advanced payment may be required, and, in such cases, orders are only processed upon our bank's confirmation of money transfer. Banking expenses shall be fully supported by the CUSTOMER. In specific cases, the production will take place prior to bank validation of money transfer.

For Portugal and Spain, invoices will be due within 30 days from issue date. Advanced payment may be required.

Once an order is accepted by NZYTech, it can only be cancelled in cases where production on demand did not take place. In the specific cases of Services, including Gene Synthesis, Cloning, Mutagenesis, Protein Expression, Peptide Synthesis, DNA sequenc ing

and Oligonucleotides, services that are only produced on demand, NZYTech will not accept the cancelation of any such orders and the CUSTOMER will be responsible for payment of the total amount of the invoice in case of cancellation.

Shipping Costs

Spain (Main Land): 9 €
Portugal (Main Land): 5 €
Austria, Belgium, Denmark, France, Germany, Ireland, Italy, Luxembourg, Poland, Sweden, The Netherlands, United Kingdom: 25€
Bulgaria, Croatia, Czech Republic, Estonia, Finland, Greece, Hungary, Latvia, Lithuania, Romania, Slovakia, Slovenia: 50€
Albania, Andorra, Belarus, Bosnia Herzegovina, Cyprus, Gibraltar, Iceland, Kosovo, Lichtenstein, Macedonia, Malta, Moldavia, Monaco, Montenegro, Norway, San Marino, Serbia, Switzerland, Ukraine, Vatican: 125€
All other geographic areas: Upon quotation (in these cases shipping costs are additional to the price of the products and fully supported by the client).
Products that require ultra-low temperature shipping will have an extra cost for dry ice (29 € / shipment).
Custom fees, if any, related to the clearance of goods upon product arrival to the destiny country are of CUSTOMER responsibility.

Eurofins Genomics

Eurofins Genomics Products and Services will be shipped directly by Eurofins.
Shipping Costs for Portugal and Spain: 8,5€ for orders below 200€ (Without VAT).
Eurofins and NZYTech Orders cannot be combined to save shipping.

Product Shipping and Delivery

All products are transported in the appropriated conditions to maintain intact all the properties inherent to their expected output. NZYTech can ship at different temperatures products to be stored according to product label temperature indications in the cases where this does not affect product quality. Regarding Incoterms, NZYTech can deliver goods with the following Delivery Terms: DAP – delivered At Place of Destination, where we handle the shipment from our facilities to Customer's address (all shipping and customs fees on NZYTech's responsibility); DPU – Delivery at Place Unloaded, formerly referred as DAT – Delivery at Terminal, or EXW – Ex-Works, when using a Customer's courier account (all shipping and customs fees on Customer's responsibility). In specific cases, like CAZymes, Analytical Products, Molecular Diagnostics kits, Molecular Services, custom and bulk orders can take longer to produce and ship the goods. All Services, including gene synthesis, DNA sequencing and oligonucleotides, are only produced on demand and, therefore, each order has its own deadline. For most countries, the delivery occurs within five working days, except in case of stock rupture.
In case a customer requires any certification to be sent with the goods, i.e., Certificate of Origin or ATR forms, these requirements must be stated upon placement of the order, as these documents will be provided at an additional cost.

Return Policy

NZYTech CUSTOMER Service is available to assist you in every way possible if a problem arises with your order. The CUSTOMER must inspect all packages immediately upon receipt and store the goods at the designated storage temperature.

CUSTOMER will only have 14 calendar days to notify NZYTech if any damage or discrepancy occurs. After this period, NZYTech will assume that the products were properly delivered and no longer accepts any complaint regarding packaging, delivery or other. In case of any damage occur, please retain the damaged goods, packing material and shipping documents and please notify our Customer Service through e-mail at info@nzytech.com. If the damage requires you to return the goods to NZYTech, our Customer Service will provide assistance, shipping instructions and authorizations. If an item is shipped to you incorrectly, as the result of a mistake from our Logistics team, please contact our Customer Service through e-mail at info@nzytech.com, and we will take a quick and appropriate action to correct the problem. At NZYTech sole discretion, returns may be accepted for items stored at room temperature and that have been ordered by mistake but will be subjected to a processing fee of 30% to cover costs.

For e-commerce online orders carried out by consumers, if applicable, the return period without any cause is 14 calendar days from date of receipt of goods.

