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(54) Title: PLANTS HAVING INCREASED TOLERANCE TO HERBICIDES

(57) **Abrégé/Abstract:**

The present invention refers to a method for controlling undesired vegetation at a plant cultivation site, the method comprising the steps of providing, at said site, a plant that comprises at least one nucleic acid comprising a nucleotide sequence encoding protoporphyrinogen oxidase (PPO) which is resistant or tolerant to a PPO-inhibiting herbicide by applying to said site an effective amount of said herbicide. The invention further refers to plants comprising wild-type or mutated PPO enzymes, and methods of obtaining such plants.

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(54) Title: PLANTS HAVING INCREASED TOLERANCE TO HERBICIDES

(57) Abstract: The present invention refers to a method for controlling undesired vegetation at a plant cultivation site, the method comprising the steps of providing, at said site, a plant that comprises at least one nucleic acid comprising a nucleotide sequence encoding protoporphyrinogen oxidase (PPO) which is resistant or tolerant to a PPO-inhibiting herbicide by applying to said site an effective amount of said herbicide. The invention further refers to plants comprising wild-type or mutated PPO enzymes, and methods of obtaining such plants.

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LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

CECI EST LE TOME 1 DE 2
CONTENANT LES PAGES 1 À 264

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THIS IS VOLUME 1 OF 2
CONTAINING PAGES 1 TO 264

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PLANTS HAVING INCREASED TOLERANCE TO HERBICIDES

FIELD OF THE INVENTION

5 The present invention relates in general to methods for conferring on plants agricultural level tolerance to herbicides. Particularly, the invention refers to plants having an increased tolerance to PPO-inhibiting herbicides. More specifically, the present invention relates to methods and plants obtained by mutagenesis and cross-breeding and transformation that have an increased tolerance to PPO-inhibiting herbicides.

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BACKGROUND OF THE INVENTION

Herbicides that inhibit protoporphyrinogen oxidase (hereinafter referred to as Protox or PPO; EC:1.3.3.4), a key enzyme in the biosynthesis of protoporphyrin IX, have been used
 15 for selective weed control since the 1960s. PPO catalyzes the last common step in chlorophyll and heme biosynthesis which is the oxidation of protoporphyrinogen IX to protoporphyrin IX. (Matringe et al. 1989. Biochem. 1. 260: 231). PPO-inhibiting herbicides include many different structural classes of molecules (Duke et al. 1991. Weed Sci. 39: 465; Nandihalli et al. 1992. Pesticide Biochem. Physiol. 43: 193; Matringe et al. 1989. FEBS Lett.
 20 245: 35; Yanase and Andoh. 1989. Pesticide Biochem. Physiol. 35: 70). These herbicidal compounds include the diphenylethers {e.g. lactofen, (+-)-2-ethoxy-1-methyl-2-oxoethyl 5-{2-chloro-4-(trifluoromethyl)phenoxy}-2-nitrobenzoate; acifluorfen, 5-{2-chloro-4-(trifluoromethyl)phenoxy}-2-nitrobenzoic acid; its methyl ester; or oxyfluorfen, 2-chloro-1-(3-ethoxy-4-nitrophenoxy)-4-(trifluorobenzene)}, oxidiazoles, (e.g. oxidiazon, 3-{2,4-dichloro-5-(1-methylethoxy)phenyl}-5-(1,1-dimethylethyl)-1,3,4-oxadiazol-2-(3H)-one), cyclic imides
 25 (e.g. S-23142, N-(4-chloro-2-fluoro-5-propargyloxyphenyl)-3,4,5,6-tetrahydrophthalimide; chlorophthalim, N-(4-chlorophenyl)-3,4,5,6-tetrahydrophthalimide), phenyl pyrazoles (e.g. TNPP-ethyl, ethyl 2-{1-(2,3,4-trichlorophenyl)-4-nitropyrazolyl-5-oxy}propionate; M&B 39279), pyridine derivatives (e.g. LS 82-556), and phenopylate and its O-phenylpyrrolidino-
 30 and piperidinocarbamate analogs. Many of these compounds competitively inhibit the normal reaction catalyzed by the enzyme, apparently acting as substrate analogs.

Application of PPO-inhibiting herbicides results in the accumulation of protoporphyrinogen IX in the chloroplast and mitochondria, which is believed to leak into the cytosol where it is
 35 oxidized by a peroxidase. When exposed to light, protoporphyrin IX causes formation of singlet oxygen in the cytosol and the formation of other reactive oxygen species, which can cause lipid peroxidation and membrane disruption leading to rapid cell death (Lee et al. 1993. Plant Physiol. 102: 881).

40 Not all PPO enzymes are sensitive to herbicides which inhibit plant PPO enzymes. Both the

- Escherichia coli and Bacillus subtilis PPO enzymes (Sasarmen et al. 1993. Can. J. Microbiol. 39: 1155; Dailey et al. 1994. J. Biol. Chem. 269: 813) are resistant to these herbicidal inhibitors. Mutants of the unicellular alga Chlamydomonas reinhardtii resistant to the phenylimide herbicide S-23142 have been reported (Kataoka et al. 1990. J. Pesticide Sci. 15: 449; Shibata et al. 1992. In Research in Photosynthesis, Vol. III, N. Murata, ed. Kluwer:Netherlands. pp. 567-70). At least one of these mutants appears to have an altered PPO activity that is resistant not only to the herbicidal inhibitor on which the mutant was selected, but also to other classes of protox inhibitors (Oshio et al. 1993. Z. Naturforsch. 48c: 339; Sato et al. 1994. In ACS Symposium on Porphyrin Pesticides, S. Duke, ed. ACS Press: Washington, D.C.). A mutant tobacco cell line has also been reported that is resistant to the inhibitor S-21432 (Che et al. 1993. Z. Naturforsch. 48c: 350). Auxotrophic E. coli mutants have been used to confirm the herbicide resistance of cloned plant PPO-inhibiting herbicides.
- Three main strategies are available for making plants tolerant to herbicides, i.e. (1) detoxifying the herbicide with an enzyme which transforms the herbicide, or its active metabolite, into non-toxic products, such as, for example, the enzymes for tolerance to bromoxynil or to basta (EP242236, EP337899); (2) mutating the target enzyme into a functional enzyme which is less sensitive to the herbicide, or to its active metabolite, such as, for example, the enzymes for tolerance to glyphosate (EP293356, Padgett S. R. et al., J.Biol. Chem., 266, 33, 1991); or (3) overexpressing the sensitive enzyme so as to produce quantities of the target enzyme in the plant which are sufficient in relation to the herbicide, in view of the kinetic constants of this enzyme, so as to have enough of the functional enzyme available despite the presence of its inhibitor. The third strategy was described for successfully obtaining plants which were tolerant to PPO inhibitors (see e.g. US5,767,373 or US5,939,602, and patent family members thereof.). In addition, US 2010/0100988 and WO 2007/024739 discloses nucleotide sequences encoding amino acid sequences having enzymatic activity such that the amino acid sequences are resistant to PPO inhibitor herbicidal chemicals, in particular 3-phenyluracil inhibitor specific PPO mutants.
- WO 2012/080975 discloses plants the tolerance of which to a PPO-inhibiting herbicide named (1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione) had been increased by transforming said plants with nucleic acids encoding mutated PPO mutated enzymes. In particular, WO 2012/080975 discloses that the introduction of nucleic acids which code for a mutated PPO of an Amaranthus type II PPO in which the Arginine at position 128 had been replaced by a leucine, alanine, or valine, and the phenylalanine at position 420 had been replaced by a methionine, cysteine, isoleucine, leucine, or threonine, confers increased tolerance/resistance to a benzoxazinone-derivative herbicide. WO 2013/189984 discloses plants the tolerance of which to PPO inhibitors had been increased by transforming said plants with nucleic acids encoding mutated PPO enzymes, in which the Leucine corresponding to position 397 of an Amaranthus type II PPO had been replaced, and the

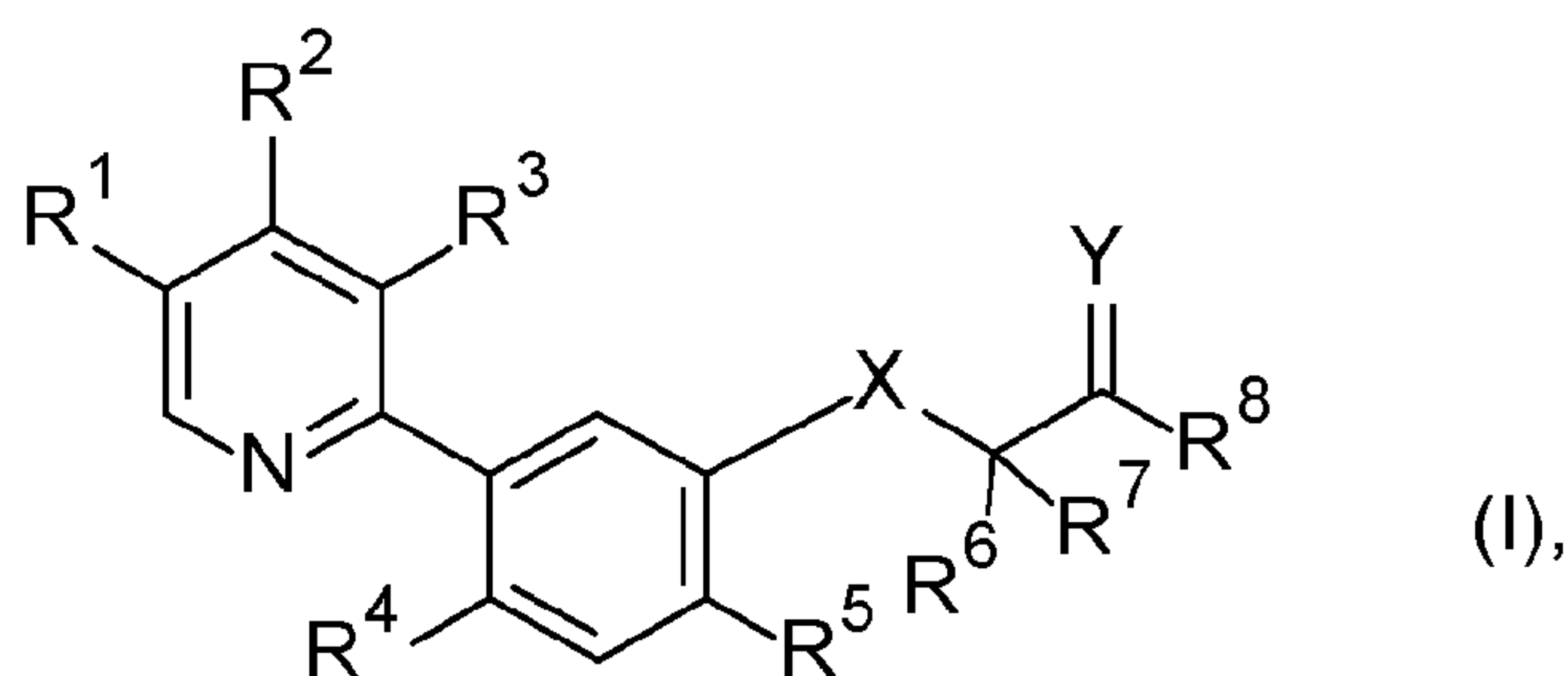
phenylalanine corresponding to position 420 of an *Amaranthus* type II PPO had been replaced. WO2015/022636 discloses plants the tolerance of which to PPO inhibitors had been increased by transforming said plants with nucleic acids encoding mutated PPO enzymes, in which the Arginine corresponding to position 128 of an *Amaranthus* type II PPO had been replaced, and the phenylalanine corresponding to position 420 of an *Amaranthus* type II PPO had been replaced, but the replacement occurred with amino acids, which are different from those disclosed in WO 2012/080975. WO2015/092706 describes PPO polypeptides from a plurality of organisms, which PPO polypeptides had been mutated to comprise the advantageous mutations employed for the *Amaranthus* type II PPO. WO2015/022640 discloses PPO polypeptides from *Alopecurus myosuroides* and mutants thereof, which confer tolerance to a broad spectrum of PPO inhibiting herbicides.

The inventors of the present invention have now surprisingly found that those types of mutants confer increased tolerance/resistance to a new class of PPO inhibitors, hereinafter described as phenylpyridines or phenylpyridine herbicides. Thus, to date, the prior art has not described phenylpyridine tolerant plants containing a mutated PPO nucleic acid according to the present invention, which are tolerant/resistant to a broad selection of phenylpyridines. Therefore, what is needed in the art are crop plants and crop plants having increased tolerance to phenylpyridines and containing at least one wildtype and/or mutated PPO nucleic acid according to the present invention. Also needed are methods for controlling weed growth in the vicinity of such crop plants or crop plants. These compositions and methods would allow for the use of spray over techniques when applying herbicides to areas containing crop plants or crop plants.

SUMMARY OF THE INVENTION

The problem is solved by the present invention which refers to a method for controlling undesired vegetation at a plant cultivation site, the method comprising the steps of:

- a) providing, at said site, a plant that comprises at least one nucleic acid comprising a nucleotide sequence encoding a protoporphyrinogen oxidase (PPO) polypeptide which is resistant or tolerant to a "PPO inhibiting herbicide";
 - b) applying to said site an effective amount of said herbicide,
- wherein the PPO inhibiting herbicide is a phenylpyridine of formula (I)



wherein the variables have the following meanings:

- 5 R¹ halogen, C₁-C₄-haloalkyl or SO₂CH₃;
 R² H, CH₃ or NH₂;
 R³ halogen;
 R⁴ H or halogen;
 R⁵ halogen or CN;
 R⁶ H or CH₃;
 10 R⁷ C₁-C₆-alkoxy, C₁-C₆-haloalkoxy, C₃-C₆-alkenyloxy, C₃-C₆-alkynyloxy;
 R⁸ OR⁹, SR⁹, NR¹⁰R¹¹, NR⁹S(O)R¹⁰, NR⁹S(O)₂R¹⁰, NR⁹S(O)NR¹⁰R¹¹, or
 NR⁹S(O)₂NR¹⁰R¹¹,
 wherein
 15 R⁹ is hydrogen, C₁-C₆-alkyl, C₃-C₆-alkenyl, C₃-C₆-alkynyl, C₁-C₆-haloalkyl, C₃-
 C₆-haloalkenyl, C₃-C₆-haloalkynyl, C₁-C₆-cyanoalkyl, C₁-C₆-alkoxy-C₁-C₆-
 alkyl, C₁-C₆-alkoxy-C₁-C₆-alkoxy-C₁-C₆-alkyl, di(C₁-C₆-alkoxy)C₁-C₆-alkyl,
 C₁-C₆-haloalkoxy-C₁-C₆-alkyl, C₃-C₆-alkenyloxy-C₁-C₆-alkyl, C₃-C₆-
 haloalkenyloxy-C₁-C₆-alkyl, C₃-C₆-alkenyloxy-C₁-C₆-alkoxy-C₁-C₆-alkyl, C₁-
 20 C₆-alkylthio-C₁-C₆-alkyl, C₁-C₆-alkylsulfinyl-C₁-C₆-alkyl, C₁-C₆-alkylsulfonyl-
 C₁-C₆-alkyl, C₁-C₆-alkylcarbonyl-C₁-C₆-alkyl, C₁-C₆-alkoxycarbonyl-C₁-C₆-
 alkyl, C₁-C₆-haloalkoxycarbonyl-C₁-C₆-alkyl, C₃-C₆-alkenyloxycarbonyl-C₁-
 C₆-alkyl, amino, (C₁-C₆-alkyl)amino, di(C₁-C₆-alkyl)amino, (C₁-C₆-
 alkylcarbonyl)amino, amino-C₁-C₆-alkyl, (C₁-C₆-alkyl)amino-C₁-C₆-alkyl,
 25 di(C₁-C₆-alkyl)amino-C₁-C₆-alkyl, aminocarbonyl-C₁-C₆-alkyl, (C₁-C₆-
 alkyl)aminocarbonyl-C₁-C₆-alkyl, di(C₁-C₆-alkyl)aminocarbonyl-C₁-C₆-alkyl,
 -N=CR¹²R¹³, wherein R¹² and R¹³ independently of one another are H, C₁-
 C₄-alkyl or phenyl;
 C₃-C₆-cycloalkyl, C₃-C₆-cycloalkyl-C₁-C₆-alkyl, C₃-C₆-heterocyclyl, C₃-C₆-
 heterocyclyl-C₁-C₆-alkyl, phenyl, phenyl-C₁-C₄-alkyl or a 5- or 6 membered
 30 heteroaryl,
 wherein each phenyl or heteroaryl ring can be substituted by one to
 four substituents selected from R¹⁴ or a 3- to 7-membered
 carbocyclus,
 which carbocyclus optionally has in addition to carbon atoms
 35 one or two ring members selected from the group consisting of -
 N(R¹²)-, -N=N-, -C(=O)-, -O- and -S-, and
 which carbocyclus is optionally substituted with one to four
 substituents selected from R¹⁴;
 wherein R¹⁴ is halogen, NO₂, CN, C₁-C₄-alkyl, C₁-C₄-
 40 haloalkyl, C₁-C₄-alkoxy or C₁-C₄-alkoxy-
 carbonyl;

R¹⁰, R¹¹ independently of one another are R⁹, or together form a 3- to 7-membered carbocyclus,

which carbocyclus optionally has in addition to carbon atoms one or two ring members selected from the group consisting of -N(R¹²)-, -N=N-, -C(=O)-, -O- and -S-, and

which carbocyclus is optionally substituted with one to four substituents selected from R¹⁴;

X O or S; and

Y O or S;

including their agriculturally acceptable salts, and wherein the effective amount of said herbicide does not kill or inhibit the growth of the herbicide-tolerant plant of a).

In one embodiment, the herbicide resistant or tolerant PPO polypeptide comprises one or more of the following motifs 1, 2, and/or 3:

- a. Motif 1: SQ[N/K/H]KRYI, wherein the Arg at position 5 within said motif is substituted by any other amino acid;
- b. Motif 2: TLGTLFSS, wherein the Leu at position 2 within said motif is substituted by any other amino acid;
- c. Motif 3: [F/Y]TTF[V/I]GG, wherein the Phe at position 4 within said motif is substituted by any other amino acid.

In another embodiment, the herbicide resistant or tolerant PPO polypeptide comprises a variant of the amino acid sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, which variant comprises one or more of the following substitutions:

- a. the amino acid corresponding to Arg128 of SEQ ID NO: 1 is substituted by any other amino acid.
- b. the amino acid corresponding to Leu397 of SEQ ID NO: 1 is substituted by any other amino acid.
- c. the amino acid corresponding to Phe420 of SEQ ID NO: 1 is substituted by any other amino acid.

In still another embodiment, the herbicide resistant or tolerant PPO polypeptide comprises the amino acid sequence of SEQ ID NO: 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328,

329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, or a variant thereof.

In still another embodiment, the herbicide resistant or tolerant PPO polypeptide comprises the amino acid sequence of SEQ ID NO: 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, or 262.

Another object refers to a method of identifying a nucleotide sequence encoding a mutated PPO which is resistant or tolerant to a phenylpyridine herbicide, the method comprising:

- a) generating a library of mutated PPO-encoding nucleic acids,
- b) screening a population of the resulting mutated PPO-encoding nucleic acids by expressing each of said nucleic acids in a cell or plant and treating said cell or plant with a phenylpyridine,
- c) comparing the phenylpyridine herbicide-tolerance levels provided by said population of mutated PPO encoding nucleic acids with the phenylpyridine -tolerance level provided by a control PPO-encoding nucleic acid,
- d) selecting at least one mutated PPO-encoding nucleic acid that provides a significantly increased level of tolerance to a phenylpyridine as compared to that provided by the control PPO-encoding nucleic acid.

In a preferred embodiment, the mutated PPO-encoding nucleic acid selected in step d) provides at least 2-fold as much tolerance to a phenylpyridine as compared to that provided by the control PPO-encoding nucleic acid.

The resistance or tolerance can be determined by generating a transgenic plant comprising a nucleic acid sequence of the library of step a) and comparing said transgenic plant with a control plant.

Another object refers to a method of identifying a plant or algae containing a nucleic acid encoding a mutated PPO which is resistant or tolerant to a phenylpyridine, the method

comprising:

- a) identifying an effective amount of a phenylpyridine in a culture of plant cells or green algae.
- b) treating said plant cells or green algae with a mutagenizing agent,
- 5 c) contacting said mutagenized cells population with an effective amount of phenylpyridine herbicide, identified in a),
- d) selecting at least one cell surviving these test conditions,
- e) PCR-amplification and sequencing of PPO genes from cells selected in d) and comparing such sequences to wild-type PPO gene sequences, respectively.

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In a preferred embodiment, the mutagenizing agent is ethylmethanesulfonate.

In another embodiment, the invention refers to a plant cell transformed by and expressing a wild-type or a mutated PPO nucleic acid according to the present invention or a plant which
 15 has been mutated to obtain a plant expressing, preferably over-expressing a wild-type or a mutated PPO nucleic acid according to the present invention, wherein expression of said nucleic acid in the plant cell results in increased resistance or tolerance to a phenylpyridine as compared to a wild type variety of the plant cell.

