The present invention, therefore, aims to provide fusarium toxin-cleaving polypeptide variants of a fusarium toxin carboxylesterase of SEQ ID No. 46, by which it is possible to cleave at least one fusarium toxin to non-toxic or less toxic products in an oxygen-independent and cofactor-free manner, wherein the polypeptide variants have increased temperature stabilities and increased temperature activities as compared to fusarium toxin carboxylesterase of SEQ ID No. 46.

To solve this object, the present invention is essentially characterized by fusarium toxin-cleaving polypeptide variants of a fusarium toxin carboxylesterase of SEQ ID No. 46, characterized in that the polypeptide variants each possess an amino acid sequence truncated by 47 amino acids at the N-terminus, the amino acid sequences sharing at least 70%, preferably 80%, particularly preferably 100%, sequence identity, namely SEQ ID No. 1, with the amino acid sequence section 48-540 of SEQ ID No. 46, that the temperature stability (T(50%) of the polypeptide of SEQ ID No. 46 is determined to be 42°C and that of the polypeptide variant of SEQ ID No. 1 is determined to be 45°, or modifications of SEQ ID No. 1 having a relative increase of T(50%) compared to the parental enzyme of SEQ ID No. 1, wherein on at least one position selected from the group consisting of 10, 33, 66, 107, 140, 144, 149, 151, 157, 199, 266, 267, 270, 272, 275, 280, 284, 286, 293, 302, 312, 329, 332, 360, 363, 364, 365, 367, 371, 372, 377, 389, 391, 394, 418, 419, 424, 427, 429, 430, 436, 440, 443, 447, 453, 455, 456, 457, 462, 463, 464, 465, 469, 473, 478, 487 and 490 an amino acid substitution is contained as modification, and that the amino acid substituents at positions 10 and 456 are selected from Q, E, N, H, K and R, at positions 33, 107, 293 and 332 from E, Q, D, K, R and N, at positions 66, 463 and 478 from D, E, K, N, Q and R, at positions 140 and 490 from P, A, S and N, at positions 144 and 367 from I, L, M and V, at positions 149, 270, 312, 329 and 372 from F, Y, W and H, at positions 151 and 453 from D, E, K and R, at positions 157 and 462 from F, H, W and Y, at positions 199, 302, 365 and 464 from I, L, M and V, at positions 266 and 455 and from A, S and T, at positions 267, 394 and 429 from A, N, P and S, at position 272 from H, N, Q and S, at position 275 from A, D, E, G, K, N, Q, R and S, at position 280 from A, D, E, K, N, P, Q, R and S, at position 284 from A, N, P, S, T and V, at position 286 from A, D, E, K, N, P, R and S, at positions 360, 377, 391, 419 and 427 from A, I, L S, T and V, at positions 363, 443 and 457 from A, S, T and V, at position 364 from H, I, L, M, N, Q, S and V, at position 371 from A, I, L, M, S, T and V, at position 389 from I, L, M and V, at positions 418, 430, 447 and 473 from A, G and S, at position 424 from A, D, E, G, K, R and S, at position 436 from A, G, S and T, at position 440 from A, G, S and T, at position 465 from A, G, H, N, Q, S and T, at position 469 from D, E, K and R and/or at position 487 from N, D, Q, H and S.

It has surprisingly turned out that an amino acid sequence truncated by 47 amino acids relative to SEQ ID No. 46 is both significantly more active than said sequence and also has increased temperature stability as compared to said sequence. In that polypeptide variants of SEQ ID No. 1 are formed, in particular polypeptide variants having amino acid sequences sharing at least 70% sequence identity with SEQ ID No. 1, and comprising amino acid substitutions on at least one position selected from the group consisting of 10, 33, 66, 107, 140, 144, 149, 151, 157, 199, 266, 267, 270, 272, 275, 280, 284, 286, 293, 302, 312, 329, 332, 360, 363, 364, 365, 367, 371, 372, 377, 389, 391, 394, 418, 419, 424, 427, 429, 430, 436, 440, 443, 447, 453, 455, 456, 457, 462, 463, 464, 465, 469, 473, 478, 487 and 490, a temperature stability enhancement by at least 4% as compared to that of the fusarium toxin carboxylesterase of SEQ ID No. 1 has been achieved. The use of such polypeptide variants having fusarium toxin-cleaving properties has enabled the detoxification of fusarium toxins at elevated temperatures, for instance during technological processes. This is, in particular, enabled by the temperature activity being also enhanced in addition to the temperature stability. In particular, it will thereby be safeguarded that the enzymatic activity of the polypeptide variants will even be maintained at elevated temperature stresses as might, for instance, also occur during transport in containers.