Discontinuation of Products

We reserve the right to discontinue any product without prior notice, unless NZYTech has provided a long-term confirmation of delivery.

Gene Synthesis and Custom Cloning: Representations and Indemnities

NZYTech can clone synthetic genes into custom vectors. CUSTOMER will provide the custom vectors necessary for NZYTech to provide the requested services. Such custom vectors shall remain the property of CUSTOMER throughout the cloning and sequencing process. CUSTOMER hereby grants NZYTech a limited, non-exclusive, royalty-free license to use the custom vectors and the gene sequences for the purpose of performing the services. By agreeing to the terms and conditions of this Agreement and providing NZYTech with the custom vectors and the gene sequence, CUSTOMER, at its own risk and liability, represents and warrants that it has the power and authority to grant the foregoing license, or otherwise has obtained all licenses and rights, including all intellectual property rights, necessary for NZYTech to provide the requested services.

For custom cloning projects, no turnaround guarantee is offered. If NZYTech fails to clone the DNA fragment in three attempts (for commercially available vectors shipped directly from the manufacturer) or two attempts (for all other vector preparations), NZYTech reserves the right to ship the gene cloned into our in-house vector or as a linear PCR fragment and refund to CUSTOMER the custom cloning fee.

All genes resulting from gene synthesis and/or cloning services are stored at NZYTech for a three-month period. After this period, nucleic acids provided to CUSTOMERS are destroyed. Custom proteins are not stored in-house after dispatch to clients.

Peptide Synthesis: Representations and Indemnities

Unless otherwise stated, all peptide quantities/amounts mentioned on our website and all our documents including but not limited to quotation, projects, reports, invoices are gross weights. Gross weight includes not only the target peptides but also fragment peptides, salts and residual water. Net peptide weight indicates the actual weight of the peptide component of your sample, and is usually 60-70% of the total gross peptide weight. Custom peptides are not stored in-house after dispatch to clients.

Disputes and applicable law

These terms and conditions are subject to Portuguese law and, in the event of any dispute, the parties shall recourse to the courts of the city ("comarca") of Lisbon.

Information made available on a permanent basis in Compliance with article 10 of the E-commerce law (Decree-Law n.º 7/2004, of 7 january, as amended) and seller of the goods and services.

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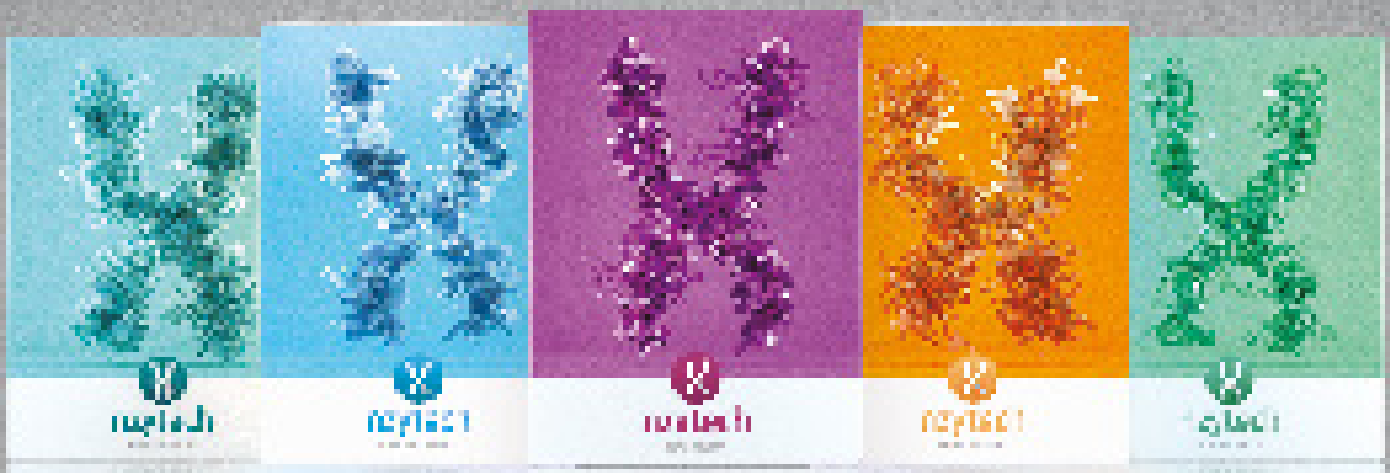
Catalogues by NZY Tech



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genes & genomes

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