20 In another embodiment, the invention refers to a plant that expresses a mutagenized or recombinant mutated PPO polypeptide, and wherein said mutated PPO confers upon the plant increased phenylpyridine tolerance as compared to the corresponding wild-type variety of the plant when expressed therein.

25 In another embodiment, the invention refers to a plant comprising a plant cell according to the present invention, wherein expression of the nucleic acid in the plant results in the plant's increased resistance to phenylpyridine herbicide as compared to a wild type variety of the plant.

30 The plants of the present invention can be transgenic or non-transgenic.

Preferably, the expression of the nucleic acid of the invention in the plant results in the plant's increased resistance to phenylpyridine herbicides as compared to a wild type variety of the plant.

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In another embodiment, the invention refers to a method for growing the plant according to the present invention while controlling weeds in the vicinity of said plant, said method comprising the steps of:

- a) growing said plant ; and
- 40 b) applying a herbicide composition comprising a phenylpyridine herbicide to the plant and weeds, wherein the herbicide normally inhibits protoporphyrinogen oxidase, at a level of the herbicide that would inhibit the growth of a corresponding wild-type plant.

In another embodiment, the invention refers to a seed produced by a transgenic plant comprising a plant cell of the present invention, or to a seed produced by the non-transgenic plant that expresses a mutagenized PPO polypeptide, wherein the seed is true
5 breeding for an increased resistance to a phenylpyridine herbicide as compared to a wild type variety of the seed.

In another embodiment, the invention refers to a method of producing a transgenic plant cell with an increased resistance to a phenylpyridine herbicide as compared to a wild type
10 variety of the plant cell comprising, transforming the plant cell with an expression cassette comprising a wild-type or a mutated PPO nucleic acid.

In another embodiment, the invention refers to a method of producing a transgenic plant comprising, (a) transforming a plant cell with an expression cassette comprising a wild-type
15 or a mutated PPO nucleic acid, and (b) generating a plant with an increased resistance to phenylpyridine herbicide from the plant cell.

Preferably, the expression cassette further comprises a transcription initiation regulatory region and a translation initiation regulatory region that are functional in the plant.
20

In another embodiment, the invention relates to using the mutated PPO of the invention as selectable marker. The invention provides a method of identifying or selecting a transformed plant cell, plant tissue, plant or part thereof comprising a) providing a transformed plant cell, plant tissue, plant or part thereof, wherein said transformed plant
25 cell, plant tissue, plant or part thereof comprises an isolated nucleic acid encoding a mutated PPO polypeptide of the invention as described hereinafter, wherein the polypeptide is used as a selection marker, and wherein said transformed plant cell, plant tissue, plant or part thereof may optionally comprise a further isolated nucleic acid of interest; b) contacting the transformed plant cell, plant tissue, plant or part thereof with at least one PPO-inhibiting
30 inhibiting compound; c) determining whether the plant cell, plant tissue, plant or part thereof is affected by the inhibitor or inhibiting compound; and d) identifying or selecting the transformed plant cell, plant tissue, plant or part thereof.

The invention is also embodied in purified mutated PPO proteins that contain the mutations
35 described herein, which are useful in molecular modeling studies to design further improvements to herbicide tolerance. Methods of protein purification are well known, and can be readily accomplished using commercially available products or specially designed methods, as set forth for example, in Protein Biotechnology, Walsh and Headon (Wiley, 1994).
40

In another embodiment, the invention relates to a combination useful for weed control, comprising (a) a polynucleotide encoding a mutated PPO polypeptide according to the

present invention, which polynucleotide is capable of being expressed in a plant to thereby provide to that plant tolerance to a phenylpyridine herbicide; and (b) a phenylpyridine herbicide.

- 5 In another embodiment, the invention relates to a process for preparing a combination useful for weed control comprising (a) providing a polynucleotide encoding a mutated PPO polypeptide according to the present invention, which polynucleotide is capable of being expressed in a plant to thereby provide to that plant tolerance to a phenylpyridine herbicide; and (b) providing a phenylpyridine herbicide.

10

In a preferred embodiment, said step of providing a polynucleotide comprises providing a plant containing the polynucleotide.

15

In another preferred embodiment, said step of providing a polynucleotide comprises providing a seed containing the polynucleotide.

In another preferred embodiment, said process further comprises a step of applying the phenylpyridine herbicide to the seed.

20

In another embodiment, the invention relates to the use of a combination useful for weed control, comprising (a) a polynucleotide encoding a mutated PPO polypeptide according to the present invention, which polynucleotide is capable of being expressed in a plant to thereby provide to that plant tolerance to a phenylpyridine herbicide; and (b) a phenylpyridine herbicide, to control weeds at a plant cultivation site.

25

BRIEF DESCRIPTION OF THE DRAWINGS

30 **Figure 1** shows transgenic T2 Arabidopsis plants, four weeks old, were sprayed in the greenhouse with the indicated amount of methyl 2-[2-chloro-5-[3-chloro-5-(trifluoromethyl)-2-pyridyl]-4-fluoro-phenoxy]-2-methoxy-acetate + 1% (v/v) MSO. AMATU = Amaranthus tuberculatum; ALOMY = Alopecurus myosuroides

Figure 1A:

- 1 = wildtype (non-transgenic)
 35 2= AMATU_PPO2_R128M_F420V
 3= AMATU_PPO2_R128M_F420I
 4= AMATU_PPO2_R128M_F420L
 5 = AMATU_PPO2_R128M_F420M
 6 = ALOMY_PPO2_F438V
 40 7 = ALOMY_PPO2_F438I
 8 = ALOMY_PPO2_F438M
 9= ALOMY_PPO2_R137L_F438V

Figure 1B

- 10= ALOMY_PPO2_R137L_F438L
 11 = ALOMY_PPO2_R137L_F438M
 5 12 = AMATU_PPO2_L397E_F420V
 13 = AMATU_PPO2_L397E_F420M
 14 = AMATU_PPO2_L397Q_F420V
 15 = AMATU_PPO2_L397Q_F420M
 16 = AMATU_PPO2_L397C_F420M
 10 17 = AMATU_PPO2_L397G_F420M

Figure 1C

- 18 = AMATU_PPO2_R128L_F420L
 19 = AMATU_PPO2_R128I_F420V
 15 20 = ALOMY_PPO2_L415A_F438M
 21 = ALOMY_PPO2_L415C_F438M
 22 = ALOMY_PPO2_L415G_F438M
 23 = ALOMY_PPO2_L415E_F438M
 24 = ALOMY_PPO2_L415Q_F438M
 20 25 = hemG_tplAMATU_PPO2

Figure 1D

- 1 = wildtype (non-transgenic)
 2 = AMATU_PPO2_R128A_F420V
 25 3 = AMATU_PPO2_L397D_F420V
 4 = Arabidopsis thaliana_PPO1_S305L_Y426M

Figure 2A: T2 soybean events were transformed with the indicated *Amaranthus* PPO2 variant. Greenhouse grown plants at the V2 stage were sprayed with the indicated amount of herbicide methyl 2-[2-chloro-5-[3-chloro-5-(trifluoromethyl)-2-pyridyl]-4-fluoro-phenoxy]-2-methoxy-acetate (herbicide 1) + 1% v/v methylated seed oil. Images were taken 3 days after treatment and are representative of replicates.

Figure 2B: T2 soybean events were transformed with the indicated *Amaranthus* PPO2 variant. Greenhouse grown plants at the V2 stage were sprayed with the indicated amount of herbicide prop-2-ynyl 2-[2-chloro-5-[3-chloro-5-(trifluoromethyl)-2-pyridyl]-4-fluoro-phenoxy]-2-methoxy-acetate (herbicide 2) + 1% v/v methylated seed oil. Images were taken 3 days after treatment and are representative of replicates.

Figure 2C: T2 soybean events were transformed with the indicated *Amaranthus* PPO2 variant. Greenhouse grown plants at the V2 stage were sprayed with the indicated amount of herbicide prop-2-ynyl 2-[2-chloro-5-[3-chloro-5-(trifluoromethyl)-2-pyridyl]-4-fluoro-phenoxy]-

2-methoxy-acetate (herbicide 2) + 1% v/v methylated seed oil. Images were taken 3 days after treatment and are representative of replicates.

Figure 2D: T2 maize events were transformed with the *Amaranthus* PPO2 variants: (1) R128A F420I; (2) R128A F420I; (3) L397E F420M; (4) L397D F420M; (5) Untransformed. Greenhouse grown plants at the V2 stage were sprayed with the indicated amount of herbicide methyl 2-[2-chloro-5-[3-chloro-5-(trifluoromethyl)-2-pyridyl]-4-fluoro-phenoxy]-2-methoxy-acetate (herbicide 1) + 1% v/v methylated seed oil. Images were taken 3 days after treatment

DETAILED DESCRIPTION

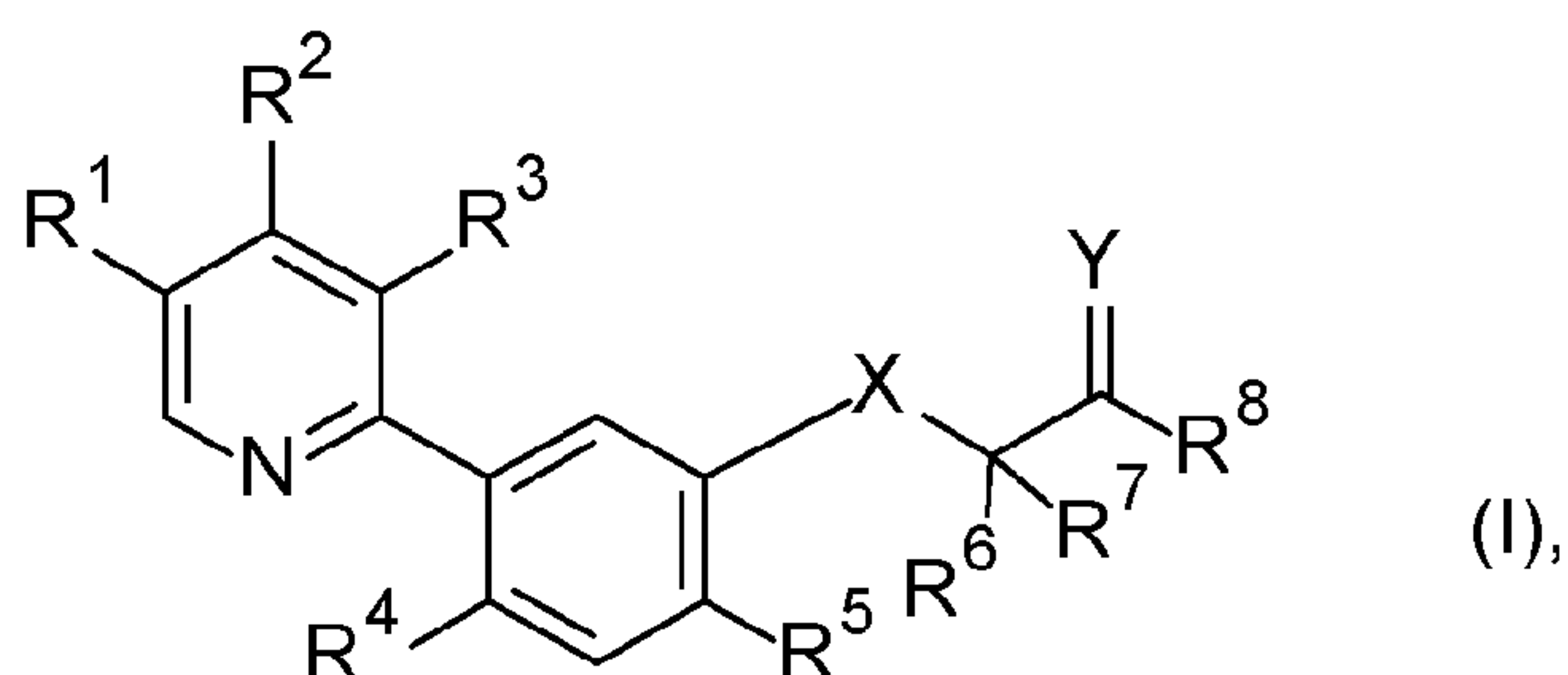
The articles "a" and "an" are used herein to refer to one or more than one (i.e., to at least one) of the grammatical object of the article. By way of example, "an element" means one or more elements.

As used herein, the word "comprising," or variations such as "comprises" or "comprising," will be understood to imply the inclusion of a stated element, integer or step, or group of elements, integers or steps, but not the exclusion of any other element, integer or step, or group of elements, integers or steps.

The inventors of the present invention have found, that the tolerance or resistance of a plant to a phenylpyridine herbicide could be remarkably increased by overexpressing a nucleic acid encoding PPO polypeptides described hereinafter.

The present invention refers to a method for controlling undesired vegetation at a plant cultivation site, the method comprising the steps of:

- providing, at said site, a plant that comprises at least one nucleic acid comprising a nucleotide sequence encoding a protoporphyrinogen oxidase (mutated PPO) which is resistant or tolerant to a PPO-inhibiting herbicide,
 - applying to said site an effective amount of said herbicide,
- wherein the PPO inhibiting herbicide is a phenylpyridine of formula (I)



wherein the variables have the following meanings:

R¹ halogen, C₁-C₄-haloalkyl or SO₂CH₃;

R² H, CH₃ or NH₂;

5 R³ halogen;

R⁴ H or halogen;

R⁵ halogen or CN;

R⁶ H or CH₃;

R⁷ C₁-C₆-alkoxy, C₁-C₆-haloalkoxy, C₃-C₆-alkenyloxy, C₃-C₆-alkynyloxy;

10 R⁸ OR⁹, SR⁹, NR¹⁰R¹¹, NR⁹S(O)R¹⁰, NR⁹S(O)₂R¹⁰, NR⁹S(O)NR¹⁰R¹¹, or
NR⁹S(O)₂NR¹⁰R¹¹,

wherein

15 R⁹ is hydrogen, C₁-C₆-alkyl, C₃-C₆-alkenyl, C₃-C₆-alkynyl, C₁-C₆-haloalkyl, C₃-
C₆-haloalkenyl, C₃-C₆-haloalkynyl, C₁-C₆-cyanoalkyl, C₁-C₆-alkoxy-C₁-C₆-
alkyl, C₁-C₆-alkoxy-C₁-C₆-alkoxy-C₁-C₆-alkyl, di(C₁-C₆-alkoxy)C₁-C₆-alkyl,
C₁-C₆-haloalkoxy-C₁-C₆-alkyl, C₃-C₆-alkenyloxy-C₁-C₆-alkyl, C₃-C₆-
haloalkenyloxy-C₁-C₆-alkyl, C₃-C₆-alkenyloxy-C₁-C₆-alkoxy-C₁-C₆-alkyl, C₁-
20 C₆-alkylthio-C₁-C₆-alkyl, C₁-C₆-alkylsulfinyl-C₁-C₆-alkyl, C₁-C₆-alkylsulfonyl-
C₁-C₆-alkyl, C₁-C₆-alkylcarbonyl-C₁-C₆-alkyl, C₁-C₆-alkoxycarbonyl-C₁-C₆-
alkyl, C₁-C₆-haloalkoxycarbonyl-C₁-C₆-alkyl, C₃-C₆-alkenyloxycarbonyl-C₁-
C₆-alkyl, amino, (C₁-C₆-alkyl)amino, di(C₁-C₆-alkyl)amino, (C₁-C₆-
alkylcarbonyl)amino, amino-C₁-C₆-alkyl, (C₁-C₆-alkyl)amino-C₁-C₆-alkyl,
25 di(C₁-C₆-alkyl)amino-C₁-C₆-alkyl, aminocarbonyl-C₁-C₆-alkyl, (C₁-C₆-
alkyl)aminocarbonyl-C₁-C₆-alkyl, di(C₁-C₆-alkyl)aminocarbonyl-C₁-C₆-alkyl,
-N=CR¹²R¹³, wherein R¹² and R¹³ independently of one another are H, C₁-
C₄-alkyl or phenyl;
C₃-C₆-cycloalkyl, C₃-C₆-cycloalkyl-C₁-C₆-alkyl, C₃-C₆-heterocyclyl, C₃-C₆-
heterocyclyl-C₁-C₆-alkyl, phenyl, phenyl-C₁-C₄-alkyl or a 5- or 6 membered
heteroaryl,

30 wherein each phenyl or heteroaryl ring can be substituted by one to
four substituents selected from R¹⁴ or a 3- to 7-membered
carbocyclus,

35 which carbocyclus optionally has in addition to carbon atoms
one or two ring members selected from the group consisting of -
N(R¹²)-, -N=N-, -C(=O)-, -O- and -S-, and
which carbocyclus is optionally substituted with one to four
substituents selected from R¹⁴;

40 wherein R¹⁴ is halogen, NO₂, CN, C₁-C₄-alkyl, C₁-C₄-
haloalkyl, C₁-C₄-alkoxy or C₁-C₄-alkoxy-
carbonyl;

R¹⁰, R¹¹ independently of one another are R⁹, or together form a 3- to 7-
membered carbocyclus,

which carbocyclous optionally has in addition to carbon atoms one or two ring members selected from the group consisting of -N(R¹²)-, -N=N-, -C(=O)-, -O- and -S-, and

which carbocyclous is optionally substituted with one to four substituents selected from R¹⁴;

X O or S; and

Y O or S;

including their agriculturally acceptable salts, and wherein the effective amount of said herbicide does not kill or inhibit the growth of the herbicide-tolerant plant of a).

The term “control of undesired vegetation” is to be understood as meaning the killing of weeds and/or otherwise retarding or inhibiting the normal growth of the weeds. Weeds, in the broadest sense, are understood as meaning all those plants which grow in locations where they are undesired, e.g. (crop) plant cultivation sites. The weeds of the present invention include, for example, dicotyledonous and monocotyledonous weeds.

Dicotyledonous weeds include, but are not limited to, weeds of the genera: Sinapis, Lepidium, Galium, Stellaria, Matricaria, Anthemis, Galinsoga, Chenopodium, Urtica, Senecio, Amaranthus, Portulaca, Xanthium, Convolvulus, Ipomoea, Polygonum, Sesbania, Ambrosia, Cirsium, Carduus, Sonchus, Solanum, Rorippa, Rotala, Lindernia, Lamium, Veronica, Abutilon, Emex, Datura, Viola, Galeopsis, Papaver, Centaurea, Trifolium, Ranunculus, and Taraxacum. Monocotyledonous weeds include, but are not limited to, weeds of the genera: Echinochloa, Setaria, Panicum, Digitaria, Phleum, Poa, Festuca, Eleusine, Brachiaria, Lolium, Bromus, Avena, Cyperus, Sorghum, Agropyron, Cynodon, Monochoria, Fimbristylis, Sagittaria, Eleocharis, Scirpus, Paspalum, Ischaemum, Sphenoclea, Dactyloctenium, Agrostis, Alopecurus, and Apera. In addition, the weeds of the present invention can include, for example, crop plants that are growing in an undesired location. For example, a volunteer maize plant that is in a field that predominantly comprises soybean plants can be considered a weed, if the maize plant is undesired in the field of soybean plants.

The term “plant” is used in its broadest sense as it pertains to organic material and is intended to encompass eukaryotic organisms that are members of the Kingdom Plantae, examples of which include but are not limited to vascular plants, vegetables, grains, flowers, trees, herbs, bushes, grasses, vines, ferns, mosses, fungi and algae, etc, as well as clones, offsets, and parts of plants used for asexual propagation (e.g. cuttings, pipings, shoots, rhizomes, underground stems, clumps, crowns, bulbs, corms, tubers, rhizomes, plants/tissues produced in tissue culture, etc.). The term “plant” further encompasses whole plants, ancestors and progeny of the plants and plant parts, including seeds, shoots, stems, leaves, roots (including tubers), flowers, florets, fruits, pedicles, peduncles, stamen, anther, stigma, style, ovary, petal, sepal, carpel, root tip, root cap, root hair, leaf hair, seed hair, pollen grain, microspore, cotyledon, hypocotyl, epicotyl, xylem, phloem, parenchyma, endosperm, a companion cell, a guard cell, and any other known organs, tissues, and cells

of a plant, and tissues and organs, wherein each of the aforementioned comprise the gene/nucleic acid of interest. The term "plant" also encompasses plant cells, suspension cultures, callus tissue, embryos, meristematic regions, gametophytes, sporophytes, pollen and microspores, again wherein each of the aforementioned comprises the gene/nucleic acid of interest.