According to the invention, a particularly strong increase in the temperature stability is achieved in that the amino acid substituents at positions 10 and 456 are selected from Q, E, N, H, K and R, at positions 33, 107, 293 and 332 from E, Q, D, K, R and N, at positions 66, 463 and 478 from D, E, K, N, Q and R, at positions 140 and 490 from P, A, S and N, at positions 144 and 367 from I, L, M and V, at positions 149, 270, 312, 329 and 372 from F, Y, W and H, at positions 151 and 453 from D, E, K and R, at positions 157 and 462 from F, H, W and Y, at positions 199, 302, 365 and 464 from I, L, M and V, at positions 266 and 455 and from A, S and T, at positions 267, 394 and 429 from A, N, P and S, at position 272 from H, N, Q and S, at position 275 from A, D, E, G, K, N, Q, R and S, at position 280 from A, D, E, K, N, P, Q, R and S, at position 284 from A, N, P, S, T and V, at position 286 from A, D, E, K, N, P, R and S, at positions 360, 377, 391, 419 and 427 from A, I, L S, T and V, at positions 363, 443 and 457 from A, S, T and V, at position 364 from H, I, L, M, N, Q, S and V, at position 371 from A, I, L, M, S, T and V, at position 389 from I, L, M and V, at positions 418, 430, 447 and 473 from A, G and S, at position 424 from A, D, E, G, K, R and S, at position 436 from A, G, S and T, at position 440 from A, G, S and T, at position 465 from A, G, H, N, Q, S and T, at position 469 from D, E, K and R, and/or

at position 487 from N, D, Q, H and S, whereat the amino acids originally present on the cited positions having been substituted in any event.

The term "carboxylesterase" refers to any enzyme, polypeptide or polypeptide variant capable of cleaving carboxylic ester compounds to the respective alcohol compounds and carboxylic acid compounds by means of water. The term "fusarium toxin carboxylesterase" refers to any enzyme, polypeptide or polypeptide variant capable of hydrolyzing at least one fusarium toxin by hydrolytically cleaving at least one tricarballylic acid (propane-1,2,3-tricarboxylic acid) off the same. A "fusarium toxin-cleaving property" as described herein refers to the capability of hydrolytically cleaving off at least one tricarballylic acid residue from a least one fusarium toxin, in particular from FA1-2, FB1-4, FC1-2, FC4, HFC1, AAL-TA1-2 und AAL-TB1-2 or derivatives or degradation products thereof.

The terms used below are taken from the technical terminology and, unless otherwise stated, are each used in their conventional meanings. Thus, the term "polynucleotide" refers to any kind of genetic material of any length and sequence, such as single-stranded and double-stranded DNA and RNA molecules, including regulatory elements, structural elements, groups of genes, plasmids, entire genomes and fragments thereof. The term "polypeptide" comprises proteins such as enzymes, antibodies and polypeptides with up to 500 amino acids, such as peptide inhibitors, domains of proteins, yet even short polypeptides with small sequence lengths, e.g. less than 10 amino acids, such as receptors, ligands, peptide hormones, tags and the like. The term "position" in a polynucleotide or polypeptide refers to a single, specific base or amino acid in the sequence of said polynucleotide or polypeptide, respectively. The names of the amino acids are abbreviated by the one- or three-letter codes familiar to the skilled person in the art.

The term "unit" or "U" refers to the measure of the catalytic activity of an enzyme, polypeptide or polypeptide variant and is defined as the number of micromoles (µmol) of substrate, i.e. fumonisin B1 in this case, that are reacted or cleaved per minute under defined conditions. Thus, if at least one tricarballylic acid residue is cleaved off from 60 µmol FB1 within 15 min, this corresponds to a catalytic activity of 4 units. For FB1 cleavage, the reaction conditions are defined as follows: The reaction is carried out in 20 mM Tris-HCl buffer (pH 8.0) with 0.1 mg/ml bovine serum albumin at a temperature of 30°C for 30 min. The substrate concentration in the reaction is 100 µM FB1.