Plants that are particularly useful in the methods of the invention include all plants which belong to the superfamily Viridiplantae, in particular monocotyledonous and dicotyledonous plants including fodder or forage legumes, ornamental plants, food crops, trees or shrubs selected from the list comprising Acer spp., Actinidia spp., Abelmoschus spp., Agave sisalana, Agropyron spp., Agrostis stolonifera, Allium spp., Amaranthus spp., Ammophila arenaria, Ananas comosus, Annona spp., Apium graveolens, Arachis spp, Artocarpus spp., Asparagus officinalis, Avena spp. (e.g. Avena sativa, Avena fatua, Avena byzantina, Avena fatua var. sativa, Avena hybrida), Averrhoa carambola, Bambusa sp., Benincasa hispida, Bertholletia excelsea, Beta vulgaris, Brassica spp. (e.g. Brassica napus, Brassica rapa ssp. [canola, oilseed rape, turnip rape]), Cadaba farinosa, Camellia sinensis, Canna indica, Cannabis sativa, Capsicum spp., Carex elata, Carica papaya, Carissa macrocarpa, Carya spp., Carthamus tinctorius, Castanea spp., Ceiba pentandra, Cichorium endivia, Cinnamomum spp., Citrullus lanatus, Citrus spp., Cocos spp., Coffea spp., Colocasia esculenta, Cola spp., Corchorus sp., Coriandrum sativum, Corylus spp., Crataegus spp., Crocus sativus, Cucurbita spp., Cucumis spp., Cynara spp., Daucus carota, Desmodium spp., Dimocarpus longan, Dioscorea spp., Diospyros spp., Echinochloa spp., Elaeis (e.g. Elaeis guineensis, Elaeis oleifera), Eleusine coracana, Eragrostis tef, Erianthus sp., Eriobotrya japonica, Eucalyptus sp., Eugenia uniflora, Fagopyrum spp., Fagus spp., Festuca arundinacea, Ficus carica, Fortunella spp., Fragaria spp., Ginkgo biloba, Glycine spp. (e.g. Glycine max, Soja hispida or Soja max), Gossypium hirsutum, Helianthus spp. (e.g. Helianthus annuus), Hemerocallis fulva, Hibiscus spp., Hordeum spp. (e.g. Hordeum vulgare), Ipomoea batatas, Juglans spp., Lactuca sativa, Lathyrus spp., Lens culinaris, Linum usitatissimum, Litchi chinensis, Lotus spp., Luffa acutangula, Lupinus spp., Luzula sylvatica, Lycopersicon spp. (e.g. Lycopersicon esculentum, Lycopersicon lycopersicum, Lycopersicon pyriforme), Macrotyloma spp., Malus spp., Malpighia emarginata, Mammea americana, Mangifera indica, Manihot spp., Manilkara zapota, Medicago sativa, Melilotus spp., Mentha spp., Miscanthus sinensis, Momordica spp., Morus nigra, Musa spp., Nicotiana spp., Olea spp., Opuntia spp., Ornithopus spp., Oryza spp. (e.g. Oryza sativa, Oryza latifolia), Panicum miliaceum, Panicum virgatum, Passiflora edulis, Pastinaca sativa, Pennisetum sp., Persea spp., Petroselinum crispum, Phalaris arundinacea, Phaseolus spp., Phleum pratense, Phoenix spp., Phragmites australis, Physalis spp., Pinus spp., Pistacia vera, Pisum spp., Poa spp., Populus spp., Prosopis spp., Prunus spp., Psidium spp., Punica granatum, Pyrus communis, Quercus spp., Raphanus sativus, Rheum rhabarbarum, Ribes spp., Ricinus communis, Rubus spp., Saccharum spp., Salix sp., Sambucus spp., Secale cereale, Sesamum spp., Sinapis sp., Solanum spp. (e.g. Solanum tuberosum, Solanum integrifolium or Solanum lycopersicum), Sorghum bicolor, Spinacia spp.,

- Syzygium spp., Tagetes spp., Tamarindus indica, Theobroma cacao, Trifolium spp.,
 Tripsacum dactyloides, Triticosecale rimpai, Triticum spp. (e.g. Triticum aestivum, Triticum
 durum, Triticum turgidum, Triticum hybernum, Triticum macha, Triticum sativum, Triticum
 monococcum or Triticum vulgare), Tropaeolum minus, Tropaeolum majus, Vaccinium spp.,
 5 Vicia spp., Vigna spp., Viola odorata, Vitis spp., Zea mays, Zizania palustris, Ziziphus spp.,
 amaranth, artichoke, asparagus, broccoli, Brussels sprouts, cabbage, canola, carrot,
 cauliflower, celery, collard greens, flax, kale, lentil, oilseed rape, okra, onion, potato, rice,
 soybean, strawberry, sugar beet, sugar cane, sunflower, tomato, squash, tea and algae,
 amongst others. According to a preferred embodiment of the present invention, the plant is
 10 a crop plant. Examples of crop plants include inter alia soybean, sunflower, canola, alfalfa,
 rapeseed, cotton, tomato, potato or tobacco. Further preferably, the plant is a
 monocotyledonous plant, such as sugarcane. Further preferably, the plant is a cereal, such
 as rice, maize, wheat, barley, millet, rye, sorghum or oats.
- 15 In a preferred embodiment, the plant has been previously produced by a process
 comprising recombinantly preparing a plant by introducing and over-expressing a wild-type
 or mutated PPO transgene according to the present invention, as described in greater detail
 hereinafter.
- 20 In another preferred embodiment, the plant has been previously produced by a process
 comprising in situ mutagenizing plant cells, to obtain plant cells which express a mutated
 PPO.
- As disclosed herein, the nucleic acids of the invention find use in enhancing the herbicide
 25 tolerance of plants that comprise in their genomes a gene encoding a herbicide-tolerant
 wild-type or mutated PPO protein. Such a gene may be an endogenous gene or a
 transgene, as described hereinafter.
- Therefore, in another embodiment the present invention refers to a method of increasing or
 30 enhancing the phenylpyridine herbicide tolerance or resistance of a plant, the method
 comprising overexpressing a nucleic acid encoding a PPO polypeptide which comprises
 one or more of the following motifs 1, 2, and/or 3:
- a. Motif 1: SQ[N/K/H]KRYI, wherein the Arg at position 5 within said motif is substituted by
 any other amino acid;
 - 35 b. Motif 2: TLGTLFSS, wherein the Leu at position 2 within said motif is substituted by
 any other amino acid;
 - c. Motif 3: [F/Y]TTF[V/I]GG, wherein the Phe at position 4 within said motif is substituted
 by any other amino acid.
- 40 In another embodiment the present invention refers to a method of increasing or enhancing
 the phenylpyridine herbicide tolerance or resistance of a plant, the method comprising
 overexpressing a nucleic acid encoding a herbicide resistant or tolerant PPO polypeptide

which comprises a variant of the amino acid sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, which variant comprises one or more of the following substitutions:

- a. the amino acid corresponding to Arg128 of SEQ ID NO: 1 is substituted by any other amino acid.
- b. the amino acid corresponding to Leu397 of SEQ ID NO: 1 is substituted by any other amino acid.
- c. the amino acid corresponding to Phe420 of SEQ ID NO: 1 is substituted by any other amino acid.

In another embodiment the present invention refers to a method of increasing or enhancing the phenylpyridine herbicide tolerance or resistance of a plant, the method comprising overexpressing a nucleic acid encoding a herbicide resistant or tolerant PPO polypeptide which comprises the amino acid sequence of SEQ ID NO: 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, or a variant thereof.

In another embodiment the present invention refers to a method of increasing or enhancing the phenylpyridine herbicide tolerance or resistance of a plant, the method comprising overexpressing a nucleic acid encoding a herbicide resistant or tolerant PPO polypeptide which comprises the amino acid sequence of SEQ ID NO: 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, or 262.

Additionally, in certain embodiments, the nucleic acids of the present invention can be stacked with any combination of polynucleotide sequences of interest in order to create plants with a desired phenotype. For example, the nucleic acids of the present invention
 5 may be stacked with any other polynucleotides encoding polypeptides having pesticidal and/or insecticidal activity, such as, for example, the *Bacillus thuringiensis* toxin proteins (described in U.S. Patent Nos. 5,366,892; 5,747,450; 5,737,514; 5,723,756; 5,593,881; and Geiser et al (1986) Gene 48: 109),

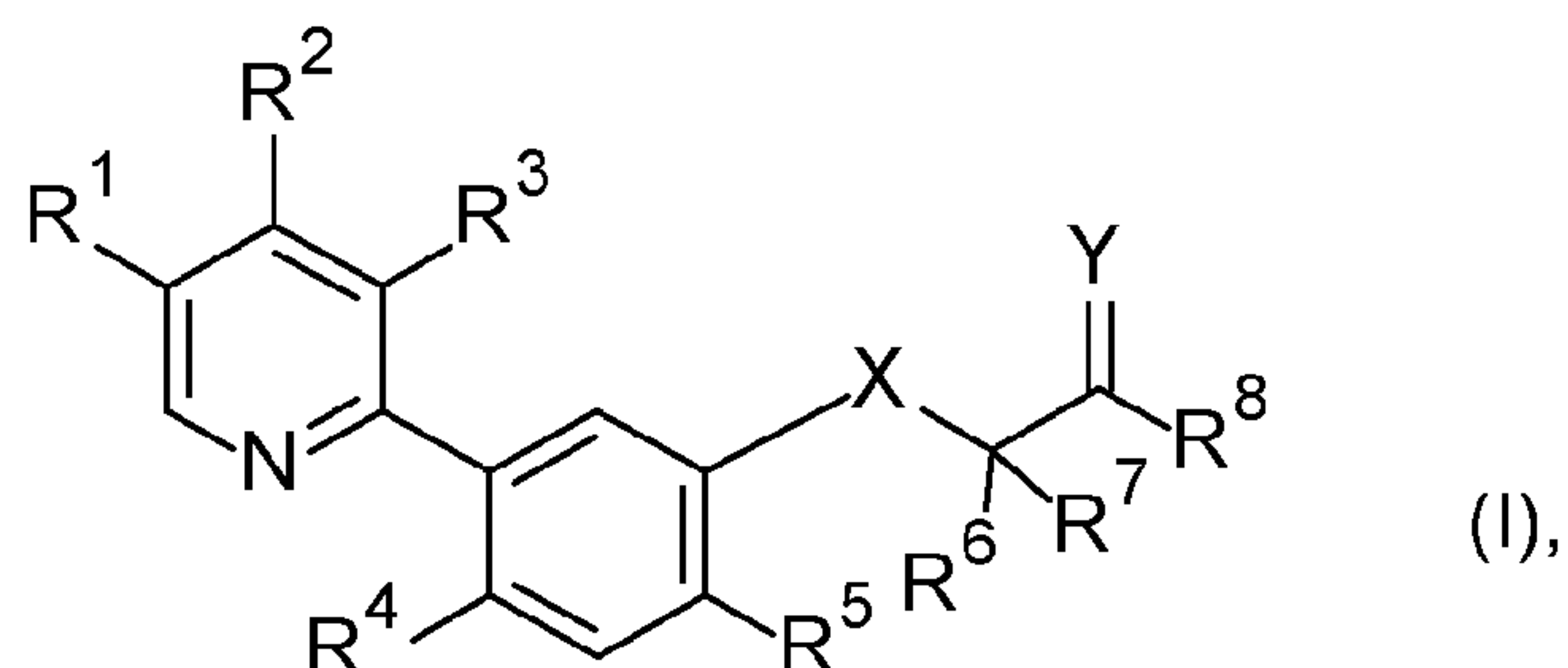
10 By way of example, polynucleotides that may be stacked with the nucleic acids of the present invention include nucleic acids encoding polypeptides conferring resistance to pests/pathogens such as viruses, nematodes, insects or fungi, and the like. Exemplary polynucleotides that may be stacked with nucleic acids of the invention include polynucleotides encoding: polypeptides having pesticidal and/or insecticidal activity, such
 15 as other *Bacillus thuringiensis* toxic proteins (described in U.S. Pat. Nos. 5,366,892; 5,747,450; 5,737,514; 5,723,756; 5,593,881; and Geiser et al., (1986) Gene 48:109), lectins (Van Damme et al. (1994) Plant Mol. Biol. 24:825, pentin (described in U.S. Pat. No. 5,981,722), and the like; traits desirable for disease or herbicide resistance (e.g., fumonisin detoxification genes (U.S. Pat. No. 5,792,931); avirulence and disease resistance genes
 20 (Jones et al. (1994) Science 266:789; Martin et al., (1993) Science 262:1432; Mindrinos et al. (1994) Cell 78:1089); acetolactate synthase (ALS) mutants that lead to herbicide resistance such as the S4 and/or Hra mutations; glyphosate resistance (e.g., 5-enol-pyrovyl-shikimate-3-phosphate-synthase (EPSPS) gene, described in U.S. Pat. Nos. 4,940,935 and 5,188,642; or the glyphosate N-acetyltransferase (GAT) gene, described in
 25 Castle et al. (2004) Science, 304:1151-1154; and in U.S. Patent App. Pub. Nos. 20070004912, 20050246798, and 20050060767)); glufosinate resistance (e.g., phosphinothricin acetyl transferase genes PAT and BAR, described in U.S. Pat. Nos. 5,561,236 and 5,276,268); resistance to herbicides including sulfonyl urea, DHT (2,4D), and PPO herbicides (e.g., glyphosate acetyl transferase, aryloxy alkanoate dioxygenase,
 30 acetolactate synthase, and protoporphyrinogen oxidase); a cytochrome P450 or variant thereof that confers herbicide resistance or tolerance to, inter alia, HPPD herbicides (U.S. patent application Ser. No. 12/156,247; U.S. Pat. Nos. 6,380,465; 6,121,512; 5,349,127; 6,649,814; and 6,300,544; and PCT Patent App. Pub. No. WO2007000077); and traits desirable for processing or process products such as high oil (e.g., U.S. Pat. No.
 35 6,232,529); modified oils (e.g., fatty acid desaturase genes (U.S. Pat. No. 5,952,544; WO 94/11516)); modified starches (e.g., ADPG pyrophosphorylases (AGPase), starch synthases (SS), starch branching enzymes (SBE), and starch debranching enzymes (SDBE)); and polymers or bioplastics (e.g., U.S. Pat. No. 5,602,321; beta-ketothiolase, polyhydroxybutyrate synthase, and acetoacetyl-CoA reductase (Schubert et al. (1988) J.
 40 Bacteriol. 170:5837-5847) facilitate expression of polyhydroxyalkanoates (PHAs)); the disclosures of which are herein incorporated by reference.

In a preferred embodiment, the plant comprises at least one additional heterologous nucleic acid comprising a nucleotide sequence encoding a herbicide tolerance enzyme selected, for example, from the group consisting of 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS), Glyphosate acetyl transferase (GAT), cytochrome P450 monooxygenase, 5 phosphinothricin acetyltransferase (PAT), Acetohydroxyacid synthase (AHAS; EC 4.1.3.18, also known as acetolactate synthase or ALS), hydroxyphenyl pyruvate dioxygenase (HPPD), Phytoene desaturase (PD) and dicamba degrading enzymes as disclosed in WO 02/068607, or phenoxyaceticacid- and phenoxypropionicacid-derivative degrading enzymes as disclosed in WO 2008141154 or WO 2005107437. The combinations generated can 10 also include multiple copies of any one of the polynucleotides of interest.

Generally, the term "herbicide" is used herein to mean an active ingredient that kills, controls or otherwise adversely modifies the growth of plants. The preferred amount or concentration of the herbicide is an "effective amount" or "effective concentration." By 15 "effective amount" and "effective concentration" is intended an amount and concentration, respectively, that is sufficient to kill or inhibit the growth of a similar, wild-type, plant, plant tissue, plant cell, or host cell, but that said amount does not kill or inhibit as severely the growth of the herbicide-resistant plants, plant tissues, plant cells, and host cells of the present invention. Typically, the effective amount of a herbicide is an amount that is 20 routinely used in agricultural production systems to kill weeds of interest. Such an amount is known to those of ordinary skill in the art. Herbicidal activity is exhibited by herbicides useful for the the present invention when they are applied directly to the plant or to the locus of the plant at any stage of growth or before planting or emergence. The effect observed depends upon the plant species to be controlled, the stage of growth of the plant, the application 25 parameters of dilution and spray drop size, the particle size of solid components, the environmental conditions at the time of use, the specific compound employed, the specific adjuvants and carriers employed, the soil type, and the like, as well as the amount of chemical applied. These and other factors can be adjusted as is known in the art to promote non-selective or selective herbicidal action. Generally, it is preferred to apply the herbicide 30 postemergence to relatively immature undesirable vegetation to achieve the maximum control of weeds.

By a "herbicide-tolerant" or "herbicide-resistant" plant, it is intended that a plant that is tolerant or resistant to at least one herbicide at a level that would normally kill, or inhibit the 35 growth of, a normal or wild-type plant. By "herbicide-tolerant wildtype or mutated PPO protein" or "herbicide -resistant wildtype or mutated PPO protein", it is intended that such a PPO protein displays higher PPO activity, relative to the PPO activity of a wild-type PPO protein, when in the presence of at least one herbicide that is known to interfere with PPO activity and at a concentration or level of the herbicide that is known to inhibit the PPO 40 activity of the wild-type mutated PPO protein. Furthermore, the PPO activity of such a herbicide-tolerant or herbicide-resistant mutated PPO protein may be referred to herein as "herbicide-tolerant" or "herbicide-resistant" PPO activity.

In a particularly preferred embodiment, the herbicides useful for the present invention refer phenylpyridines of formula (I)



5 wherein the variables have the following meanings:

R¹ halogen, C₁-C₄-haloalkyl or SO₂CH₃;

R² H, CH₃ or NH₂;

R³ halogen;

10 R⁴ H or halogen;

R⁵ halogen or CN;

R⁶ H or CH₃;

R⁷ C₁-C₆-alkoxy, C₁-C₆-haloalkoxy, C₃-C₆-alkenyloxy, C₃-C₆-alkynyloxy, C₁-C₆-alkylthio, C₁-C₆-haloalkylthio, C₃-C₆-alkenylthio or C₃-C₆-alkynylthio;

15 preferably C₁-C₆-alkoxy, C₁-C₆-haloalkoxy, C₃-C₆-alkenyloxy, C₃-C₆-alkynyloxy;

R⁸ OR⁹, SR⁹, NR¹⁰R¹¹, NR⁹S(O)R¹⁰, NR⁹S(O)₂R¹⁰, NR⁹S(O)NR¹⁰R¹¹, or NR⁹S(O)₂NR¹⁰R¹¹,

wherein

20 R⁹ is hydrogen, C₁-C₆-alkyl, C₃-C₆-alkenyl, C₃-C₆-alkynyl, C₁-C₆-haloalkyl, C₃-C₆-haloalkenyl, C₃-C₆-haloalkynyl, C₁-C₆-cyanoalkyl, C₁-C₆-alkoxy-C₁-C₆-alkyl, C₁-C₆-alkoxy-C₁-C₆-alkoxy-C₁-C₆-alkyl, di(C₁-C₆-alkoxy)C₁-C₆-alkyl, C₁-C₆-haloalkoxy-C₁-C₆-alkyl, C₃-C₆-alkenyloxy-C₁-C₆-alkyl, C₃-C₆-haloalkenyloxy-C₁-C₆-alkyl, C₃-C₆-alkenyloxy-C₁-C₆-alkoxy-C₁-C₆-alkyl, C₁-C₆-alkylthio-C₁-C₆-alkyl, C₁-C₆-alkylsulfinyl-C₁-C₆-alkyl, C₁-C₆-alkylsulfonyl-C₁-C₆-alkyl, C₁-C₆-alkylcarbonyl-C₁-C₆-alkyl, C₁-C₆-alkoxycarbonyl-C₁-C₆-alkyl, C₁-C₆-haloalkoxycarbonyl-C₁-C₆-alkyl, C₃-C₆-alkenyloxycarbonyl-C₁-C₆-alkyl, amino, (C₁-C₆-alkyl)amino, di(C₁-C₆-alkyl)amino, (C₁-C₆-alkylcarbonyl)amino, amino-C₁-C₆-alkyl, (C₁-C₆-alkyl)amino-C₁-C₆-alkyl, di(C₁-C₆-alkyl)amino-C₁-C₆-alkyl, aminocarbonyl-C₁-C₆-alkyl, (C₁-C₆-alkyl)aminocarbonyl-C₁-C₆-alkyl, di(C₁-C₆-alkyl)aminocarbonyl-C₁-C₆-alkyl, -N=CR¹²R¹³, wherein R¹² and R¹³ independently of one another are H, C₁-C₄-alkyl or phenyl;

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C₃-C₆-cycloalkyl, C₃-C₆-cycloalkyl-C₁-C₆-alkyl, C₃-C₆-heterocyclyl, C₃-C₆-heterocyclyl-C₁-C₆-alkyl, phenyl, phenyl-C₁-C₄-alkyl or a 5- or 6 membered heteroaryl,

wherein each cycloalkyl, heterocyclyl, phenyl or heteroaryl ring can be substituted by one to four substituents selected from R^{14} or a 3- to 7-membered carbocyclus,

which carbocyclus optionally has in addition to carbon atoms one or two ring members selected from the group consisting of $-N(R^{12})-$, $-N=N-$, $-C(=O)-$, $-O-$ and $-S-$, and

which carbocyclus is optionally substituted with one to four substituents selected from R^{14} ;

wherein R^{14} is halogen, NO_2 , CN , C_1-C_4 -alkyl, C_1-C_4 -haloalkyl, C_1-C_4 -alkoxy or C_1-C_4 -alkoxycarbonyl;

R^{10} , R^{11} independently of one another are R^9 , or together form a 3- to 7-membered carbocyclus,

which carbocyclus optionally has in addition to carbon atoms one or two ring members selected from the group consisting of $-N(R^{12})-$, $-N=N-$, $-C(=O)-$, $-O-$ and $-S-$, and

which carbocyclus is optionally substituted with one to four substituents selected from R^{14} ;

X O or S; and

Y O or S;

including their agriculturally acceptable salts.