By "catalytic activity", "catalytic enzyme activity" or "activity" of an enzyme or polypeptide solution or solution of a polypeptide variant, the enzymatic concentration of the enzyme or polypeptide solution, or solution of the polypeptide variant, is defined, indicated in units per milliliter of solution.

The term "specific activity" is defined as the catalytic activity per milligram of enzyme, polypeptide or polypeptide variant and is calculated from the ratio of the catalytic activity of an enzyme solution to the mass concentration (mass per unit volume) of the enzyme in said solution. If, for instance, an enzyme solution has a catalytic activity of 50 U/ml and a mass concentration of 1 mg/ml, its specific activity is 50 U/mg.

The term "temperature stability" refers to the property of enzymes, polypeptides or polypeptide variants to maintain their catalytic activities after temporary exposure to elevated temperatures (preincubation). The temperature stability is determined by measuring, and comparing, the activity of an enzyme or polypeptide solution, or solution of a polypeptide variant, after a 5-minute heat treatment and without heat treatment at identical, defined conditions. The temperature stability is thus a measure for the resistance of enzymes to temporal heat exposure. The temperature at which the residual activity of the heat-treated enzyme is 50% as compared to the non-heat-treated 100% control is the measure for the temperature stability and is abbreviated by T(50%). If, for instance, the activity of an enzyme solution is 50 U/ml without preincubation and 25 U/ml after a 5-minute preincubation at 50°C, the temperature stability of the enzyme is 50°C, or the enzyme is temperature-stable up to 50°C. The increases in the T(50%) of polypeptide variants relative to the parental polypeptide of SEQ ID No. 1 is defined as a measure for the increased temperature stability and can be indicated relatively as a percentage value or absolutely in degree Celsius.

The term "temperature activity" defines the temperature at which the enzyme, polypeptide or polypeptide variant exhibits the highest activity, the catalytic activity being measured over a period of 30 minutes.

The terms "polypeptide variant'" or "variant", in particular, refer to polypeptide sequences possessing at least one amino acid substitution as compared to SEQ ID No. 46, wherein the enzymatic function, i.e. the fusarium toxin-cleaving property, remains maintained. Moreover, a "polypeptide variant" may additionally comprise amino acid insertions or

deletions, in particular a C- or N-terminally extended or truncated sequence, relative to the polypeptide sequence of SEQ ID No. 46. An enzymatic function is substantially maintained if the enzymatic reaction mechanism remains unchanged, i.e. the fusarium toxin is hydrolyzed on the same site and the specific activity of the variant is at least 10%, preferably at least 50%, more preferably at least 90%, yet in particular >100%, based on the original, parental polypeptide of SEQ ID No. 46.

Amino acid substitutions at defined positions are described by the following nomenclature: original amino acid; position; new amino acid. If, for instance, glycine substitutes for a proline at position 134, this is indicated by Pro134Gly or P134G. Multiple mutations are separated by a plus sign or a slash. If, for instance, proline is substituted by glycine at position 134, and arginine is substituted by lysine at position 136, this is indicated by Pro134Gly+Arg136Lys or Pro134Gly/Arg136Lys or P134G+R136K or P134G/R136K, respectively. If an amino acid is substituted by two or several alternative amino acids at one position, the alternative amino acids are separated by a comma or a slash. If, for instance, proline is substituted at position 134 not only by glycine, but also by serine, valine and methionine, this is indicated by Pro134Gly, Ser,Val,Met or Pro134Gly/Ser/Val/Met or P134G,S,V,M or P134G/S/V/M. If, for instance, a substitution or exchange of an amino acid at a defined position is not defined in detail, this is to be interpreted such that said amino acid may be replaced by any other amino acid. If, for instance, a mutation of proline at position 134 is not defined in detail, the proline can be substituted by one of the following amino acids: A, R, N, D, C, Q, E, G, H, I, L, K, M, F, S, T, W, Y or V.