If the phenylpyridines of formula (I), the herbicidal compounds B and/or the safeners C as described herein are capable of forming geometrical isomers, for example E/Z isomers, it is possible to use both, the pure isomers and mixtures thereof, in the compositions according to the invention.

If the phenylpyridines of formula (I), the herbicidal compounds B and/or the safeners C as described herein have one or more centres of chirality and, as a consequence, are present as enantiomers or diastereomers, it is possible to use both, the pure enantiomers and diastereomers and their mixtures, in the compositions according to the invention.

If the phenylpyridines of formula (I), the herbicidal compounds B and/or the safeners C as described herein have ionizable functional groups, they can also be employed in the form of their agriculturally acceptable salts. Suitable are, in general, the salts of those cations and the acid addition salts of those acids whose cations and anions, respectively, have no adverse effect on the activity of the active compounds.

Preferred cations are the ions of the alkali metals, preferably of lithium, sodium and potassium, of the alkaline earth metals, preferably of calcium and magnesium, and of the transition metals, preferably of manganese, copper, zinc and iron, further ammonium and substituted ammonium in which one to four hydrogen atoms are replaced by C_1-C_4 -alkyl,

hydroxy-C₁-C₄-alkyl, C₁-C₄-alkoxy-C₁-C₄-alkyl, hydroxy-C₁-C₄-alkoxy-C₁-C₄-alkyl, phenyl or benzyl, preferably ammonium, methylammonium, isopropylammonium, dimethylammonium, diisopropylammonium, trimethylammonium, heptylammonium, dodecylammonium, tetradecylammonium, tetramethylammonium, tetraethylammonium, tetrabutylammonium, 2-hydroxyethylammonium (olamine salt), 2-(2-hydroxyeth-1-oxy)eth-1-ylammonium (diglycolamine salt), di(2-hydroxyeth-1-yl)ammonium (diolamine salt), tris(2-hydroxyethyl)ammonium (trolamine salt), tris(2-hydroxypropyl)ammonium, benzyltrimethylammonium, benzyltriethylammonium, N,N,N-trimethylethanolammonium (choline salt), furthermore phosphonium ions, sulfonium ions, preferably tri(C₁-C₄-alkyl)sulfonium, such as trimethylsulfonium, and sulfoxonium ions, preferably tri(C₁-C₄-alkyl)sulfoxonium, and finally the salts of polybasic amines such as N,N-bis-(3-aminopropyl)methylamine and diethylenetriamine.

Anions of useful acid addition salts are primarily chloride, bromide, fluoride, iodide, hydrogensulfate, methylsulfate, sulfate, dihydrogenphosphate, hydrogenphosphate, nitrate, bicarbonate, carbonate, hexafluorosilicate, hexafluorophosphate, benzoate and also the anions of C₁-C₄-alkanoic acids, preferably formate, acetate, propionate and butyrate.

Herbicidal compounds B and/or safeners C as described herein having a carboxyl group can be employed in the form of the acid, in the form of an agriculturally suitable salt as mentioned above or else in the form of an agriculturally acceptable derivative, for example as amides, such as mono- and di-C₁-C₆-alkylamides or arylamides, as esters, for example as allyl esters, propargyl esters, C₁-C₁₀-alkyl esters, alkoxyalkyl esters, tefuryl ((tetrahydrofuran-2-yl)methyl) esters and also as thioesters, for example as C₁-C₁₀-alkylthio esters. Preferred mono- and di-C₁-C₆-alkylamides are the methyl and the dimethylamides. Preferred arylamides are, for example, the anilides and the 2-chloroanilides. Preferred alkyl esters are, for example, the methyl, ethyl, propyl, isopropyl, butyl, isobutyl, pentyl, mexyl (1-methylhexyl), meptyl (1-methylheptyl), heptyl, octyl or isooctyl (2-ethylhexyl) esters. Preferred C₁-C₄-alkoxy-C₁-C₄-alkyl esters are the straight-chain or branched C₁-C₄-alkoxy ethyl esters, for example the 2-methoxyethyl, 2-ethoxyethyl, 2-butoxyethyl (butotyl), 2-butoxypropyl or 3-butoxypropyl ester. An example of a straight-chain or branched C₁-C₁₀-alkylthio ester is the ethylthio ester.

The organic moieties mentioned in the definition of the variables R¹ to R¹⁴, are - like the term halogen - collective terms for individual enumerations of the individual group members. The term halogen denotes in each case fluorine, chlorine, bromine or iodine. All hydrocarbon chains, e.g. all alkyl, alkenyl, alkynyl, alkoxy chains, can be straight-chain or branched, the prefix C_n-C_m denoting in each case the possible number of carbon atoms in the group.

Examples of such meanings are:

- C₁-C₄-alkyl and also the C₁-C₄-alkyl moieties of phenyl-C₁-C₄-alkyl: for example CH₃, C₂H₅, n-propyl, CH(CH₃)₂, n-butyl, CH(CH₃)-C₂H₅, CH₂-CH(CH₃)₂ and C(CH₃)₃;
- C₁-C₆-alkyl and also the C₁-C₆-alkyl moieties of C₁-C₆-alkoxy-C₁-C₆-alkyl, C₁-C₆-alkoxy-C₁-C₆-alkoxy-C₁-C₆-alkyl, di(C₁-C₆-alkoxy)C₁-C₆-alkyl, C₁-C₆-haloalkoxy-C₁-C₆-alkyl, C₃-C₆-alkenyloxy-C₁-C₆-alkyl, C₃-C₆-haloalkenyloxy-C₁-C₆-alkyl, C₃-C₆-alkenyloxy-C₁-C₆-alkoxy-C₁-C₆-alkyl, C₁-C₆-alkylthio-C₁-C₆-alkyl, C₁-C₆-alkylsulfinyl-C₁-C₆-alkyl, C₁-C₆-alkylsulfonyl-C₁-C₆-alkyl, C₁-C₆-alkylcarbonyl-C₁-C₆-alkyl, C₁-C₆-alkoxycarbonyl-C₁-C₆-alkyl, C₁-C₆-haloalkoxycarbonyl-C₁-C₆-alkyl, C₃-C₆-alkenyloxycarbonyl-C₁-C₆-alkyl, (C₁-C₆-alkylcarbonyl)amino, amino-C₁-C₆-alkyl, (C₁-C₆-alkyl)amino-C₁-C₆-alkyl, di(C₁-C₆-alkyl)amino-C₁-C₆-alkyl, aminocarbonyl-C₁-C₆-alkyl, (C₁-C₆-alkyl)aminocarbonyl-C₁-C₆-alkyl, di(C₁-C₆-alkyl)aminocarbonyl-C₁-C₆-alkyl, C₃-C₆-cycloalkyl-C₁-C₆-alkyl: C₁-C₄-alkyl as mentioned above, and also, for example, n-pentyl, 1-methylbutyl, 2-methylbutyl, 3-methylbutyl, 2,2-dimethylpropyl, 1-ethylpropyl, n-hexyl, 1,1-dimethylpropyl, 1,2-dimethylpropyl, 1-methylpentyl, 2-methylpentyl, 3-methylpentyl, 4-methylpentyl, 1,1-dimethylbutyl, 1,2-dimethylbutyl, 1,3-dimethylbutyl, 2,2-dimethylbutyl, 2,3-dimethylbutyl, 3,3-dimethylbutyl, 1-ethylbutyl, 2-ethylbutyl, 1,1,2-trimethylpropyl, 1,2,2-trimethylpropyl, 1-ethyl-1-methylpropyl or 1-ethyl-2-methylpropyl, preferably methyl, ethyl, n-propyl, 1-methylethyl, n-butyl, 1,1-dimethylethyl, n-pentyl or n-hexyl;
- C₁-C₄-haloalkyl: C₁-C₄-alkyl as mentioned above which is partially or fully substituted by fluorine, chlorine, bromine and/or iodine, for example, chloromethyl, dichloromethyl, trichloromethyl, fluoromethyl, difluoromethyl, trifluoromethyl, chlorofluoromethyl, dichlorofluoromethyl, chlorodifluoromethyl, bromomethyl, iodomethyl, 2-fluoroethyl, 2-chloroethyl, 2-bromoethyl, 2-iodoethyl, 2,2-difluoroethyl, 2,2,2-trifluoroethyl, 2-chloro-2-fluoroethyl, 2-chloro-2,2-difluoroethyl, 2,2-dichloro-2-fluoroethyl, 2,2,2-trichloroethyl, pentafluoroethyl, 2-fluoropropyl, 3-fluoropropyl, 2,2-difluoropropyl, 2,3-difluoropropyl, 2-chloropropyl, 3-chloropropyl, 2,3-dichloropropyl, 2-bromopropyl, 3-bromopropyl, 3,3,3-trifluoropropyl, 3,3,3-trichloropropyl, 2,2,3,3,3-pentafluoropropyl, heptafluoropropyl, 1-(fluoromethyl)-2-fluoroethyl, 1-(chloromethyl)-2-chloroethyl, 1-(bromomethyl)-2-bromoethyl, 4-fluorobutyl, 4-chlorobutyl, 4-bromobutyl, nonafluorobutyl, 1,1,2,2,-tetrafluoroethyl and 1-trifluoromethyl-1,2,2,2-tetrafluoroethyl;
- C₁-C₆-haloalkyl and also the C₁-C₆-haloalkyl moieties of C₁-C₆-haloalkylthio: C₁-C₄-haloalkyl as mentioned above, and also, for example, 5-fluoropentyl, 5-chloropentyl, 5-bromopentyl, 5-iodopentyl, undecafluoropentyl, 6-fluorohexyl, 6-chlorohexyl, 6-bromohexyl, 6-iodohexyl and dodecafluorohexyl;
- C₃-C₆-alkenyl and also the C₃-C₆-alkenyl moieties of C₃-C₆-alkenyloxy, C₃-C₆-alkenylthio, C₃-C₆-alkenyloxy-C₁-C₆-alkyl, C₃-C₆-alkenyloxy-C₁-C₆-alkoxy-C₁-C₆-alkyl, C₃-C₆-alkenyloxycarbonyl-C₁-C₆-alkyl: for example 1-propenyl, 2-propenyl, 1-methylethenyl, 1-butenyl, 2-butenyl, 3-butenyl, 1-methyl-1-propenyl, 2-methyl-1-propenyl, 1-methyl-2-propenyl, 2-methyl-2-propenyl, 1-pentenyl, 2-pentenyl, 3-pentenyl, 4-pentenyl, 1-methyl-1-butenyl, 2-methyl-1-butenyl, 3-methyl-1-butenyl, 1-methyl-2-butenyl, 2-methyl-2-butenyl, 3-methyl-2-butenyl, 1-methyl-3-butenyl, 2-methyl-3-butenyl, 3-methyl-3-butenyl, 1,1-dimethyl-2-propenyl, 1,2-dimethyl-1-propenyl, 1,2-dimethyl-2-propenyl, 1-ethyl-1-propenyl, 1-ethyl-2-

- propenyl, 1-hexenyl, 2-hexenyl, 3-hexenyl, 4-hexenyl, 5-hexenyl, 1-methyl-1-pentenyl, 2-methyl-1-pentenyl, 3-methyl-1-pentenyl, 4-methyl-1-pentenyl, 1-methyl-2-pentenyl, 2-methyl-2-pentenyl, 3-methyl-2-pentenyl, 4-methyl-2-pentenyl, 1-methyl-3-pentenyl, 2-methyl-3-pentenyl, 3-methyl-3-pentenyl, 4-methyl-3-pentenyl, 1-methyl-4-pentenyl, 2-methyl-4-pentenyl, 3-methyl-4-pentenyl, 4-methyl-4-pentenyl, 1,1-dimethyl-2-butenyl, 1,1-dimethyl-3-butenyl, 1,2-dimethyl-1-butenyl, 1,2-dimethyl-2-butenyl, 1,2-dimethyl-3-butenyl, 1,3-dimethyl-1-butenyl, 1,3-dimethyl-2-butenyl, 1,3-dimethyl-3-butenyl, 2,2-dimethyl-3-butenyl, 2,3-dimethyl-1-butenyl, 2,3-dimethyl-2-butenyl, 2,3-dimethyl-3-butenyl, 3,3-dimethyl-1-butenyl, 3,3-dimethyl-2-butenyl, 1-ethyl-1-butenyl, 1-ethyl-2-butenyl, 1-ethyl-3-butenyl, 2-ethyl-1-butenyl, 2-ethyl-2-butenyl, 2-ethyl-3-butenyl, 1,1,2-trimethyl-2-propenyl, 1-ethyl-1-methyl-2-propenyl, 1-ethyl-2-methyl-1-propenyl and 1-ethyl-2-methyl-2-propenyl;
- C₃-C₆-haloalkenyl and also the C₃-C₆-haloalkenyl moieties of C₃-C₆-haloalkenyloxy-C₁-C₆-alkyl: a C₃-C₆-alkenyl radical as mentioned above which is partially or fully substituted by fluorine, chlorine, bromine and/or iodine, for example 2-chloroprop-2-en-1-yl, 3-chloroprop-2-en-1-yl, 2,3-dichloroprop-2-en-1-yl, 3,3-dichloroprop-2-en-1-yl, 2,3,3-trichloro-2-en-1-yl, 2,3-dichlorobut-2-en-1-yl, 2-bromoprop-2-en-1-yl, 3-bromoprop-2-en-1-yl, 2,3-dibromoprop-2-en-1-yl, 3,3-dibromoprop-2-en-1-yl, 2,3,3-tribromo-2-en-1-yl or 2,3-dibromobut-2-en-1-yl;
 - C₃-C₆-alkynyl and also the C₃-C₆-alkynyl moieties of C₃-C₆-alkynyloxy, C₃-C₆-alkynylthio: for example 1-propynyl, 2-propynyl, 1-butylnyl, 2-butylnyl, 3-butylnyl, 1-methyl-2-propynyl, 1-pentylnyl, 2-pentylnyl, 3-pentylnyl, 4-pentylnyl, 1-methyl-2-butylnyl, 1-methyl-3-butylnyl, 2-methyl-3-butylnyl, 3-methyl-1-butylnyl, 1,1-dimethyl-2-propynyl, 1-ethyl-2-propynyl, 1-hexynyl, 2-hexynyl, 3-hexynyl, 4-hexynyl, 5-hexynyl, 1-methyl-2-pentylnyl, 1-methyl-3-pentylnyl, 1-methyl-4-pentylnyl, 2-methyl-3-pentylnyl, 2-methyl-4-pentylnyl, 3-methyl-1-pentylnyl, 3-methyl-4-pentylnyl, 4-methyl-1-pentylnyl, 4-methyl-2-pentylnyl, 1,1-dimethyl-2-butylnyl, 1,1-dimethyl-3-butylnyl, 1,2-dimethyl-3-butylnyl, 2,2-dimethyl-3-butylnyl, 3,3-dimethyl-1-butylnyl, 1-ethyl-2-butylnyl, 1-ethyl-3-butylnyl, 2-ethyl-3-butylnyl and 1-ethyl-1-methyl-2-propynyl;
 - C₃-C₆-haloalkynyl: a C₃-C₆-alkynyl radical as mentioned above which is partially or fully substituted by fluorine, chlorine, bromine and/or iodine, for example 1,1-difluoroprop-2-yn-1-yl, 3-chloroprop-2-yn-1-yl, 3-bromoprop-2-yn-1-yl, 3-iodoprop-2-yn-1-yl, 4-fluorobut-2-yn-1-yl, 4-chlorobut-2-yn-1-yl, 1,1-difluorobut-2-yn-1-yl, 4-iodobut-3-yn-1-yl, 5-fluoropent-3-yn-1-yl, 5-iodopent-4-yn-1-yl, 6-fluorohex-4-yn-1-yl or 6-iodohex-5-yn-1-yl;
 - C₁-C₄-alkoxy and also the C₁-C₄-alkoxy moieties of C₁-C₆-alkoxycarbonyl: for example methoxy, ethoxy, propoxy, 1-methylethoxy butoxy, 1-methylpropoxy, 2-methylpropoxy and 1,1-dimethylethoxy;
 - C₁-C₆-alkoxy and also the C₁-C₆-alkoxy moieties of C₁-C₆-alkoxy-C₁-C₆-alkyl, C₁-C₆-alkoxy-C₁-C₆-alkoxy-C₁-C₆-alkyl, di(C₁-C₆-alkoxy)C₁-C₆-alkyl, C₃-C₆-alkenyloxy-C₁-C₆-alkoxy-C₁-C₆-alkyl, C₁-C₆-alkoxycarbonyl-C₁-C₆-alkyl: C₁-C₄-alkoxy as mentioned above, and also, for example, pentoxy, 1-methylbutoxy, 2-methylbutoxy, 3-methoxylbutoxy, 1,1-dimethylpropoxy, 1,2-dimethylpropoxy, 2,2-dimethylpropoxy, 1-ethylpropoxy, hexoxy, 1-

methylpentoxy, 2-methylpentoxy, 3-methylpentoxy, 4-methylpentoxy, 1,1-dimethylbutoxy, 1,2-dimethylbutoxy, 1,3-dimethylbutoxy, 2,2-dimethylbutoxy, 2,3-dimethylbutoxy, 3,3-dimethylbutoxy, 1-ethylbutoxy, 2-ethylbutoxy, 1,1,2-trimethylpropoxy, 1,2,2-trimethylpropoxy, 1-ethyl-1-methylpropoxy and 1-ethyl-2-methylpropoxy.

- 5 - C₁-C₄-haloalkoxy: a C₁-C₄-alkoxy radical as mentioned above which is partially or fully substituted by fluorine, chlorine, bromine and/or iodine, i.e., for example, fluoromethoxy, difluoromethoxy, trifluoromethoxy, chlorodifluoromethoxy, bromodifluoromethoxy, 2-fluoroethoxy, 2-chloroethoxy, 2-bromomethoxy, 2-iodoethoxy, 2,2-difluoroethoxy, 2,2,2-trifluoroethoxy, 2-chloro-2-fluoroethoxy, 2-chloro-2,2-difluoroethoxy, 2,2-dichloro-2-fluoroethoxy, 2,2,2-trichloroethoxy, pentafluoroethoxy, 2-fluoropropoxy, 3-fluoropropoxy, 2-chloropropoxy, 3-chloropropoxy, 2-bromopropoxy, 3-bromopropoxy, 2,2-difluoropropoxy, 2,3-difluoropropoxy, 2,3-dichloropropoxy, 3,3,3-trifluoropropoxy, 3,3,3-trichloropropoxy, 2,2,3,3,3-pentafluoropropoxy, heptafluoropropoxy, 1-(fluoromethyl)-2-fluoroethoxy, 1-(chloromethyl)-2-chloroethoxy, 1-(bromomethyl)-2-bromoethoxy, 4-fluorobutoxy, 4-chlorobutoxy, 4-bromobutoxy and nonafluorobutoxy;
- 10 - C₁-C₆-haloalkoxy and also the C₁-C₆-haloalkoxy moieties of C₁-C₆-haloalkoxy-C₁-C₆-alkyl, C₁-C₆-haloalkoxycarbonyl-C₁-C₆-alkyl : a C₁-C₄-haloalkoxy as mentioned above, and also, for example, 5-fluoropentoxy, 5-chloropentoxy, 5-bromopentoxy, 5-iodopentoxy, undecafluoropentoxy, 6-fluorohexoxy, 6-chlorohexoxy, 6-bromohexoxy, 6-iodohexoxy and dodecafluorohexoxy;
- 15 - C₁-C₄-alkylthio: for example methylthio, ethylthio, propylthio, 1-methylethylthio, butylthio, 1-methylpropylthio, 2-methylpropylthio and 1,1-dimethylethylthio;
- C₁-C₆-alkylthio and also the C₁-C₆-alkylthio moieties of C₁-C₆-alkylthio-C₁-C₆-alkyl: C₁-C₄-alkylthio as mentioned above, and also, for example, pentylthio, 1-methylbutylthio, 2-methylbutylthio, 3-methylbutylthio, 2,2-dimethylpropylthio, 1-ethylpropylthio, hexylthio, 1,1-dimethylpropylthio, 1,2-dimethylpropylthio, 1-methylpentylthio, 2-methylpentylthio, 3-methylpentylthio, 4-methylpentylthio, 1,1-dimethylbutylthio, 1,2-dimethylbutylthio, 1,3-dimethylbutylthio, 2,2-dimethylbutylthio, 2,3-dimethylbutylthio, 3,3-dimethylbutylthio, 1-ethylbutylthio, 2-ethylbutylthio, 1,1,2-trimethylpropylthio, 1,2,2-trimethylpropylthio, 1-ethyl-1-methylpropylthio and 1-ethyl-2-methylpropylthio;
- 20 - C₁-C₆-alkylsulfinyl (C₁-C₆-Alkyl-S(=O)-) and also the C₁-C₆-alkylsulfinyl moieties of C₁-C₆-alkylsulfinyl-C₁-C₆-alkyl, : for example methylsulfinyl, ethylsulfinyl, propylsulfinyl, 1-methylethylsulfinyl, butylsulfinyl, 1-methylpropylsulfinyl, 2-methylpropylsulfinyl, 1,1-dimethylethylsulfinyl, pentylsulfinyl, 1-methylbutylsulfinyl, 2-methylbutylsulfinyl, 3-methylbutylsulfinyl, 2,2-dimethylpropylsulfinyl, 1-ethylpropylsulfinyl, 1,1-dimethylpropylsulfinyl, 1,2-dimethylpropylsulfinyl, hexylsulfinyl, 1-methylpentylsulfinyl, 2-methylpentylsulfinyl, 3-methylpentylsulfinyl, 4-methylpentylsulfinyl, 1,1-dimethylbutylsulfinyl, 1,2-dimethylbutylsulfinyl, 1,3-dimethylbutylsulfinyl, 2,2-dimethylbutylsulfinyl, 2,3-dimethylbutylsulfinyl, 3,3-dimethylbutylsulfinyl, 1-ethylbutylsulfinyl, 2-ethylbutylsulfinyl, 1,1,2-trimethylpropylsulfinyl, 1,2,2-trimethylpropylsulfinyl, 1-ethyl-1-methylpropylsulfinyl and 1-ethyl-2-methylpropylsulfinyl;
- 25 - C₁-C₆-alkylsulfonyl (C₁-C₆-alkyl-S(O)₂-) and also the C₁-C₆-alkylsulfonyl moieties of C₁-C₆-alkylsulfonyl-C₁-C₆-alkyl, : for example methylsulfonyl, ethylsulfonyl, propylsulfonyl, 1-methylethylsulfonyl, butylsulfonyl, 1-methylpropylsulfonyl, 2-methylpropylsulfonyl, 1,1-dimethylethylsulfonyl, pentylsulfonyl, 1-methylbutylsulfonyl, 2-methylbutylsulfonyl, 3-methylbutylsulfonyl, 2,2-dimethylpropylsulfonyl, 1-ethylpropylsulfonyl, 1,1-dimethylpropylsulfonyl, 1,2-dimethylpropylsulfonyl, hexylsulfonyl, 1-methylpentylsulfonyl, 2-methylpentylsulfonyl, 3-methylpentylsulfonyl, 4-methylpentylsulfonyl, 1,1-dimethylbutylsulfonyl, 1,2-dimethylbutylsulfonyl, 1,3-dimethylbutylsulfonyl, 2,2-dimethylbutylsulfonyl, 2,3-dimethylbutylsulfonyl, 3,3-dimethylbutylsulfonyl, 1-ethylbutylsulfonyl, 2-ethylbutylsulfonyl, 1,1,2-trimethylpropylsulfonyl, 1,2,2-trimethylpropylsulfonyl, 1-ethyl-1-methylpropylsulfonyl and 1-ethyl-2-methylpropylsulfonyl;
- 30 - C₁-C₆-alkylsulfonyl (C₁-C₆-alkyl-S(O)₂-) and also the C₁-C₆-alkylsulfonyl moieties of C₁-C₆-alkylsulfonyl-C₁-C₆-alkyl, : for example methylsulfonyl, ethylsulfonyl, propylsulfonyl, 1-methylethylsulfonyl, butylsulfonyl, 1-methylpropylsulfonyl, 2-methylpropylsulfonyl, 1,1-dimethylethylsulfonyl, pentylsulfonyl, 1-methylbutylsulfonyl, 2-methylbutylsulfonyl, 3-methylbutylsulfonyl, 2,2-dimethylpropylsulfonyl, 1-ethylpropylsulfonyl, 1,1-dimethylpropylsulfonyl, 1,2-dimethylpropylsulfonyl, hexylsulfonyl, 1-methylpentylsulfonyl, 2-methylpentylsulfonyl, 3-methylpentylsulfonyl, 4-methylpentylsulfonyl, 1,1-dimethylbutylsulfonyl, 1,2-dimethylbutylsulfonyl, 1,3-dimethylbutylsulfonyl, 2,2-dimethylbutylsulfonyl, 2,3-dimethylbutylsulfonyl, 3,3-dimethylbutylsulfonyl, 1-ethylbutylsulfonyl, 2-ethylbutylsulfonyl, 1,1,2-trimethylpropylsulfonyl, 1,2,2-trimethylpropylsulfonyl, 1-ethyl-1-methylpropylsulfonyl and 1-ethyl-2-methylpropylsulfonyl;
- 35 - C₁-C₆-alkylsulfonyl (C₁-C₆-alkyl-S(O)₂-) and also the C₁-C₆-alkylsulfonyl moieties of C₁-C₆-alkylsulfonyl-C₁-C₆-alkyl, : for example methylsulfonyl, ethylsulfonyl, propylsulfonyl, 1-methylethylsulfonyl, butylsulfonyl, 1-methylpropylsulfonyl, 2-methylpropylsulfonyl, 1,1-dimethylethylsulfonyl, pentylsulfonyl, 1-methylbutylsulfonyl, 2-methylbutylsulfonyl, 3-methylbutylsulfonyl, 2,2-dimethylpropylsulfonyl, 1-ethylpropylsulfonyl, 1,1-dimethylpropylsulfonyl, 1,2-dimethylpropylsulfonyl, hexylsulfonyl, 1-methylpentylsulfonyl, 2-methylpentylsulfonyl, 3-methylpentylsulfonyl, 4-methylpentylsulfonyl, 1,1-dimethylbutylsulfonyl, 1,2-dimethylbutylsulfonyl, 1,3-dimethylbutylsulfonyl, 2,2-dimethylbutylsulfonyl, 2,3-dimethylbutylsulfonyl, 3,3-dimethylbutylsulfonyl, 1-ethylbutylsulfonyl, 2-ethylbutylsulfonyl, 1,1,2-trimethylpropylsulfonyl, 1,2,2-trimethylpropylsulfonyl, 1-ethyl-1-methylpropylsulfonyl and 1-ethyl-2-methylpropylsulfonyl;
- 40 - C₁-C₆-alkylsulfonyl (C₁-C₆-alkyl-S(O)₂-) and also the C₁-C₆-alkylsulfonyl moieties of C₁-C₆-alkylsulfonyl-C₁-C₆-alkyl, : for example methylsulfonyl, ethylsulfonyl, propylsulfonyl, 1-methylethylsulfonyl, butylsulfonyl, 1-methylpropylsulfonyl, 2-methylpropylsulfonyl, 1,1-dimethylethylsulfonyl, pentylsulfonyl, 1-methylbutylsulfonyl, 2-methylbutylsulfonyl, 3-methylbutylsulfonyl, 2,2-dimethylpropylsulfonyl, 1-ethylpropylsulfonyl, 1,1-dimethylpropylsulfonyl, 1,2-dimethylpropylsulfonyl, hexylsulfonyl, 1-methylpentylsulfonyl, 2-methylpentylsulfonyl, 3-methylpentylsulfonyl, 4-methylpentylsulfonyl, 1,1-dimethylbutylsulfonyl, 1,2-dimethylbutylsulfonyl, 1,3-dimethylbutylsulfonyl, 2,2-dimethylbutylsulfonyl, 2,3-dimethylbutylsulfonyl, 3,3-dimethylbutylsulfonyl, 1-ethylbutylsulfonyl, 2-ethylbutylsulfonyl, 1,1,2-trimethylpropylsulfonyl, 1,2,2-trimethylpropylsulfonyl, 1-ethyl-1-methylpropylsulfonyl and 1-ethyl-2-methylpropylsulfonyl;

C₆-alkylsulfonyl-C₁-C₆-alkyl,: for example methylsulfonyl, ethylsulfonyl, propylsulfonyl, 1-methylethylsulfonyl, butylsulfonyl, 1-methylpropylsulfonyl, 2-methyl-propylsulfonyl, 1,1-dimethylethylsulfonyl, pentylsulfonyl, 1-methylbutylsulfonyl, 2-methylbutylsulfonyl, 3-methylbutylsulfonyl, 1,1-dimethylpropylsulfonyl, 1,2-dimethylpropylsulfonyl, 2,2-dimethylpropylsulfonyl, 1-ethylpropylsulfonyl, hexylsulfonyl, 1-methylpentylsulfonyl, 2-methylpentylsulfonyl, 3-methylpentylsulfonyl, 4-methylpentylsulfonyl, 1,1-dimethylbutylsulfonyl, 1,2-dimethylbutylsulfonyl, 1,3-dimethylbutylsulfonyl, 2,2-dimethylbutylsulfonyl, 2,3-dimethylbutylsulfonyl, 3,3-dimethylbutylsulfonyl, 1-ethylbutylsulfonyl, 2-ethylbutylsulfonyl, 1,1,2-trimethyl-propylsulfonyl, 1,2,2-trimethylpropylsulfonyl, 1-ethyl-1-methylpropylsulfonyl and 1-ethyl-2-methylpropylsulfonyl;

- (C₁-C₄-alkyl)amino: for example methylamino, ethylamino, propylamino, 1-methylethylamino, butylamino, 1-methylpropylamino, 2-methylpropylamino or 1,1-dimethylethylamino;

- (C₁-C₆-alkyl)amino and also the (C₁-C₆-alkyl)amino moieties of (C₁-C₆-alkyl)amino-C₁-C₆-alkyl, (C₁-C₆-alkyl)aminocarbonyl-C₁-C₆-alkyl: (C₁-C₄-alkylamino) as mentioned above, and also, for example, pentylamino, 1-methylbutylamino, 2-methylbutylamino, 3-methylbutylamino, 2,2-dimethylpropylamino, 1-ethylpropylamino, hexylamino, 1,1-dimethylpropylamino, 1,2-dimethylpropylamino, 1-methylpentylamino, 2-methylpentylamino, 3-methylpentylamino, 4-methylpentylamino, 1,1-dimethylbutylamino, 1,2-dimethylbutylamino, 1,3-dimethylbutylamino, 2,2-dimethylbutylamino, 2,3-dimethylbutylamino, 3,3-dimethylbutylamino, 1-ethylbutylamino, 2-ethylbutylamino, 1,1,2-trimethylpropylamino, 1,2,2-trimethyl-propylamino, 1-ethyl-1-methylpropylamino or 1-ethyl-2-methylpropylamino;

- di(C₁-C₆-alkyl)amino and also the di(C₁-C₆-alkyl)amino moieties of di(C₁-C₆-alkyl)amino-C₁-C₆-alkyl, di(C₁-C₆-alkyl)aminocarbonyl-C₁-C₆-alkyl: di(C₁-C₄-alkyl)amino as mentioned above, and also, for example, N-methyl-N-pentylamino, N-methyl-N-(1-methylbutyl)amino, N-methyl-N-(2-methylbutyl)amino, N-methyl-N-(3-methylbutyl)amino, N-methyl-N-(2,2-dimethylpropyl)amino, N-methyl-N-(1-ethylpropyl)amino, N-methyl-N-hexylamino, N-methyl-N-(1,1-dimethylpropyl)amino, N-methyl-N-(1,2-dimethylpropyl)amino, N-methyl-N-(1-methylpentyl)amino, N-methyl-N-(2-methylpentyl)amino, N-methyl-N-(3-methylpentyl)amino, N-methyl-N-(4-methylpentyl)amino, N-methyl-N-(1,1-dimethylbutyl)amino, N-methyl-N-(1,2-dimethylbutyl)amino, N-methyl-N-(1,3-dimethylbutyl)amino, N-methyl-N-(2,2-dimethylbutyl)amino, N-methyl-N-(2,3-dimethylbutyl)amino, N-methyl-N-(3,3-dimethylbutyl)amino, N-methyl-N-(1-ethylbutyl)amino, N-methyl-N-(2-ethylbutyl)amino, N-methyl-N-(1,1,2-trimethylpropyl)amino, N-methyl-N-(1,2,2-trimethylpropyl)amino, N-methyl-N-(1-ethyl-1-methylpropyl)amino, N-methyl-N-(1-ethyl-2-methylpropyl)amino, N-ethyl-N-pentylamino, N-ethyl-N-(1-methylbutyl)amino, N-ethyl-N-(2-methylbutyl)amino, N-ethyl-N-(3-methylbutyl)amino, N-ethyl-N-(2,2-dimethylpropyl)amino, N-ethyl-N-(1-ethylpropyl)amino, N-ethyl-N-hexylamino, N-ethyl-N-(1,1-dimethylpropyl)amino, N-ethyl-N-(1,2-dimethylpropyl)amino, N-ethyl-N-(1-methylpentyl)amino, N-ethyl-N-(2-methylpentyl)amino, N-ethyl-N-(3-methylpentyl)amino, N-ethyl-N-(4-methylpentyl)amino, N-ethyl-N-(1,1-dimethylbutyl)amino, N-ethyl-N-(1,2-

dimethylbutyl)amino, N-ethyl-N-(1,3-dimethylbutyl)amino, N-ethyl-N-(2,2-dimethylbutyl)amino, N-ethyl-N-(2,3-dimethylbutyl)amino, N-ethyl-N-(3,3-dimethylbutyl)amino, N-ethyl-N-(1-ethylbutyl)amino, N-ethyl-N-(2-ethylbutyl)amino, N-ethyl-N-(1,1,2-trimethylpropyl)amino, N-ethyl-N-(1,2,2-trimethylpropyl)amino, N-ethyl-N-(1-ethyl-1-methylpropyl)amino, N-ethyl-N-(1-ethyl-2-methylpropyl)amino, N-propyl-N-pentylamino, N-butyl-N-pentylamino, N,N-dipentylamino, N-propyl-N-hexylamino, N-butyl-N-hexylamino, N-pentyl-N-hexylamino or N,N-dihexylamino;

- C₃-C₆-cycloalkyl and also the cycloalkyl moieties of C₃-C₆-cycloalkyl-C₁-C₆-alkyl: monocyclic saturated hydrocarbons having 3 to 6 ring members, such as cyclopropyl, cyclobutyl, cyclopentyl and cyclohexyl;

- C₃-C₆-heterocyclyl: aliphatic heterocycle having 3 to 6 ring members which, in addition to carbon atoms, contains 1 to 4 nitrogen atoms, or 1 to 3 nitrogen atoms and an oxygen or sulphur atom, or an oxygen or a sulphur atom, for example three- or four-membered heterocycles like 2-oxetanyl, 3-oxetanyl, 2-thietanyl, 3-thietanyl, 1-azetidiny, 2-azetidiny, 1-azetiny, 2-azetiny; five-membered saturated heterocycles like 2-tetrahydrofuranyl, 3-tetrahydrofuranyl, 2-tetrahydrothienyl, 3-tetrahydrothienyl, 1-pyrrolidinyl, 2-pyrrolidinyl, 3-pyrrolidinyl, 3-isoxazolidinyl, 4-isoxazolidinyl, 5-isoxazolidinyl, 2-isothiazolidinyl, 3-isothiazolidinyl, 4-isothiazolidinyl, 5-isothiazolidinyl, 1-pyrazolidinyl, 3-pyrazolidinyl, 4-pyrazolidinyl, 5-pyrazolidinyl, 2-oxazolidinyl, 4-oxazolidinyl, 5-oxazolidinyl, 2-thiazolidinyl, 4-thiazolidinyl, 5-thiazolidinyl, 1-imidazolidinyl, 2-imidazolidinyl, 4-imidazolidinyl, 3-oxazolidinyl, 1,2,4-oxadiazolidin-3-yl, 1,2,4-oxadiazolidin-5-yl, 3-thiazolidinyl, 1,2,4-thiadiazolidin-3-yl, 1,2,4-thiadiazolidin-5-yl, 1,2,4-triazolidin-3-yl, 1,2,4-oxadiazolidin-2-yl, 1,2,4-oxadiazolidin-4-yl, 1,3,4-oxadiazolidin-2-yl, 1,2,4-thiadiazolidin-2-yl, 1,2,4-thiadiazolidin-4-yl, 1,3,4-thiadiazolidin-2-yl, 1,2,4-triazolidin-1-yl, 1,3,4-triazolidin-2-yl; six-membered saturated heterocycles like 1-piperidinyl, 2-piperidinyl, 3-piperidinyl, 4-piperidinyl, 1,3-dioxan-5-yl, 1,4-dioxanyl, 1,3-dithian-5-yl, 1,3-dithianyl, 1,3-oxathian-5-yl, 1,4-oxathianyl, 2-tetrahydropyranyl, 3-tetrahydropyranyl, 4-tetrahydropyranyl, 2-tetrahydrothiopyranyl, 3-tetrahydrothiopyranyl, 4-tetrahydrothiopyranyl, 1-hexahydropyridazinyl, 3-hexahydropyridazinyl, 4-hexahydropyridazinyl, 1-hexahydropyrimidinyl, 2-hexahydropyrimidinyl, 4-hexahydropyrimidinyl, 5-hexahydropyrimidinyl, 1-piperazinyl, 2-piperazinyl, 1,3,5-hexahydrotriazin-1-yl, 1,3,5-hexahydrotriazin-2-yl, 1,2,4-hexahydrotriazin-1-yl, 1,2,4-hexahydrotriazin-3-yl, tetrahydro-1,3-oxazin-1-yl, tetrahydro-1,3-oxazin-2-yl, tetrahydro-1,3-oxazin-6-yl, 1-morpholinyl, 2-morpholinyl, 3-morpholinyl;

- 5- or 6 membered heteroaryl: aromatic heteroaryl having 5 or 6 ring members which, in addition to carbon atoms, contains 1 to 4 nitrogen atoms, or 1 to 3 nitrogen atoms and an oxygen or sulphur atom, or an oxygen or a sulphur atom, for example 5-membered aromatic rings like furyl (for example 2-furyl, 3-furyl), thienyl (for example 2-thienyl, 3-thienyl), pyrrolyl (for example pyrrol-2-yl, pyrrol-3-yl), pyrazolyl (for example pyrazol-3-yl, pyrazol-4-yl), isoxazolyl (for example isoxazol-3-yl, isoxazol-4-yl, isoxazol-5-yl), isothiazolyl (for example isothiazol-3-yl, isothiazol-4-yl, isothiazol-5-yl), imidazolyl (for example imidazole-2-yl, imidazole-4-yl), oxazolyl (for example oxazol-2-yl, oxazol-4-yl, oxazol-5-yl),

thiazolyl (for example thiazol-2-yl, thiazol-4-yl, thiazol-5-yl), oxadiazolyl (for example 1,2,3-oxadiazol-4-yl, 1,2,3-oxadiazol-5-yl, 1,2,4-oxadiazol-3-yl, 1,2,4-oxadiazol-5-yl, 1,3,4-oxadiazol-2-yl), thiadiazolyl (for example 1,2,3-thiadiazol-4-yl, 1,2,3-thiadiazol-5-yl, 1,2,4-thiadiazol-3-yl, 1,2,4-thiadiazol-5-yl, 1,3,4-thiadiazolyl-2-yl), triazolyl (for example 1,2,3-triazol-4-yl, 1,2,4-triazol-3-yl); 1-tetrazolyl; 6-membered aromatic rings like pyridyl (for example pyridine-2-yl, pyridine-3-yl, pyridine-4-yl), pyrazinyl (for example pyridazin-3-yl, pyridazin-4-yl), pyrimidinyl (for example pyrimidin-2-yl, pyrimidin-4-yl, pyrimidin-5-yl), pyrazin-2-yl, triazinyl (for example 1,3,5-triazin-2-yl, 1,2,4-triazin-3-yl, 1,2,4-triazin-5-yl, 1,2,4-triazin-6-yl);

10 - 3- to 7-membered carbocyclus: a three- to seven-membered monocyclic, saturated, partial unsaturated or aromatic cycle having three to seven ring members which comprises apart from carbon atoms optionally one or two ring members selected from the group consisting of -N(R¹²)-, -N=N-, -C(=O)-, -O- and -S-.

15

The preferred embodiments of the invention mentioned herein below have to be understood as being preferred either independently from each other or in combination with one another.

20 According to a preferred embodiment of the invention preference is given to those phenylpyridines of formula (I), wherein the variables, either independently of one another or in combination with one another, have the following meanings:

Preferred are the phenylpyridines of formula (I), wherein

R¹ is halogen or C₁-C₄-haloalkyl;

25 particularly preferred Cl, CF₃ or CF₂H;
also particularly preferred C₁-C₄-haloalkyl;
especially preferred CF₃ or CF₂H;
more preferred CF₃.

30 Also preferred are the phenylpyridines of formula (I) wherein

R² is H or CH₃;

particularly preferred H;
also particularly preferred CH₃.

35 Also preferred are the phenylpyridines of formula (I) wherein

R³ is F, Cl or Br;

preferably F or Cl;
particularly preferred F;
also particularly preferred Cl.

40

Also preferred are the phenylpyridines of formula (I) wherein

R⁴ is H, F or Cl;

particularly preferred H or F;
 especially preferred H;
 also particularly preferred H or Cl;
 especially preferred Cl;
 5 also particularly preferred F or Cl;
 especially preferred F.

Also preferred are the phenylpyridines of formula (I) wherein
 R⁵ is F, Cl, Br or CN;

10 particularly preferred F, Cl or CN;
 especially preferred Cl or CN;
 more preferred Cl;
 also more preferred CN;
 also especially preferred F or Cl;
 15 more preferred F.

Also preferred are the phenylpyridines of formula (I) wherein
 R⁶ is H;
 also preferred CH₃.

20

Also preferred are the phenylpyridines of formula (I) wherein
 R⁷ is C₁-C₆-alkoxy, C₁-C₆-haloalkoxy, C₃-C₆-alkenyloxy, C₃-C₆-alkynyloxy;
 preferably C₁-C₆-alkoxy or C₁-C₆-haloalkoxy;
 particularly preferred C₁-C₄-alkoxy or C₁-C₄-haloalkoxy;
 25 also particularly preferred C₁-C₆-alkoxy;
 especially preferred C₁-C₄-alkoxy;
 more preferred OCH₃ or OC₂H₅;
 most preferred is OCH₃.