The term “sequence identity” refers to a percentual sequence identity. For amino acid sequences and nucleotide sequences, the sequence identity can be determined visually, yet preferably calculated by a computer program. The amino acid sequence having the sequence SEQ ID No. 1 is defined as reference sequence. A sequence comparison is also performed within sequence sections, a section meaning a continuous sequence of the reference sequence. Normally, the length of the sequence sections for nucleotide sequences is 18 to 600, preferably 45 to 200, more preferably 100 to 150, nucleotides. Normally, the length of the sequence sections for peptide sequences is 3 to 200, more preferably 15 to 65, most preferably 30 to 50, amino acids. There is a plurality of purchasable or costlessly available bioinformatic programs that can be used for the determination of homology and are constantly updated. Examples include GCG Wisconsin Bestfit package (Devereux et al. 1984), BLAST (Altschul et al. 1990) or BLAST 2

(Tatusova und Madden 1999). Due to the different adjustment options of these algorithms, it may happen that different results are output at identical input sequences. It is, therefore, necessary to define the search algorithm and its respective settings. In the present case, the sequence identity was assessed using the programs NCBI BLAST (Basic Local Alignment Search Tool), in particular BLASTP for polypeptides and BLASTN for polynucleotides, which are available on the website of the National Center for Biotechnology Information (NCBI; http://www.ncbi.nlm.nih.gov/). It is thereby possible to compare two or several sequences with one another according to the algorithm of Altschul et al., 1997 (Nucleic Acids Res., 25:3389-3402). In this case, the program versions of August 12, 2014, were used. As program setings, the base settings were applied, in particular for the amino acid comparison: "max target sequence" = 100; "expected threshold" = 10; "word size" = 3; "matrix" = BLOSOM62; "gap costs" = "Existence: 11; Extension: 1"; "computational adjustment" = "Conditional compositional score matrix adjustment"; and for the nucleotide sequence comparison: Word Size: 11; Expect value: 10; Gap costs: Existence = 5 , Extension = 2; Filter = low complexity activated; Match/Mismatch Scores: 2,-3; Filter String: L; m.

According to a preferred further development of the invention, the amino acid substitution is selected from the group consisting of 10Q, 33E, 66D, 107E, 140P, 144M, 149F, 151R, 157Y, 199I, 266S, 267P, 270F, 272H, 275E, 275A, 280D, 280P, 284T, 284P, 286P, 286R, 293E, 302I, 312F, 329F, 332E, 360V, 363T, 364H, 364L, 365I, 367H, 371V, 371M, 372F, 377V, 389L, 391V, 394P, 418A, 419V, 424A, 424K, 427V, 429P, 430A, 436A, 436S, 440G, 440S, 443T, 447A, 453R, 455S, 456Q, 457T, 462Y, 463D, 464I, 465H, 465S, 465G, 469K, 473A, 478D, 487N und 490P. In that the polypeptide variants comprise at least one such substitution, the temperature stability and the temperature activity can even be more selectively enhanced, wherein other enzyme parameters such as the specific activity, pH stability or pH activity can likewise be improved, which, however, at least exhibit the values of the fusarium toxin carboxylesterase of SEQ ID No. 1.

According to a further development of the invention, the polypeptide variants on at least one position selected from the group consisting of 66, 199, 302, 377, 394, 424, 430 and 463 each comprise an amino acid substitution and a temperature stability increased by at least 6% as compared to that of fusarium toxins carboxylesterase of SEQ ID No. 1. Such polypeptide variants enable the cleavage of fusarium toxins during technological processes at elevated temperatures, such as the production of pasta and other corn products such as polenta, popcorn, cornflakes, corn bread or tortillas, and starch

liquefaction processes, saccharification processes or fermentation processes such as, in particular, the mashing or fermentation process in the production of bioethanol.

According to a preferred further development of the invention, the amino acid substitution is selected from the group consisting of 66D, 199I, 302I, 377V, 394P, 424A, 430A und 463D. Such a substitution enables an increase of the temperature stability and of the temperature activity of the polypeptide variants by at least 3°C relative to the fusarium toxin carboxylesterase of SEQ ID No. 1.