30

Also preferred are the phenylpyridines of formula (I) wherein
 R⁸ is OR⁹, SR⁹, NR¹⁰R¹¹, NR⁹S(O)₂R⁹ or NR⁹S(O)₂NR¹⁰R¹¹;
 particularly preferred OR⁹, NR¹⁰R¹¹, NR⁹S(O)₂R⁹ or NR⁹S(O)₂NR¹⁰R¹¹;
 especially preferred OR⁹ or NR⁹S(O)₂R⁹.

35

Also preferred are the phenylpyridines of formula (I) wherein

40

R⁹ is hydrogen, C₁-C₆-alkyl, C₃-C₆-alkenyl, C₃-C₆-alkynyl, C₁-C₆-haloalkyl, C₃-C₆-
 haloalkenyl, C₃-C₆-haloalkynyl, C₁-C₆-cyanoalkyl, C₁-C₆-alkoxy-C₁-C₆-alkyl, C₁-
 C₆-alkoxy-C₁-C₆-alkoxy-C₁-C₆-alkyl, di(C₁-C₆-alkoxy)C₁-C₆-alkyl, C₁-C₆-halo-
 alkoxy-C₁-C₆-alkyl, C₃-C₆-alkenyloxy-C₁-C₆-alkyl, C₃-C₆-haloalkenyloxy-C₁-C₆-
 alkyl, C₃-C₆-alkenyloxy-C₁-C₆-alkoxy-C₁-C₆-alkyl, C₁-C₆-alkylthio-C₁-C₆-alkyl, C₁-
 C₆-alkylsulfinyl-C₁-C₆-alkyl, C₁-C₆-alkylsulfonyl-C₁-C₆-alkyl, C₁-C₆-alkylcarbonyl-
 C₁-C₆-alkyl, C₁-C₆-alkoxycarbonyl-C₁-C₆-alkyl, C₁-C₆-haloalkoxycarbonyl-C₁-C₆-

alkyl, C₃-C₆-alkenyloxycarbonyl-C₁-C₆-alkyl, amino, (C₁-C₆-alkyl)amino, di(C₁-C₆-alkyl)amino, (C₁-C₆-alkylcarbonyl)amino, amino-C₁-C₆-alkyl, (C₁-C₆-alkyl)amino-C₁-C₆-alkyl, di(C₁-C₆-alkyl)amino-C₁-C₆-alkyl, aminocarbonyl-C₁-C₆-alkyl, (C₁-C₆-alkyl)aminocarbonyl-C₁-C₆-alkyl, di(C₁-C₆-alkyl)aminocarbonyl-C₁-C₆-alkyl, -N=CR¹²R¹³, wherein R¹² and R¹³ independently of one another are H, C₁-C₄-alkyl or phenyl;

C₃-C₆-cycloalkyl, C₃-C₆-cycloalkyl-C₁-C₆-alkyl, C₃-C₆-heterocyclyl, phenyl, phenyl-C₁-C₄-alkyl or a 5- or 6 membered heteroaryl, wherein each cycloalkyl, heterocyclyl, phenyl or heteroaryl ring can be substituted by one to four substituents selected from R¹⁴ or a 3- to 7-membered carbocyclus, which carbocyclus optionally has in addition to carbon atoms one or two ring members selected from the group consisting of -N(R¹²)-, -N=N-, -C(=O)-, -O- and -S-, and which carbocyclus is optionally substituted with one to four substituents selected from R¹⁴;

wherein R¹⁴ is halogen, NO₂, CN, C₁-C₄-alkyl, C₁-C₄-haloalkyl, C₁-C₄-alkoxy or C₁-C₄-alkoxycarbonyl;

preferably hydrogen, C₁-C₆-alkyl, C₃-C₆-alkenyl, C₃-C₆-alkynyl, C₁-C₆-haloalkyl, C₁-C₆-alkoxy-C₁-C₆-alkyl, di(C₁-C₆-alkoxy)C₁-C₆-alkyl, C₁-C₆-alkylcarbonyl-C₁-C₆-alkyl, C₁-C₆-alkoxycarbonyl-C₁-C₆-alkyl or C₃-C₆-cycloalkyl-C₁-C₆-alkyl;

particularly preferred hydrogen, C₁-C₆-alkyl, C₃-C₆-alkenyl, C₃-C₆-alkynyl or C₁-C₆-haloalkyl;

especially preferred hydrogen, C₁-C₆-alkyl, or C₃-C₆-alkynyl;

more preferred hydrogen, CH₃, C₂H₅ or CH₂C≡CH.

Also preferred are the phenylpyridines of formula (I) wherein R¹⁰ is H or C₁-C₆-alkyl; more preferred H; also more preferred C₁-C₆-alkyl.

Also preferred are the phenylpyridines of formula (I) wherein R¹¹ is C₁-C₆-alkyl.

Also preferred are the phenylpyridines of formula (I) wherein R¹² is phenyl or CH₃; particularly preferred phenyl; also particularly preferred C₁-C₄-alkyl.

Also preferred are the phenylpyridines of formula (I) wherein

R¹³ is phenyl or CH₃;
 particularly preferred phenyl;
 also particularly preferred C₁-C₄-alkyl.

- 5 Also preferred are the phenylpyridines of formula (I) wherein
 R¹⁴ is halogen or C₁-C₆-alkyl;
 particularly preferred F, Cl or CH₃;
 also particularly preferred halogen;
 especially preferred F or Cl;
 10 also particularly preferred C₁-C₆-alkyl;
 especially preferred CH₃.

- Also preferred are the phenylpyridines of formula (I) wherein
 X is O;
 15 also preferred S.

- Also preferred are the phenylpyridines of formula (I) wherein
 Y is O;
 also preferred S.

- 20 Also preferred are the phenylpyridines of formula (I) wherein
 R¹ is halogen or C₁-C₄-haloalkyl;
 particularly preferred Cl, CF₃ or CF₂H;
 also particularly preferred C₁-C₄-haloalkyl;
 25 especially preferred CF₃ or CF₂H;
 more preferred CF₃;

- R² is H or CH₃;
 particularly preferred H;
 also particularly preferred CH₃;

- 30 R³ is F or Cl;
 particularly preferred F;
 also particularly preferred Cl;

- R⁴ is H, F or Cl;
 particularly preferred H or F;
 35 especially preferred H;
 also particularly preferred H or Cl;
 especially preferred Cl;
 also particularly preferred F or Cl;
 especially preferred F;

- 40 R⁵ is F, Cl, Br or CN;
 particularly preferred F, Cl or CN;
 especially preferred Cl or CN;

more preferred Cl;
 also more preferred CN;
 also especially preferred F or Cl;
 more preferred F;

5 R⁶ is H;

also preferred CH₃;

R⁷ is C₁-C₆-alkoxy or C₁-C₆-haloalkoxy;

particularly preferred C₁-C₄-alkoxy or C₁-C₄-haloalkoxy;

also particularly preferred C₁-C₆-alkoxy;

10 especially preferred C₁-C₄-alkoxy;

more preferred OCH₃ or OC₂H₅;

most preferred is OCH₃;

R⁸ is OR⁹, SR⁹, NR¹⁰R¹¹, NR⁹S(O)₂R⁹ or NR⁹S(O)₂NR¹⁰R¹¹;

particularly preferred OR⁹, NR¹⁰R¹¹, NR⁹S(O)₂R⁹ or NR⁹S(O)₂NR¹⁰R¹¹;

15 especially preferred OR⁹ or NR⁹S(O)₂R⁹;

R⁹ is hydrogen, C₁-C₆-alkyl, C₃-C₆-alkenyl, C₃-C₆-alkynyl, C₁-C₆-haloalkyl, C₁-C₆-alkoxy-C₁-C₆-alkyl, di(C₁-C₆-alkoxy)C₁-C₆-alkyl, C₁-C₆-alkylcarbonyl-C₁-C₆-alkyl, C₁-C₆-alkoxycarbonyl-C₁-C₆-alkyl or C₃-C₆-cycloalkyl-C₁-C₆-alkyl;

particularly preferred hydrogen, C₁-C₆-alkyl, C₃-C₆-alkenyl, C₃-C₆-alkynyl or C₁-C₆-

20 haloalkyl;

especially preferred hydrogen, C₁-C₆-alkyl, or C₃-C₆-alkynyl;

more preferred hydrogen, CH₃, C₂H₅ or CH₂C≡CH;

R¹⁰ is H or C₁-C₆-alkyl;

more preferred H;

25 also more preferred C₁-C₆-alkyl;

R¹¹ is C₁-C₆-alkyl;

R¹² is phenyl or CH₃;

particularly preferred phenyl;

also particularly preferred C₁-C₄-alkyl;

30 R¹³ is phenyl or CH₃;

particularly preferred phenyl;

also particularly preferred C₁-C₄-alkyl;

R¹⁴ is halogen or C₁-C₆-alkyl;

particularly preferred F, Cl or CH₃;

35 also particularly preferred halogen;

especially preferred F or Cl;

also particularly preferred C₁-C₆-alkyl;

especially preferred CH₃;

X is O;

40 also preferred S; and

Y is O;

also preferred S.

Also preferred are the phenylpyridines of formula (I) wherein

R¹ is halogen or C₁-C₄-haloalkyl;

5 R² is H;

R³ is Cl or F;

R⁴ is H or F;

R⁵ is Cl or CN;

R⁶ is H;

10 R⁷ is C₁-C₆-alkoxy;

R⁸ is OR⁹, NR¹⁰R¹¹, NR⁹S(O)₂R⁹ or NR⁹S(O)₂NR¹⁰R¹¹, wherein

R⁹ is hydrogen, C₁-C₆-alkyl, C₃-C₆-alkenyl, C₃-C₆-alkynyl, C₁-C₆-haloalkyl, C₁-C₆-alkoxy-C₁-C₆-alkyl, di(C₁-C₆-alkoxy)C₁-C₆-alkyl, , C₁-C₆-alkoxycarbonyl-C₁-C₆-alkyl or C₃-C₆-cycloalkyl-C₁-C₆-alkyl;

15 R¹⁰ is H or C₁-C₆-alkyl; and

R¹¹ is C₁-C₆-alkyl.

Also preferred are the phenylpyridines of formula (I) wherein

R¹ is C₁-C₄-haloalkyl;

20 R² and R⁶ are H;

R³, R⁴ and R⁵ are halogen;

R⁷ is C₁-C₆-alkoxy; and

R⁸ is OR⁹ or NR⁹S(O)₂R⁹, wherein R⁹ is H, C₁-C₆-alkyl or C₃-C₆-alkynyl.

25 Particularly preferred are the phenylpyridines of formula (I) wherein

R¹ is CF₃;

R² and R⁶ are H;

R³ and R⁵ are Cl;

R⁴ is F;

30 R⁷ is C₁-C₆-alkoxy; and

R⁸ is OR⁹ or NR⁹S(O)₂R⁹, wherein R⁹ is H, C₁-C₆-alkyl or C₃-C₆-alkynyl.

Also particularly preferred are the phenylpyridines of formula (I) wherein

R¹ is CF₃;

35 R² and R⁶ are H;

R³ and R⁵ are Cl;

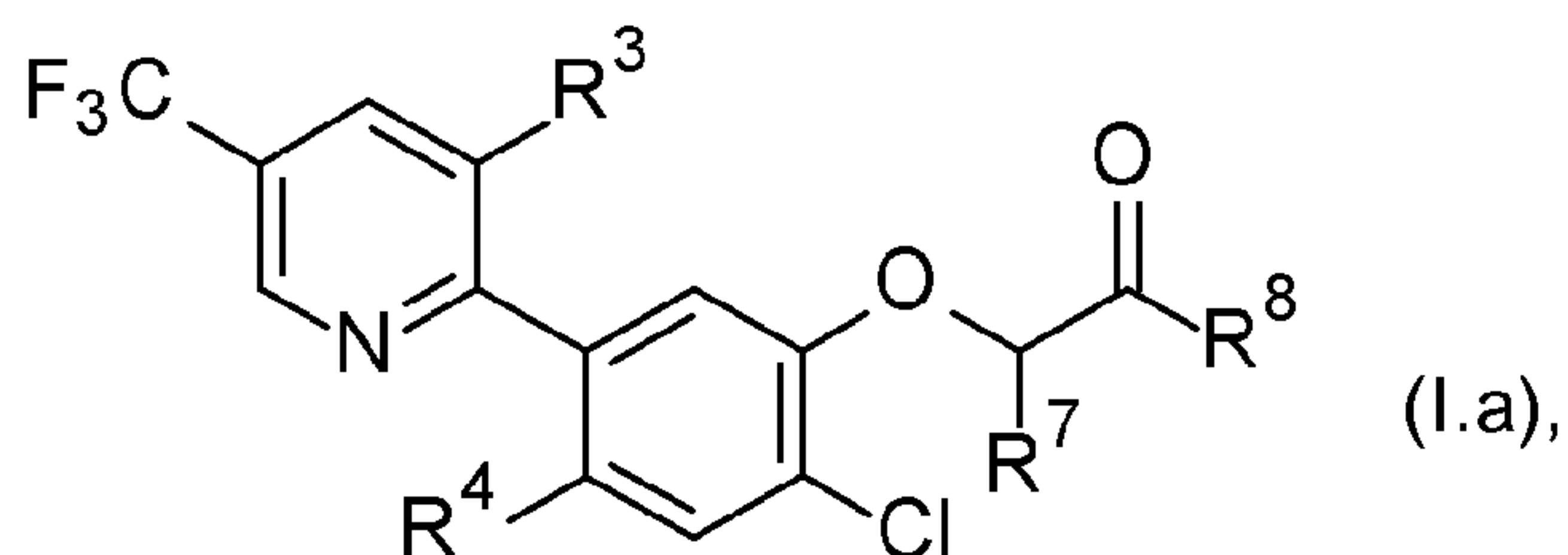
R⁴ is F;

R⁷ is OCH₃;

R⁸ is OR⁹ or NR⁹S(O)₂R⁹, wherein R⁹ is H, CH₃, C₂CH₅, CH(CH₃)₂ or CH₂C≡CH.

40

Particular preference is given to phenylpyridines of formula (I.a) (corresponds to phenylpyridines of formula (I), wherein R¹ is CF₃, R² is H, R⁵ is Cl, R⁶ is H, X and Y are O),



wherein the variables R³, R⁴, R⁷ and R⁸ have the meanings, in particular the preferred meanings, as defined above.

Special preference is given to the compounds of the formulae I.a.1 to I.a.264 of Table (I), where the definitions of the variables R³, R⁴, R⁷ and R⁸ are of particular importance for the compounds according to the invention not only in combination with one another but in each case also on their own:

Table (I)

No.	R ³	R ⁴	R ⁷	R ⁸
I.a.1	F	H	OCH ₃	OH
I.a.2	F	H	OCH ₃	OCH ₃
I.a.3	F	H	OCH ₃	OCH ₂ CH ₃
I.a.4	F	H	OCH ₃	OCH(CH ₃) ₂
I.a.5	F	H	OCH ₃	OCH ₂ CH ₂ CH ₃
I.a.6	F	H	OCH ₃	OCH ₂ CH(CH ₃) ₂
I.a.7	F	H	OCH ₃	OCH ₂ CH=CH ₂
I.a.8	F	H	OCH ₃	OCH ₃ C(CH ₃)=CH ₂
I.a.9	F	H	OCH ₃	OCH ₂ C≡CH
I.a.10	F	H	OCH ₃	OCH ₂ CF ₃
I.a.11	F	H	OCH ₃	OCH ₂ CHF ₂
I.a.12	F	H	OCH ₃	OCH ₂ OCH ₃
I.a.13	F	H	OCH ₃	OCH ₂ OCH ₂ CH ₃
I.a.14	F	H	OCH ₃	OCH ₂ CH ₂ OCH ₃
I.a.15	F	H	OCH ₃	OCH ₂ CH ₂ OCH ₂ CH ₃
I.a.16	F	H	OCH ₃	OCH ₂ CH ₂ CH ₂ OCH ₃
I.a.17	F	H	OCH ₃	OCH ₂ CH(OCH ₃) ₂
I.a.18	F	H	OCH ₃	OCH ₂ (CO)OCH ₃
I.a.19	F	H	OCH ₃	OCH ₂ (CO)OCH ₂ CH ₃
I.a.20	F	H	OCH ₃	OCH(CH ₃)(CO)OCH ₃
I.a.21	F	H	OCH ₃	OCH(CH ₃)(CO)OCH ₂ CH ₃
I.a.22	F	H	OCH ₃	OC(CH ₃) ₂ (CO)OCH ₃
I.a.23	F	H	OCH ₃	OC(CH ₃) ₂ (CO)OCH ₂ CH ₃

No.	R ³	R ⁴	R ⁷	R ⁸
l.a.24	F	H	OCH ₃	OCH ₂ -cyclopropyl
l.a.25	F	H	OCH ₃	OCH ₂ -cyclobutyl
l.a.26	F	H	OCH ₃	NHCH ₃
l.a.27	F	H	OCH ₃	N(CH ₃) ₂
l.a.28	F	H	OCH ₃	N(CH ₃)(CH ₂ CH ₃)
l.a.29	F	H	OCH ₃	N(CH ₂ CH ₃) ₂
l.a.30	F	H	OCH ₃	NHSO ₂ CH ₃
l.a.31	F	H	OCH ₃	NHSO ₂ CH ₂ CH ₃
l.a.32	F	H	OCH ₃	NHSO ₂ N(CH ₃) ₂
l.a.33	F	H	OCH ₃	NHSO ₂ N(CH ₃)[CH(CH ₃) ₂]
l.a.34	F	H	OCH ₂ CH ₃	OH
l.a.35	F	H	OCH ₂ CH ₃	OCH ₃
l.a.36	F	H	OCH ₂ CH ₃	OCH ₂ CH ₃
l.a.37	F	H	OCH ₂ CH ₃	OCH(CH ₃) ₂
l.a.38	F	H	OCH ₂ CH ₃	OCH ₂ CH ₂ CH ₃
l.a.39	F	H	OCH ₂ CH ₃	OCH ₂ CH(CH ₃) ₂
l.a.40	F	H	OCH ₂ CH ₃	OCH ₂ CH=CH ₂
l.a.41	F	H	OCH ₂ CH ₃	OCH ₃ C(CH ₃)=CH ₂
l.a.42	F	H	OCH ₂ CH ₃	OCH ₂ C≡CH
l.a.43	F	H	OCH ₂ CH ₃	OCH ₂ CF ₃
l.a.44	F	H	OCH ₂ CH ₃	OCH ₂ CHF ₂
l.a.45	F	H	OCH ₂ CH ₃	OCH ₂ OCH ₃
l.a.46	F	H	OCH ₂ CH ₃	OCH ₂ OCH ₂ CH ₃
l.a.47	F	H	OCH ₂ CH ₃	OCH ₂ CH ₂ OCH ₃
l.a.48	F	H	OCH ₂ CH ₃	OCH ₂ CH ₂ OCH ₂ CH ₃
l.a.49	F	H	OCH ₂ CH ₃	OCH ₂ CH ₂ CH ₂ OCH ₃
l.a.50	F	H	OCH ₂ CH ₃	OCH ₂ CH(OCH ₃) ₂
l.a.51	F	H	OCH ₂ CH ₃	OCH ₂ (CO)OCH ₃
l.a.52	F	H	OCH ₂ CH ₃	OCH ₂ (CO)OCH ₂ CH ₃
l.a.53	F	H	OCH ₂ CH ₃	OCH(CH ₃)(CO)OCH ₃
l.a.54	F	H	OCH ₂ CH ₃	OCH(CH ₃)(CO)OCH ₂ CH ₃
l.a.55	F	H	OCH ₂ CH ₃	OC(CH ₃) ₂ (CO)OCH ₃
l.a.56	F	H	OCH ₂ CH ₃	OC(CH ₃) ₂ (CO)OCH ₂ CH ₃
l.a.57	F	H	OCH ₂ CH ₃	OCH ₂ -cyclopropyl
l.a.58	F	H	OCH ₂ CH ₃	OCH ₂ -cyclobutyl
l.a.59	F	H	OCH ₂ CH ₃	NHCH ₃
l.a.60	F	H	OCH ₂ CH ₃	N(CH ₃) ₂
l.a.61	F	H	OCH ₂ CH ₃	N(CH ₃)(CH ₂ CH ₃)
l.a.62	F	H	OCH ₂ CH ₃	N(CH ₂ CH ₃) ₂