According to a further development of the invention, the polypeptide variants, on at least two, in particular three, positions of the amino acid sequence, selected from the group consisting of 10, 33, 66, 107, 140, 144, 149, 151, 157, 199, 266, 267, 270, 272, 275, 280, 284, 286, 293, 302, 312, 329, 332, 360, 363, 364, 365, 367, 371, 372, 377, 389, 391, 394, 418, 419, 424, 427, 429, 430, 436, 440, 443, 447, 453, 455, 456, 457, 462, 463, 464, 465, 469, 473, 478, 487 and 490, each comprise an amino acid substitution, wherein the amino acid substitution being selected from the group consisting of 10Q, 66D, 144M, 151R, 199I, 266S, 267P, 272H, 275E, 275A, 280D, 284T, 286P, 286R, 293E, 302I, 360V, 363T, 364H, 364L, 365I, 367H, 371V, 371M, 372F, 377V, 389L, 391V, 394P, 418A, 419V, 424A, 424K, 427V, 429P, 430A, 436A, 436S, 440G, 440S, 443T, 447A, 453R, 455S, 456Q, 457T, 462Y, 463D, 464I, 465H, 465S, 465G, 469K, 473A, 478D, 487N and 490P, and exhibit a temperature stability increased by at least 15% as compared to the fusarium toxin carboxylesterase of SEQ ID No. 1. It has surprisingly turned out that by substituting several amino acids their positive effects on the temperature stability are approximately additive, the temperature stability being increased by more than 7°C by inserting at least three amino acids different from the amino acids originally present in the sequence. Such an increase is sufficient to use the enzymes, for instance, for mash resting at 55°C in the production of bioethanol or to pelletize feeds at moderate temperatures of about 65 to 70°C.

According to a further development of the invention, the amino acid sequence of the polypeptide variants comprises combinations of several amino acid substitutions, the combinations of the positions being selected from the group consisting of 66/199/302/394/424/430, 66/199/302/377/394/424/430, 66/199/302/377/394/424/430/463, 66/144/199/302/360/372/377/394/424/430/443/463, 199/302/377/394/424/430/463, 66/199/302/377/394, 66/199/302/364/377/394/424/430/463, 66/199/302/377/394/424/430/463/465, 66/199/302/377/394/424/430/440/463,

66/199/302/377/394/424/430/447/463, 66/199/302/377/394/418/424/430/463, 66/199/302/377/394/424/436/430/463, 66/199/302/364/377/394/424/430/463, 66/199/302/377/394/424/430/463/490, 66/199/302/377/394/424/430/463/469, 66/199/302/377/389/394/424/430/463, 66/199/302/377/394/424/430/463/465, 66/199/302/377/394/424/430/463/464, 66/199/302/377/394/424/430/463/465, 66/199/302/377/394/424/430/440/463, 66/199/302/377/394/424/430/457/463, 66/199/302/377/394/424/430/436/463, 66/199/302/363/371/377/394/424/430/463, 66/199/302/377/394/424/430/447/453/463, 66/199/302/377/394/424/430/456/462/463, 66/199/302/377/394/419/424/427/430/463, 66/199/302/365/377/394/424/430/463/487 und 66/199/302/371/377/394/424/430/463/487. Polypeptide variants substituted in such a manner exhibit a temperature stability increased by at least 25% as compared to the fusarium toxin carboxylesterase of SEQ ID No. 1. Such combinations of substitutions enable a further increase of not only the temperature stability but also the temperature activity of the polypeptide variants.

According to a preferred further development of the invention, the amino acid sequences of the polypeptide variants are selected from the group consisting of SEQ ID Nos. 2 to 29. Such polypeptide variants have a temperature stability increased by at least 11°C, preferably at least 13°C, and even more preferably at least 15°C, as compared to the enzyme of SEQ ID No. 1, thus guaranteeing the activity of the respective polypeptide, and hence the detoxification of fusarium toxins, during or after technological processes at elevated temperature loads, such as mash resting at 65°C in the production of bioethanol or pelletizing at temperatures of about 75-80°C.

	55 °C	168
	60 °C	134
	65 °C	102
	70 °C	98
SEQ ID No. 44	10 °C	33
	20 °C	59
	30 °C	100
	35 °C	110
	40 °C	124
	45 °C	131
	50 °C	162
	55 °C	174
	60 °C	126
	65 °C	99
	70 °C	95
SEQ ID No. 45	10 °C	41
	20 °C	68
	30 °C	100
	35 °C	115
	40 °C	136
	45 °C	141
	50 °C	164
	55 °C	177
	60 °C	137
	65 °C	121
	70 °C	100

Example 5: Determination of the pelletizing stability of fusarium toxin-degrading polypeptides

Selected polypeptide variants were cloned in *Pichia pastoris* in a bioreactor using standard methods under controlled aerobic conditions and extracellularly secreted. The clear supernatant was separated from the biomass, supplemented with a carrier substance (maltodextrin) and processed to a pelletizable powder using a spray-dryer. The fusarium toxin-degrading polypeptide variants present in power form were admixed to piglet rearing feed, each at the same concentration of 100 U/kg, and processed to feed pellets in a controlled process. During the pelletizing process, the feed was moistened by hot steaming and heated in individual batches at precisely defined temperatures (75 to 95 °C in 5°C steps). This preparation phase was followed by the pelletizing process proper. The residual activities of the fusarium toxin-degrading polypeptide variants contained in the pellets were determined as described in Example 2, non-pelletized feed containing the respective fusarium toxin-degrading polypeptide variants serving as 100% controls. The enzyme activity remaining after the pelletizing process is therefore defined as residual activity. The values are indicated in Table 3.

Table 3: Pelletizing temperatures and residual activities of fusarium toxin-degrading polypeptides. <LOQ values are below detection limits (level of quantification: <0.15 U/l in the test mixture)

Enzyme	Pelletizing temperature	Residual activity %
SEQ ID No. 1	75 °C	15
	80 °C	< LOQ
	85 °C	< LOQ
	90 °C	< LOQ
SEQ ID No. 4	75 °C	57
	80 °C	46
	85°C	37
	90 °C	14
SEQ ID No. 43	75 °C	78
	80 °C	73

Claims:

1. Fusarium toxin-cleaving polypeptide variants of a fusarium toxin carboxylesterase of SEQ ID No. 46, characterized in that the polypeptide variants each possess an amino acid sequence truncated by 47 amino acids at the N-terminus, the amino acid sequences sharing at least 70%, preferably 80%, particularly preferably 100%, sequence identity, namely SEQ ID No. 1, with the amino acid sequence section 48-540 of SEQ ID No. 46 wherein the temperature stability (T(50%)) of the polypeptide of SEQ ID No. 46 is determined to be 42°C and that of the polypeptide variant of SEQ ID No. 1 is determined to be 45°, or modifications of SEQ ID No. 1 having a relative increase of T(50%) compared to the parental enzyme of SEQ ID No. 1, wherein on at least one position selected from the group consisting of 10, 33, 66, 107, 140, 144, 149, 151, 157, 199, 266, 267, 270, 272, 275, 280, 284, 286, 293, 302, 312, 329, 332, 360, 363, 364, 365, 367, 371, 372, 377, 389, 391, 394, 418, 419, 424, 427, 429, 430, 436, 440, 443, 447, 453, 455, 456, 457, 462, 463, 464, 465, 469, 473, 478, 487 and 490 an amino acid substitution is contained as modification, and that the amino acid substituents at positions 10 and 456 are selected from Q, E, N, H, K and R, at positions 33, 107, 293 and 332 from E, Q, D, K, R and N, at positions 66, 463 and 478 from D, E, K, N, Q and R, at positions 140 and 490 from P, A, S and N, at positions 144 and 367 from I, L, M and V, at positions 149, 270, 312, 329 and 372 from F, Y, W and H, at positions 151 and 453 from D, E, K and R, at positions 157 and 462 from F, H, W and Y, at positions 199, 302, 365 and 464 from I, L, M and V, at positions 266 and 455 and from A, S and T, at positions 267, 394 and 429 from A, N, P and S, at position 272 from H, N, Q and S, at position 275 from A, D, E, G, K, N, Q, R and S, at position 280 from A, D, E, K, N, P, Q, R and S, at position 284 from A, N, P, S, T and V, at position 286 from A, D, E, K, N, P, R and S, at positions 360, 377, 391, 419 and 427 from A, I, L S, T and V, at positions 363, 443 and 457 from A, S, T and V, at position 364 from H, I, L, M, N, Q, S and V, at position 371 from A, I, L, M, S, T and V, at position 389 from I, L, M and V, at positions 418, 430, 447 and 473 from A, G and S, at position 424 from A, D, E, G, K, R and S, at position 436 from A, G, S and T, at position 440 from A, G, S and T, at position 465 from A, G, H, N, Q, S and T, at position 469 from D, E, K and R and/or at position 487 from N, D, Q, H and S.