No.	R ³	R ⁴	R ⁷	R ⁸
I.a.63	F	H	OCH ₂ CH ₃	NHSO ₂ CH ₃
I.a.64	F	H	OCH ₂ CH ₃	NHSO ₂ CH ₂ CH ₃
I.a.65	F	H	OCH ₂ CH ₃	NHSO ₂ N(CH ₃) ₂
I.a.66	F	H	OCH ₂ CH ₃	NHSO ₂ N(CH ₃)[CH(CH ₃) ₂]
I.a.67	F	F	OCH ₃	OH
I.a.68	F	F	OCH ₃	OCH ₃
I.a.69	F	F	OCH ₃	OCH ₂ CH ₃
I.a.70	F	F	OCH ₃	OCH(CH ₃) ₂
I.a.71	F	F	OCH ₃	OCH ₂ CH ₂ CH ₃
I.a.72	F	F	OCH ₃	OCH ₂ CH(CH ₃) ₂
I.a.73	F	F	OCH ₃	OCH ₂ CH=CH ₂
I.a.74	F	F	OCH ₃	OCH ₃ C(CH ₃)=CH ₂
I.a.75	F	F	OCH ₃	OCH ₂ C≡CH
I.a.76	F	F	OCH ₃	OCH ₂ CF ₃
I.a.77	F	F	OCH ₃	OCH ₂ CHF ₂
I.a.78	F	F	OCH ₃	OCH ₂ OCH ₃
I.a.79	F	F	OCH ₃	OCH ₂ OCH ₂ CH ₃
I.a.80	F	F	OCH ₃	OCH ₂ CH ₂ OCH ₃
I.a.81	F	F	OCH ₃	OCH ₂ CH ₂ OCH ₂ CH ₃
I.a.82	F	F	OCH ₃	OCH ₂ CH ₂ CH ₂ OCH ₃
I.a.83	F	F	OCH ₃	OCH ₂ CH(OCH ₃) ₂
I.a.84	F	F	OCH ₃	OCH ₂ (CO)OCH ₃
I.a.85	F	F	OCH ₃	OCH ₂ (CO)OCH ₂ CH ₃
I.a.86	F	F	OCH ₃	OCH(CH ₃)(CO)OCH ₃
I.a.87	F	F	OCH ₃	OCH(CH ₃)(CO)OCH ₂ CH ₃
I.a.88	F	F	OCH ₃	OC(CH ₃) ₂ (CO)OCH ₃
I.a.89	F	F	OCH ₃	OC(CH ₃) ₂ (CO)OCH ₂ CH ₃
I.a.90	F	F	OCH ₃	OCH ₂ -cyclopropyl
I.a.91	F	F	OCH ₃	OCH ₂ -cyclobutyl
I.a.92	F	F	OCH ₃	NHCH ₃
I.a.93	F	F	OCH ₃	N(CH ₃) ₂
I.a.94	F	F	OCH ₃	N(CH ₃)(CH ₂ CH ₃)
I.a.95	F	F	OCH ₃	N(CH ₂ CH ₃) ₂
I.a.96	F	F	OCH ₃	NHSO ₂ CH ₃
I.a.97	F	F	OCH ₃	NHSO ₂ CH ₂ CH ₃
I.a.98	F	F	OCH ₃	NHSO ₂ N(CH ₃) ₂
I.a.99	F	F	OCH ₃	NHSO ₂ N(CH ₃)[CH(CH ₃) ₂]
I.a.100	F	F	OCH ₂ CH ₃	OH
I.a.101	F	F	OCH ₂ CH ₃	OCH ₃

No.	R ³	R ⁴	R ⁷	R ⁸
I.a.102	F	F	OCH ₂ CH ₃	OCH ₂ CH ₃
I.a.103	F	F	OCH ₂ CH ₃	OCH(CH ₃) ₂
I.a.104	F	F	OCH ₂ CH ₃	OCH ₂ CH ₂ CH ₃
I.a.105	F	F	OCH ₂ CH ₃	OCH ₂ CH(CH ₃) ₂
I.a.106	F	F	OCH ₂ CH ₃	OCH ₂ CH=CH ₂
I.a.107	F	F	OCH ₂ CH ₃	OCH ₃ C(CH ₃)=CH ₂
I.a.108	F	F	OCH ₂ CH ₃	OCH ₂ C≡CH
I.a.109	F	F	OCH ₂ CH ₃	OCH ₂ CF ₃
I.a.110	F	F	OCH ₂ CH ₃	OCH ₂ CHF ₂
I.a.111	F	F	OCH ₂ CH ₃	OCH ₂ OCH ₃
I.a.112	F	F	OCH ₂ CH ₃	OCH ₂ OCH ₂ CH ₃
I.a.113	F	F	OCH ₂ CH ₃	OCH ₂ CH ₂ OCH ₃
I.a.114	F	F	OCH ₂ CH ₃	OCH ₂ CH ₂ OCH ₂ CH ₃
I.a.115	F	F	OCH ₂ CH ₃	OCH ₂ CH ₂ CH ₂ OCH ₃
I.a.116	F	F	OCH ₂ CH ₃	OCH ₂ CH(OCH ₃) ₂
I.a.117	F	F	OCH ₂ CH ₃	OCH ₂ (CO)OCH ₃
I.a.118	F	F	OCH ₂ CH ₃	OCH ₂ (CO)OCH ₂ CH ₃
I.a.119	F	F	OCH ₂ CH ₃	OCH(CH ₃)(CO)OCH ₃
I.a.120	F	F	OCH ₂ CH ₃	OCH(CH ₃)(CO)OCH ₂ CH ₃
I.a.121	F	F	OCH ₂ CH ₃	OC(CH ₃) ₂ (CO)OCH ₃
I.a.122	F	F	OCH ₂ CH ₃	OC(CH ₃) ₂ (CO)OCH ₂ CH ₃
I.a.123	F	F	OCH ₂ CH ₃	OCH ₂ -cyclopropyl
I.a.124	F	F	OCH ₂ CH ₃	OCH ₂ -cyclobutyl
I.a.125	F	F	OCH ₂ CH ₃	NHCH ₃
I.a.126	F	F	OCH ₂ CH ₃	N(CH ₃) ₂
I.a.127	F	F	OCH ₂ CH ₃	N(CH ₃)(CH ₂ CH ₃)
I.a.128	F	F	OCH ₂ CH ₃	N(CH ₂ CH ₃) ₂
I.a.129	F	F	OCH ₂ CH ₃	NHSO ₂ CH ₃
I.a.130	F	F	OCH ₂ CH ₃	NHSO ₂ CH ₂ CH ₃
I.a.131	F	F	OCH ₂ CH ₃	NHSO ₂ N(CH ₃) ₂
I.a.132	F	F	OCH ₂ CH ₃	NHSO ₂ N(CH ₃)[CH(CH ₃) ₂]
I.a.133	Cl	H	OCH ₃	OH
I.a.134	Cl	H	OCH ₃	OCH ₃
I.a.135	Cl	H	OCH ₃	OCH ₂ CH ₃
I.a.136	Cl	H	OCH ₃	OCH(CH ₃) ₂
I.a.137	Cl	H	OCH ₃	OCH ₂ CH ₂ CH ₃
I.a.138	Cl	H	OCH ₃	OCH ₂ CH(CH ₃) ₂
I.a.139	Cl	H	OCH ₃	OCH ₂ CH=CH ₂
I.a.140	Cl	H	OCH ₃	OCH ₃ C(CH ₃)=CH ₂

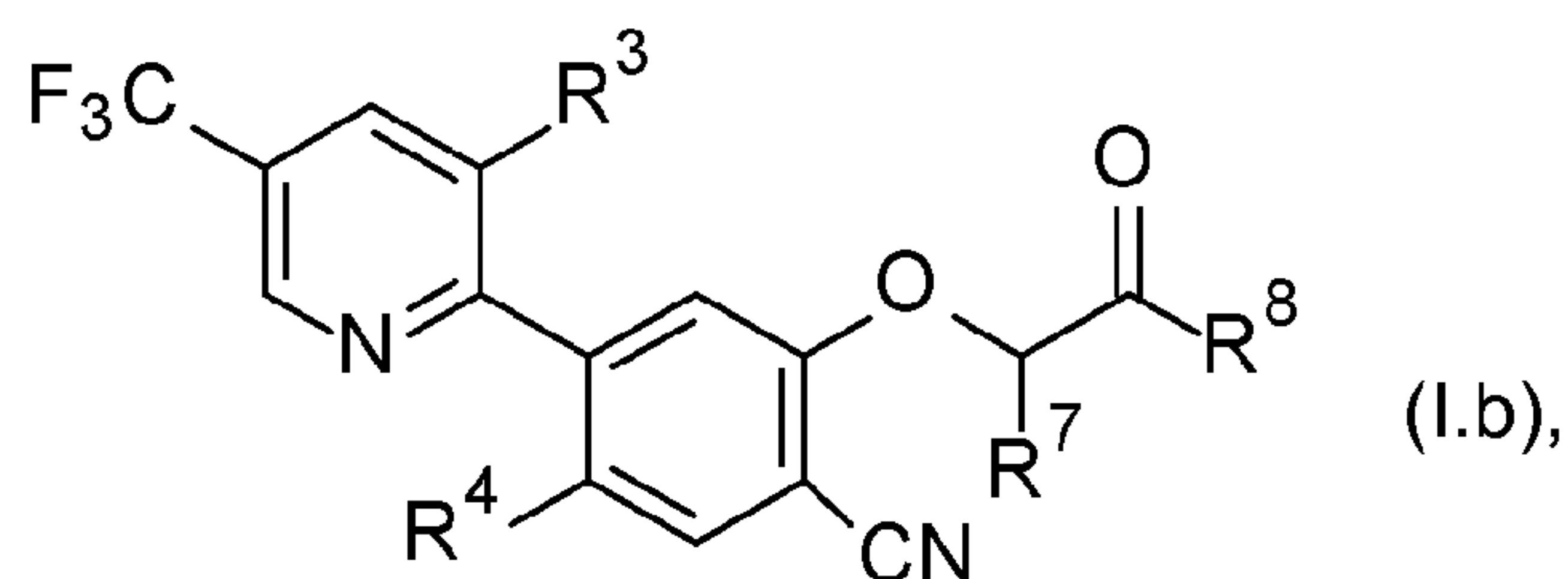
No.	R ³	R ⁴	R ⁷	R ⁸
I.a.141	Cl	H	OCH ₃	OCH ₂ C≡CH
I.a.142	Cl	H	OCH ₃	OCH ₂ CF ₃
I.a.143	Cl	H	OCH ₃	OCH ₂ CHF ₂
I.a.144	Cl	H	OCH ₃	OCH ₂ OCH ₃
I.a.145	Cl	H	OCH ₃	OCH ₂ OCH ₂ CH ₃
I.a.146	Cl	H	OCH ₃	OCH ₂ CH ₂ OCH ₃
I.a.147	Cl	H	OCH ₃	OCH ₂ CH ₂ OCH ₂ CH ₃
I.a.148	Cl	H	OCH ₃	OCH ₂ CH ₂ CH ₂ OCH ₃
I.a.149	Cl	H	OCH ₃	OCH ₂ CH(OCH ₃) ₂
I.a.150	Cl	H	OCH ₃	OCH ₂ (CO)OCH ₃
I.a.151	Cl	H	OCH ₃	OCH ₂ (CO)OCH ₂ CH ₃
I.a.152	Cl	H	OCH ₃	OCH(CH ₃)(CO)OCH ₃
I.a.153	Cl	H	OCH ₃	OCH(CH ₃)(CO)OCH ₂ CH ₃
I.a.154	Cl	H	OCH ₃	OC(CH ₃) ₂ (CO)OCH ₃
I.a.155	Cl	H	OCH ₃	OC(CH ₃) ₂ (CO)OCH ₂ CH ₃
I.a.156	Cl	H	OCH ₃	OCH ₂ -cyclopropyl
I.a.157	Cl	H	OCH ₃	OCH ₂ -cyclobutyl
I.a.158	Cl	H	OCH ₃	NHCH ₃
I.a.159	Cl	H	OCH ₃	N(CH ₃) ₂
I.a.160	Cl	H	OCH ₃	N(CH ₃)(CH ₂ CH ₃)
I.a.161	Cl	H	OCH ₃	N(CH ₂ CH ₃) ₂
I.a.162	Cl	H	OCH ₃	NHSO ₂ CH ₃
I.a.163	Cl	H	OCH ₃	NHSO ₂ CH ₂ CH ₃
I.a.164	Cl	H	OCH ₃	NHSO ₂ N(CH ₃) ₂
I.a.165	Cl	H	OCH ₃	NHSO ₂ N(CH ₃)[CH(CH ₃) ₂]
I.a.166	Cl	H	OCH ₂ CH ₃	OH
I.a.167	Cl	H	OCH ₂ CH ₃	OCH ₃
I.a.168	Cl	H	OCH ₂ CH ₃	OCH ₂ CH ₃
I.a.169	Cl	H	OCH ₂ CH ₃	OCH(CH ₃) ₂
I.a.170	Cl	H	OCH ₂ CH ₃	OCH ₂ CH ₂ CH ₃
I.a.171	Cl	H	OCH ₂ CH ₃	OCH ₂ CH(CH ₃) ₂
I.a.172	Cl	H	OCH ₂ CH ₃	OCH ₂ CH=CH ₂
I.a.173	Cl	H	OCH ₂ CH ₃	OCH ₃ C(CH ₃)=CH ₂
I.a.174	Cl	H	OCH ₂ CH ₃	OCH ₂ C≡CH
I.a.175	Cl	H	OCH ₂ CH ₃	OCH ₂ CF ₃
I.a.176	Cl	H	OCH ₂ CH ₃	OCH ₂ CHF ₂
I.a.177	Cl	H	OCH ₂ CH ₃	OCH ₂ OCH ₃
I.a.178	Cl	H	OCH ₂ CH ₃	OCH ₂ OCH ₂ CH ₃
I.a.179	Cl	H	OCH ₂ CH ₃	OCH ₂ CH ₂ OCH ₃

No.	R ³	R ⁴	R ⁷	R ⁸
I.a.180	Cl	H	OCH ₂ CH ₃	OCH ₂ CH ₂ OCH ₂ CH ₃
I.a.181	Cl	H	OCH ₂ CH ₃	OCH ₂ CH ₂ CH ₂ OCH ₃
I.a.182	Cl	H	OCH ₂ CH ₃	OCH ₂ CH(OCH ₃) ₂
I.a.183	Cl	H	OCH ₂ CH ₃	OCH ₂ (CO)OCH ₃
I.a.184	Cl	H	OCH ₂ CH ₃	OCH ₂ (CO)OCH ₂ CH ₃
I.a.185	Cl	H	OCH ₂ CH ₃	OCH(CH ₃)(CO)OCH ₃
I.a.186	Cl	H	OCH ₂ CH ₃	OCH(CH ₃)(CO)OCH ₂ CH ₃
I.a.187	Cl	H	OCH ₂ CH ₃	OC(CH ₃) ₂ (CO)OCH ₃
I.a.188	Cl	H	OCH ₂ CH ₃	OC(CH ₃) ₂ (CO)OCH ₂ CH ₃
I.a.189	Cl	H	OCH ₂ CH ₃	OCH ₂ -cyclopropyl
I.a.190	Cl	H	OCH ₂ CH ₃	OCH ₂ -cyclobutyl
I.a.191	Cl	H	OCH ₂ CH ₃	NHCH ₃
I.a.192	Cl	H	OCH ₂ CH ₃	N(CH ₃) ₂
I.a.193	Cl	H	OCH ₂ CH ₃	N(CH ₃)(CH ₂ CH ₃)
I.a.194	Cl	H	OCH ₂ CH ₃	N(CH ₂ CH ₃) ₂
I.a.195	Cl	H	OCH ₂ CH ₃	NHSO ₂ CH ₃
I.a.196	Cl	H	OCH ₂ CH ₃	NHSO ₂ CH ₂ CH ₃
I.a.197	Cl	H	OCH ₂ CH ₃	NHSO ₂ N(CH ₃) ₂
I.a.198	Cl	H	OCH ₂ CH ₃	NHSO ₂ N(CH ₃)[CH(CH ₃) ₂]
I.a.199	Cl	F	OCH ₃	OH
I.a.200	Cl	F	OCH ₃	OCH ₃
I.a.201	Cl	F	OCH ₃	OCH ₂ CH ₃
I.a.202	Cl	F	OCH ₃	OCH(CH ₃) ₂
I.a.203	Cl	F	OCH ₃	OCH ₂ CH ₂ CH ₃
I.a.204	Cl	F	OCH ₃	OCH ₂ CH(CH ₃) ₂
I.a.205	Cl	F	OCH ₃	OCH ₂ CH=CH ₂
I.a.206	Cl	F	OCH ₃	OCH ₃ C(CH ₃)=CH ₂
I.a.207	Cl	F	OCH ₃	OCH ₂ C≡CH
I.a.208	Cl	F	OCH ₃	OCH ₂ CF ₃
I.a.209	Cl	F	OCH ₃	OCH ₂ CHF ₂
I.a.210	Cl	F	OCH ₃	OCH ₂ OCH ₃
I.a.211	Cl	F	OCH ₃	OCH ₂ OCH ₂ CH ₃
I.a.212	Cl	F	OCH ₃	OCH ₂ CH ₂ OCH ₃
I.a.213	Cl	F	OCH ₃	OCH ₂ CH ₂ OCH ₂ CH ₃
I.a.214	Cl	F	OCH ₃	OCH ₂ CH ₂ CH ₂ OCH ₃
I.a.215	Cl	F	OCH ₃	OCH ₂ CH(OCH ₃) ₂
I.a.216	Cl	F	OCH ₃	OCH ₂ (CO)OCH ₃
I.a.217	Cl	F	OCH ₃	OCH ₂ (CO)OCH ₂ CH ₃
I.a.218	Cl	F	OCH ₃	OCH(CH ₃)(CO)OCH ₃

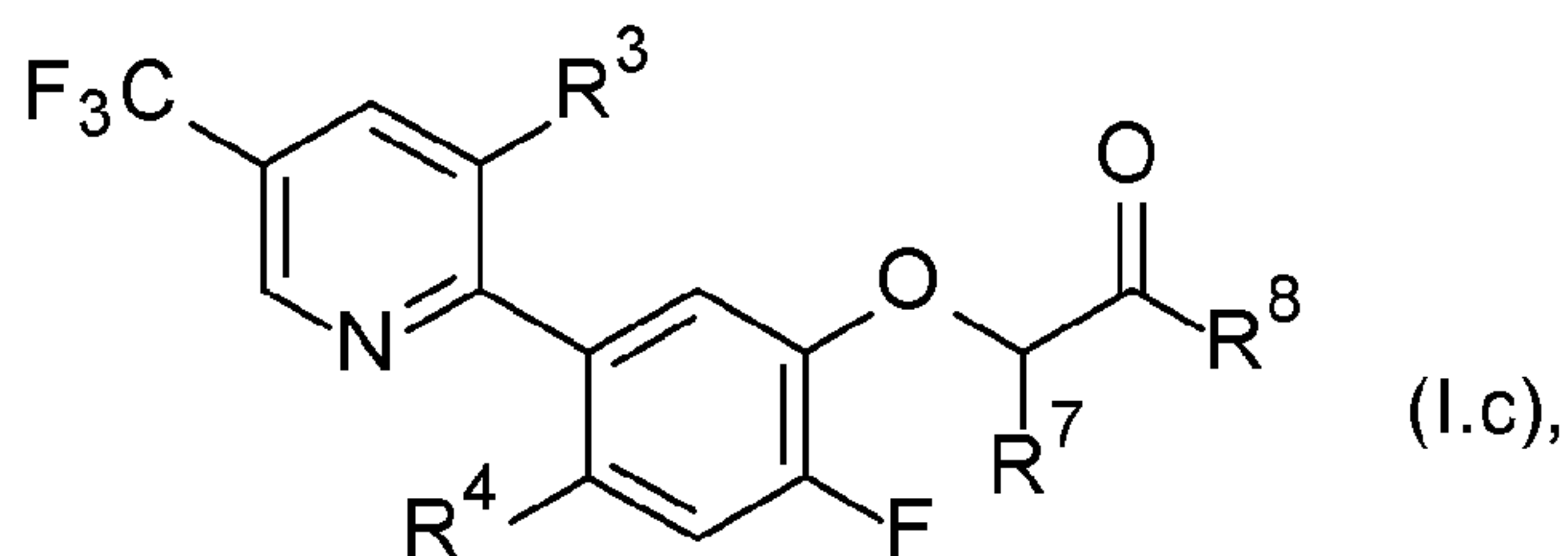
No.	R ³	R ⁴	R ⁷	R ⁸
I.a.219	Cl	F	OCH ₃	OCH(CH ₃)(CO)OCH ₂ CH ₃
I.a.220	Cl	F	OCH ₃	OC(CH ₃) ₂ (CO)OCH ₃
I.a.221	Cl	F	OCH ₃	OC(CH ₃) ₂ (CO)OCH ₂ CH ₃
I.a.222	Cl	F	OCH ₃	OCH ₂ -cyclopropyl
I.a.223	Cl	F	OCH ₃	OCH ₂ -cyclobutyl
I.a.224	Cl	F	OCH ₃	NHCH ₃
I.a.225	Cl	F	OCH ₃	N(CH ₃) ₂
I.a.226	Cl	F	OCH ₃	N(CH ₃)(CH ₂ CH ₃)
I.a.227	Cl	F	OCH ₃	N(CH ₂ CH ₃) ₂
I.a.228	Cl	F	OCH ₃	NHSO ₂ CH ₃
I.a.229	Cl	F	OCH ₃	NHSO ₂ CH ₂ CH ₃
I.a.230	Cl	F	OCH ₃	NHSO ₂ N(CH ₃) ₂
I.a.231	Cl	F	OCH ₃	NHSO ₂ N(CH ₃)[CH(CH ₃) ₂]
I.a.232	Cl	F	OCH ₂ CH ₃	OH
I.a.233	Cl	F	OCH ₂ CH ₃	OCH ₃
I.a.234	Cl	F	OCH ₂ CH ₃	OCH ₂ CH ₃
I.a.235	Cl	F	OCH ₂ CH ₃	OCH(CH ₃) ₂
I.a.236	Cl	F	OCH ₂ CH ₃	OCH ₂ CH ₂ CH ₃
I.a.237	Cl	F	OCH ₂ CH ₃	OCH ₂ CH(CH ₃) ₂
I.a.238	Cl	F	OCH ₂ CH ₃	OCH ₂ CH=CH ₂
I.a.239	Cl	F	OCH ₂ CH ₃	OCH ₃ C(CH ₃)=CH ₂
I.a.240	Cl	F	OCH ₂ CH ₃	OCH ₂ C≡CH
I.a.241	Cl	F	OCH ₂ CH ₃	OCH ₂ CF ₃
I.a.242	Cl	F	OCH ₂ CH ₃	OCH ₂ CHF ₂
I.a.243	Cl	F	OCH ₂ CH ₃	OCH ₂ OCH ₃
I.a.244	Cl	F	OCH ₂ CH ₃	OCH ₂ OCH ₂ CH ₃
I.a.245	Cl	F	OCH ₂ CH ₃	OCH ₂ CH ₂ OCH ₃
I.a.246	Cl	F	OCH ₂ CH ₃	OCH ₂ CH ₂ OCH ₂ CH ₃
I.a.247	Cl	F	OCH ₂ CH ₃	OCH ₂ CH ₂ CH ₂ OCH ₃
I.a.248	Cl	F	OCH ₂ CH ₃	OCH ₂ CH(OCH ₃) ₂
I.a.249	Cl	F	OCH ₂ CH ₃	OCH ₂ (CO)OCH ₃
I.a.250	Cl	F	OCH ₂ CH ₃	OCH ₂ (CO)OCH ₂ CH ₃
I.a.251	Cl	F	OCH ₂ CH ₃	OCH(CH ₃)(CO)OCH ₃
I.a.252	Cl	F	OCH ₂ CH ₃	OCH(CH ₃)(CO)OCH ₂ CH ₃
I.a.253	Cl	F	OCH ₂ CH ₃	OC(CH ₃) ₂ (CO)OCH ₃
I.a.254	Cl	F	OCH ₂ CH ₃	OC(CH ₃) ₂ (CO)OCH ₂ CH ₃
I.a.255	Cl	F	OCH ₂ CH ₃	OCH ₂ -cyclopropyl
I.a.256	Cl	F	OCH ₂ CH ₃	OCH ₂ -cyclobutyl
I.a.257	Cl	F	OCH ₂ CH ₃	NHCH ₃