2. Polypeptide variants according to claim 1, characterized in that the amino acid substitution is selected from the group consisting of 10Q, 66D, 144M, 151R, 199I, 266S, 267P, 272H, 275E, 275A, 280D, 284T, 286P, 286R, 293E, 302I, 360V, 363T, 364H, 364L, 365I, 367H, 371V, 371M, 372F, 377V, 389L, 391V, 394P, 418A, 419V, 424A, 424K, 427V,

429P, 430A, 436A, 436S, 440G, 440S, 443T, 447A, 453R, 455S, 456Q, 457T, 462Y, 463D, 464I, 465H, 465S, 465G, 469K, 473A, 478D, 487N and 490P.

3. Polypeptide variants according to any one of claim 1 or 2, characterized in that they comprise an amino acid substitution on at least one position selected from the group consisting of 66, 199, 302, 377, 394, 424, 430 and 463.

4. Polypeptide variants according to any one of claim 1, 2 or 3, characterized in that the amino acid substitution is selected from the group consisting of 66D, 199I, 302I, 377V, 394P, 424A, 430A and 463D.

5. Polypeptide variants according to claim 1, characterized in that the polypeptide variants comprise an amino acid substitution, on at least two, in particular three, positions of the amino acid sequence, selected from the group consisting of 10, 33, 66, 107, 140, 144, 149, 151, 157, 199, 266, 267, 270, 272, 275, 280, 284, 286, 293, 302, 312, 329, 332, 360, 363, 364, 365, 367, 371, 372, 377, 389, 391, 394, 418, 419, 424, 427, 429, 430, 436, 440, 443, 447, 453, 455, 456, 457, 462, 463, 464, 465, 469, 473, 478, 487 and 490 whereby the amino acid substitution is selected from the group consisting of 10Q, 66D, 144M, 151R, 199I, 266S, 267P, 272H, 275E, 275A, 280D, 284T, 286P, 286R, 293E, 302I, 360V, 363T, 364H, 364L, 365I, 367H, 371V, 371M, 372F, 377V, 389L, 391V, 394P, 418A, 419V, 424A, 424K, 427V, 429P, 430A, 436A, 436S, 440G, 440S, 443T, 447A, 453R, 455S, 456Q, 457T, 462Y, 463D, 464I, 465H, 465S, 465G, 469K, 473A, 478D, 487N and 490P..

6. Polypeptide variants according to claim 1 or 2, characterized in that the amino acid sequence of the polypeptide variants comprises combinations of several amino acid substitutions, whereat the combinations of the positions being selected from the group consisting of 66/199/302/394/424/430, 66/199/302/377/394/424/430, 66/199/302/377/394/424/430/463, 66/144/199/302/360/372/377/394/424/430/443/463, 199/302/377/394/424/430/463, 66/199/302/377/394, 66/199/302/364/377/394/424/430/463, 66/199/302/377/394/424/430/463/465, 66/199/302/377/394/424/430/440/463, 66/199/302/377/394/424/430/447/463, 66/199/302/377/394/418/424/430/463, 66/199/302/377/394/424/436/430/463, 66/199/302/364/377/394/424/430/463, 66/199/302/377/394/424/430/463/490, 66/199/302/377/394/424/430/463/469, 66/199/302/377/389/394/424/430/463, 66/199/302/377/394/424/430/463/465, 66/199/302/377/394/424/430/463/464, 66/199/302/377/394/424/430/463/465, 66/199/302/377/394/424/430/440/463,

66/199/302/377/394/424/430/457/463, 66/199/302/377/394/424/430/436/463, 66/199/302/363/371/377/394/424/430/463, 66/199/302/377/394/424/430/447/453/463, 66/199/302/377/394/424/430/456/462/463, 66/199/302/377/394/419/424/427/430/463, 66/199/302/365/377/394/424/430/463/487 and 66/199/302/371/377/394/424/430/463/487.

7. Polypeptide variants according to claim 6, characterized in that the amino acid sequences of the polypeptide variants are selected from the group consisting of SEQ ID Nos. 2 to 29.

8. Polypeptide variants according to claim 1 or 2, characterized in that the amino acid sequence of the polypeptide variants comprises combinations of several amino acid substitutions, the combinations of the positions being selected from the group consisting of 66/99/302/364/377/389/394/419/424/427/430/447/463/465/469, 66/199/302/377/389/394/419/424/427/430/447/463/465/469, 66/199/302/363/364/371/377/389/394/419/424/427/430/447/463/464/465/469, 66/199/302/363/371/377/389/394/419/424/427/430/447/463/464/465/469, 66/199/302/364/367/371/377/389/394/418/419/424/427/430/436/440/447/463/464/465/469/490, 66/199/302/367/371/377/389/394/418/419/424/427/430/436/440/447/463/464/465/469/490, 66/199/302/363/367/371/377/394/424/430/463/490, 66/199/302/377/394/418/419/424/427/430/436/440/447/463, 66/199/302/377/389/394/424/430/457/463/464/465/469, 66/199/302/363/371/377/389/394/419/424/427/430/440/447/457/463/464/469/490, 66/199/302/377/394/424/430/463/447/490/469/465, 66/199/302/377/394/424/430/463/490/469/465/419/427/371/487, 66/199/302/371/377/394/419/424/427/430/447/453/463/465/469/487/490, 66/199/302/367/371/377/389/394/418/419/424/427/429/430/436/440/447/457/463/464/465/469/490,66/199/302/371/377/389/394/419/424/427/430/436/447/453/456/462/463/465/469/490/487 and 66/199/302/367/371/377/389/394/418/419/424/427/429/430/436/440/447/453/456/457/462/463/464/465/469/487/490.

9. Polypeptide variants according to claim 8, characterized in that the amino acid sequences of the polypeptide variants are selected from the group consisting of SEQ ID Nos. 30 to 45.

10. Isolated polynucleotides, characterized in that the polynucleotides comprises nucleotide sequences encoding a polypeptide variant according to any one of claims 1 to 9.

11. Fusarium toxin-cleaving additive, characterized in that said additive comprises at least one polypeptide variant according to any one of claims 1 to 9 and optionally at least one supplement material.

12. Additive according to claim 11, characterized in that the supplement material is selected from the group consisting of inert carriers, vitamins, minerals, phytogenic substances, enzymes and other components for detoxifying mycotoxins, such as mycotoxin-degrading enzymes, in particular aflatoxin oxidases, ergotamine hydrolases, ergotamine amidases, zearalenone esterases, zearalenone lactonases, zearalenone hydrolases, ochratoxin amidases, fumonisin aminotransferases, aminopolyol aminoxidases, deoxynivalenol epoxide hydrolases, deoxynivalenol dehydrogenases, deoxynivalenol oxidases, trichothecene dehydrogenases, trichothecene oxidases; and mycotoxin-degrading microorganisms; and mycotoxin-binding substances, for instance microbial cell walls or inorganic materials such as bentonite.

13. Use of the additive according to any one of claim 11 or 12 for cleaving at least one fusarium toxin in, in particular pelletized, food or feed products, in particular for pigs, poultry, cattle, horses, fishes or aquaculture.

14. Use of the additive according to any one of claim 11 or 12 for cleaving at least one fusarium toxin in a process, in particular at temperatures of at least 50°C, preferably at least 70°C, for the production or processing of food or feed products.

15. Use of at least one polypeptide variant according to any one of claims 1 to 9 for use in a preparation for the prophylaxis and/or treatment of fusarium toxin mycotoxicoses.

16. Method for hydrolytically cleaving at least one fusarium toxin, characterized in that at least one fusarium toxin is contacted with at least one polypeptide variant according to any one of claims 1 to 9, or at least one additive according to any one of claim 11 or 12, and that the mixture of the polypeptide variant and the fusarium toxin is subjected to a temperature treatment at at least 50°C, preferably at least 70°C, and that the mixture is contacted with an amount of moisture sufficient for hydrolytic cleavage either during or after the temperature treatment.

17. Method according to claim 16, characterized in that the polypeptide variant, or the additive, is mixed with a feed or food product contaminated with at least one fusarium toxin, and the temperature treatment is optionally performed during a pelletizing process.

18. Method according to any one of claim 16 or 17, characterized in that the polypeptide variant is added at a concentration range from 5 U to 500 U, preferably from 10 U to 300 U, and more preferably from 15 U to 100 U, per kilogram of feed or food product.