No.	R ³	R ⁴	R ⁷	R ⁸
I.a.258	Cl	F	OCH ₂ CH ₃	N(CH ₃) ₂
I.a.259	Cl	F	OCH ₂ CH ₃	N(CH ₃)(CH ₂ CH ₃)
I.a.260	Cl	F	OCH ₂ CH ₃	N(CH ₂ CH ₃) ₂
I.a.261	Cl	F	OCH ₂ CH ₃	NHSO ₂ CH ₃
I.a.262	Cl	F	OCH ₂ CH ₃	NHSO ₂ CH ₂ CH ₃
I.a.263	Cl	F	OCH ₂ CH ₃	NHSO ₂ N(CH ₃) ₂
I.a.264	Cl	F	OCH ₂ CH ₃	NHSO ₂ N(CH ₃)[CH(CH ₃) ₂]

Also preferred are the phenylpyridines of formula (I.b), particularly preferred the phenylpyridines of formulae (I.b.1) to (I.b.264), which differ from the corresponding phenylpyridines of formulae (I.a) as well as (I.a.1) to (I.a.264) only in that R⁵ is CN:



Also preferred are the phenylpyridines of formula (I.c), particularly preferred the phenylpyridines of formulae (I.c.1) to (I.c.264), which differ from the corresponding phenylpyridines of formulae (I.a) as well as (I.a.1) to (I.a.264) only in that R⁵ is F:



To widen the spectrum of action and to achieve synergistic effects, the phenylpyridines of formula (I) may be mixed with a large number of representatives of other herbicidal or growth-regulating active ingredient groups and then applied concomitantly. Suitable components for mixtures are, for example, herbicides from the classes of the acetamides, amides, aryloxyphenoxypropionates, benzamides, benzofuran, benzoic acids, benzothiadiazinones, bipyridylum, carbamates, chloroacetamides, chlorocarboxylic acids, cyclohexanediones, dinitroanilines, dinitrophenol, diphenyl ether, glycines, imidazolinones, isoxazoles, isoxazolidinones, nitriles, N-phenylphthalimides, oxadiazoles, oxazolidinediones, oxyacetamides, phenoxycarboxylic acids, phenylcarbamates, phenylpyrazoles, phenylpyrazolines, phenylpyridazines, phosphinic acids, phosphoroamidates, phosphorodithioates, phthalamates, pyrazoles, pyridazinones,

pyridines, pyridinecarboxylic acids, pyridinecarboxamides, pyrimidinediones, pyrimidinyl(thio)benzoates, quinolinecarboxylic acids, semicarbazones, sulfonylaminocarbonyltriazolinones, sulfonylureas, tetrazolinones, thiadiazoles, thiocarbamates, triazines, triazinones, triazoles, triazolinones, triazolocarbonylcarboxamides, triazolopyrimidines, triketones, uracils, ureas.

It may furthermore be beneficial to apply the phenylpyridines of formula (I) alone or in combination with other herbicides, or else in the form of a mixture with other crop protection agents, for example together with agents for controlling pests or phytopathogenic fungi or bacteria. Also of interest is the miscibility with mineral salt solutions, which are employed for treating nutritional and trace element deficiencies. Other additives such as non-phytotoxic oils and oil concentrates may also be added.

In one embodiment of the present invention the compositions disclosed herein comprise at least one phenylpyridine of formula (I) (compound A) and at least one further active compound selected from herbicides B, preferably herbicides B of class b1) to b15), and safeners C (compound C).

In another embodiment of the present invention the compositions according to the present invention comprise at least one phenylpyridine of formula (I) and at least one further active compound B (herbicide B).

The further herbicidal compound B (component B) is preferably selected from the herbicides of class b1) to b15):

B) herbicides of class b1) to b15):

- b1) lipid biosynthesis inhibitors;
- b2) acetolactate synthase inhibitors (ALS inhibitors);
- b3) photosynthesis inhibitors;
- b4) protoporphyrinogen-IX oxidase inhibitors,
- b5) bleacher herbicides;
- b6) enolpyruvyl shikimate 3-phosphate synthase inhibitors (EPSP inhibitors);
- b7) glutamine synthetase inhibitors;
- b8) 7,8-dihydropteroate synthase inhibitors (DHP inhibitors);
- b9) mitosis inhibitors;
- b10) inhibitors of the synthesis of very long chain fatty acids (VLCFA inhibitors);
- b11) cellulose biosynthesis inhibitors;
- b12) decoupler herbicides;
- b13) auxinic herbicides;
- b14) auxin transport inhibitors; and
- b15) other herbicides selected from the group consisting of bromobutide,

chlorflurenol, chlorflurenol-methyl, cinmethylin, cumyluron, dalapon, dazomet, difenzoquat, difenzoquat-metilsulfate, dimethipin, DSMA, dymron, endothal and its salts, etobenzanid, flamprop, flamprop-isopropyl, flamprop-methyl, flamprop-M-isopropyl, flamprop-M-methyl, flurenol, flurenol-butyl, flurprimidol, fosamine, fosamine-ammonium, indanofan, indaziflam, maleic hydrazide, mefluidide, metam, methiozolin (CAS 403640-27-7), methyl azide, methyl bromide, methyl-dymron, methyl iodide, MSMA, oleic acid, oxaziclomefone, pelargonic acid, pyributicarb, quinoclamine, triaziflam, tridiphane and 6-chloro-3-(2-cyclopropyl-6-methylphenoxy)-4-pyridazinol (CAS 499223-49-3) and its salts and esters;

including their agriculturally acceptable salts or derivatives.

Preference is given to those compositions according to the present invention comprising at least one herbicide B selected from herbicides of class b2, b3, b4, b5, b6, B7, b9 b10 and b13.

Specific preference is given to those compositions according to the present invention which comprise at least one herbicide B selected from the herbicides of class b4, b6, b7, b9, b10 and b13.

Particular preference is given to those compositions according to the present invention which comprise at least one herbicide B selected from the herbicides of class b4, b6, b10 and b13.

Examples of herbicides B which can be used in combination with the phenylpyridines of formula (I) according to the present invention are:

b1) from the group of the lipid biosynthesis inhibitors:
ACC-herbicides such as alloxydim, alloxydim-sodium, butroxydim, clethodim, clodinafop, clodinafop-propargyl, cycloxydim, cyhalofop, cyhalofop-butyl, diclofop, diclofop-methyl, fenoxaprop, fenoxaprop-ethyl, fenoxaprop-P, fenoxaprop-P-ethyl, fluazifop, fluazifop-butyl, fluazifop-P, fluazifop-P-butyl, haloxyfop, haloxyfop-methyl, haloxyfop-P, haloxyfop-P-methyl, metamifop, pinoxaden, profoxydim, propaquizafop, quizalofop, quizalofop-ethyl, quizalofop-tefuryl, quizalofop-P, quizalofop-P-ethyl, quizalofop-P-tefuryl, sethoxydim, tepraloxym, tralkoxydim, 4-(4'-Chloro-4-cyclopropyl-2'-fluoro[1,1'-biphenyl]-3-yl)-5-hydroxy-2,2,6,6-tetramethyl-2H-pyran-3(6H)-one (CAS 1312337-72-6); 4-(2',4'-Dichloro-4-cyclopropyl[1,1'-biphenyl]-3-yl)-5-hydroxy-2,2,6,6-tetramethyl-2H-pyran-3(6H)-one (CAS 1312337-45-3); 4-(4'-Chloro-4-ethyl-2'-fluoro[1,1'-biphenyl]-3-yl)-5-hydroxy-2,2,6,6-tetramethyl-2H-pyran-3(6H)-one (CAS 1033757-93-5); 4-(2',4'-Dichloro-4-ethyl[1,1'-biphenyl]-3-yl)-2,2,6,6-

tetramethyl-2H-pyran-3,5(4H,6H)-dione (CAS 1312340-84-3); 5-(Acetyloxy)-4-(4'-chloro-4-cyclopropyl-2'-fluoro[1,1'-biphenyl]-3-yl)-3,6-dihydro-2,2,6,6-tetramethyl-2H-pyran-3-one (CAS 1312337-48-6); 5-(Acetyloxy)-4-(2',4'-dichloro-4-cyclopropyl- [1,1'-biphenyl]-3-yl)-3,6-dihydro-2,2,6,6-tetramethyl-2H-pyran-3-one; 5-(Acetyloxy)-4-(4'-chloro-4-ethyl-2'-fluoro[1,1'-biphenyl]-3-yl)-3,6-dihydro-2,2,6,6-tetramethyl-2H-pyran-3-one (CAS 1312340-82-1); 5-(Acetyloxy)-4-(2',4'-dichloro-4-ethyl[1,1'-biphenyl]-3-yl)-3,6-dihydro-2,2,6,6-tetramethyl-2H-pyran-3-one (CAS 1033760-55-2); 4-(4'-Chloro-4-cyclopropyl-2'-fluoro[1,1'-biphenyl]-3-yl)-5,6-dihydro-2,2,6,6-tetramethyl-5-oxo-2H-pyran-3-yl carbonic acid methyl ester (CAS 1312337-51-1); 4-(2',4'-Dichloro -4-cyclopropyl- [1,1'-biphenyl]-3-yl)-5,6-dihydro-2,2,6,6-tetramethyl-5-oxo-2H-pyran-3-yl carbonic acid methyl ester; 4-(4'-Chloro-4-ethyl-2'-fluoro[1,1'-biphenyl]-3-yl)-5,6-dihydro-2,2,6,6-tetramethyl-5-oxo-2H-pyran-3-yl carbonic acid methyl ester (CAS 1312340-83-2); 4-(2',4'-Dichloro-4-ethyl[1,1'-biphenyl]-3-yl)-5,6-dihydro-2,2,6,6-tetramethyl-5-oxo-2H-pyran-3-yl carbonic acid methyl ester (CAS 1033760-58-5); and non ACC herbicides such as benfuresate, butylate, cycloate, dalapon, dimepiperate, EPTC, esprocarb, ethofumesate, flupropanate, molinate, orbencarb, pebulate, prosulfocarb, TCA, thiobencarb, tiocarbazil, triallate and vernolate;

b2) from the group of the ALS inhibitors:

sulfonylureas such as amidosulfuron, azimsulfuron, bensulfuron, bensulfuron-methyl, chlorimuron, chlorimuron-ethyl, chlorsulfuron, cinosulfuron, cyclosulfamuron, ethametsulfuron, ethametsulfuron-methyl, ethoxysulfuron, flazasulfuron, flucetosulfuron, flupyrsulfuron, flupyrsulfuron-methyl-sodium, foramsulfuron, halosulfuron, halosulfuron-methyl, imazosulfuron, iodosulfuron, iodosulfuron-methyl-sodium, iofensulfuron, iofensulfuron-sodium, mesosulfuron, metazosulfuron, metsulfuron, metsulfuron-methyl, nicosulfuron, orthosulfamuron, oxasulfuron, primisulfuron, primisulfuron-methyl, propyrisulfuron, prosulfuron, pyrazosulfuron, pyrazosulfuron-ethyl, rimsulfuron, sulfometuron, sulfometuron-methyl, sulfosulfuron, thifensulfuron, thifensulfuron-methyl, triasulfuron, tribenuron, tribenuron-methyl, trifloxysulfuron, triflusulfuron, triflusulfuron-methyl and tritosulfuron, imidazolinones such as imazamethabenz, imazamethabenz-methyl, imazamox, imazapic, imazapyr, imazaquin and imazethapyr, triazolopyrimidine herbicides and sulfonanilides such as cloransulam, cloransulam-methyl, diclosulam, flumetsulam, florasulam, metosulam, penoxsulam, pyrimisulfan and pyroxsulam, pyrimidinylbenzoates such as bispyribac, bispyribac-sodium, pyribenzoxim, pyriftalid, pyriminobac, pyriminobac-methyl, pyriithiobac, pyriithiobac-sodium, 4-[[[2-[(4,6-dimethoxy-2-pyrimidinyl)oxy]phenyl]methyl]amino]-benzoic acid-1-methylethyl ester (CAS 420138-41-6), 4-[[[2-[(4,6-dimethoxy-2-pyrimidinyl)oxy]phenyl]methyl]amino]-benzoic acid propyl ester (CAS 420138-40-5), N-(4-bromophenyl)-2-[(4,6-dimethoxy-2-pyrimidinyl)oxy]benzenemethanamine (CAS 420138-01-8), sulfonylaminocarbonyl-triazolinone herbicides such as flucarbazone, flucarbazone-sodium, propoxycarbazon, propoxycarbazon-sodium, thienicarbazone and thienicarbazone-methyl; and triafamone;

among these, a preferred embodiment of the invention relates to those compositions comprising at least one imidazolinone herbicide;

b3) from the group of the photosynthesis inhibitors:

- 5 amicarbazone, inhibitors of the photosystem II, e.g. triazine herbicides, including of chlorotriazine, triazinones, triazindiones, methylthiotriazines and pyridazinones such as ametryn, atrazine, chloridazone, cyanazine, desmetryn, dimethametryn, hexazinone, metribuzin, prometon, prometryn, propazine, simazine, simetryn, terbumeton, terbuthylazin, terbutryn and trietazin, aryl urea such as chlorobromuron, chlorotoluron, chloroxuron,
- 10 dimefuron, diuron, fluometuron, isoproturon, isouron, linuron, metamitron, methabenzthiazuron, metobenzuron, metoxuron, monolinuron, neburon, siduron, tebuthiuron and thiadiazuron, phenyl carbamates such as desmedipham, karbutilat, phenmedipham, phenmedipham-ethyl, nitrile herbicides such as bromofenoxim, bromoxynil and its salts and esters, ioxynil and its salts and esters, uraciles such as bromacil, lenacil
- 15 and terbacil, and bentazon and bentazon-sodium, pyridate, pyridafol, pentanochlor and propanil and inhibitors of the photosystem I such as diquat, diquat-dibromide, paraquat, paraquat-dichloride and paraquat-dimetilsulfate. Among these, a preferred embodiment of the invention relates to those compositions comprising at least one aryl urea herbicide. Among these, likewise a preferred embodiment of the invention relates to those
- 20 compositions comprising at least one triazine herbicide. Among these, likewise a preferred embodiment of the invention relates to those compositions comprising at least one nitrile herbicide;

b4) from the group of the protoporphyrinogen-IX oxidase inhibitors:

- 25 acifluorfen, acifluorfen-sodium, azafenidin, bencarbazone, benzfendizone, bifenox, butafenacil, carfentrazone, carfentrazone-ethyl, chlomethoxyfen, cinidon-ethyl, fluazolate, flufenpyr, flufenpyr-ethyl, flumiclorac, flumiclorac-pentyl, flumioxazin, fluoroglycofen, fluoroglycofen-ethyl, fluthiacet, fluthiacet-methyl, fomesafen, halosafen, lactofen, oxadiargyl, oxadiazon, oxyfluorfen, pentoxazone, profluazol, pyraclonil, pyraflufen, pyraflufen-ethyl,
- 30 saflufenacil, sulfentrazone, thidiazimin, tiafenacil, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31-6; S-3100), N-ethyl-3-(2,6-dichloro-4-trifluoromethylphenoxy)-5-methyl-1*H*-pyrazole-1-carboxamide (CAS 452098-92-9), N-tetrahydrofurfuryl-3-(2,6-dichloro-4-trifluoromethylphenoxy)-5-methyl-1*H*-pyrazole-1-carboxamide (CAS 915396-43-9), N-ethyl-
- 35 3-(2-chloro-6-fluoro-4-trifluoromethylphenoxy)-5-methyl-1*H*-pyrazole-1-carboxamide (CAS 452099-05-7), N-tetrahydrofurfuryl-3-(2-chloro-6-fluoro-4-trifluoromethylphenoxy)-5-methyl-1*H*-pyrazole-1-carboxamide (CAS 452100-03-7), 3-[7-fluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2*H*-benzo[1,4]oxazin-6-yl]-1,5-dimethyl-6-thioxo-[1,3,5]triazinan-2,4-dione, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2*H*-
- 40 benzo[*b*][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione (CAS 1258836-72-4), 2-(2,2,7-Trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2*H*-benzo[1,4]oxazin-6-yl)-4,5,6,7-tetrahydro-isoindole-1,3-dione, 1-Methyl-6-trifluoromethyl-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2*H*-

benzo[1,4]oxazin-6-yl)-1H-pyrimidine-2,4-dione, methyl (*E*)-4-[2-chloro-5-[4-chloro-5-(difluoromethoxy)-1*H*-methyl-pyrazol-3-yl]-4-fluoro-phenoxy]-3-methoxy-but-2-enoate [CAS 948893-00-3], and 3-[7-Chloro-5-fluoro-2-(trifluoromethyl)-1H-benzimidazol-4-yl]-1-methyl-6-(trifluoromethyl)-1H-pyrimidine-2,4-dione (CAS 212754-02-4);

5

b5) from the group of the bleacher herbicides:

PDS inhibitors: beflubutamid, diflufenican, fluridone, flurochloridone, flurtamone, norflurazon, picolinafen, and 4-(3-trifluoromethylphenoxy)-2-(4-trifluoromethylphenyl)-pyrimidine (CAS 180608-33-7), HPPD inhibitors: benzobicyclon, benzofenap, clomazone, fenquintrione, isoxaflutole, mesotrione, pyrasulfotole, pyrazolynate, pyrazoxyfen, sulcotrione, tefuryltrione, tembotrione, topramezone and bicyclopyrone, bleacher, unknown target: aclonifen, amitrole and flumeturon;

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b6) from the group of the EPSP synthase inhibitors:

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glyphosate, glyphosate-isopropylammonium, glyposate-potassium and glyphosate-trimesium (sulfosate);

b7) from the group of the glutamine synthase inhibitors:

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bilanaphos (bialaphos), bilanaphos-sodium, glufosinate, glufosinate-P and glufosinate-ammonium;

b8) from the group of the DHP synthase inhibitors:

asulam;

25

b9) from the group of the mitosis inhibitors:

compounds of group K1: dinitroanilines such as benfluralin, butralin, dinitramine, ethalfluralin, fluchloralin, oryzalin, pendimethalin, prodiamine and trifluralin, phosphoramidates such as amiprofos, amiprofos-methyl, and butamipfos, benzoic acid herbicides such as chlorthal, chlorthal-dimethyl, pyridines such as dithiopyr and thiazopyr, benzamides such as propyzamide and tebutam; compounds of group K2: chlorpropham, propham and carbetamide, among these, compounds of group K1, in particular dinitroanilines are preferred;

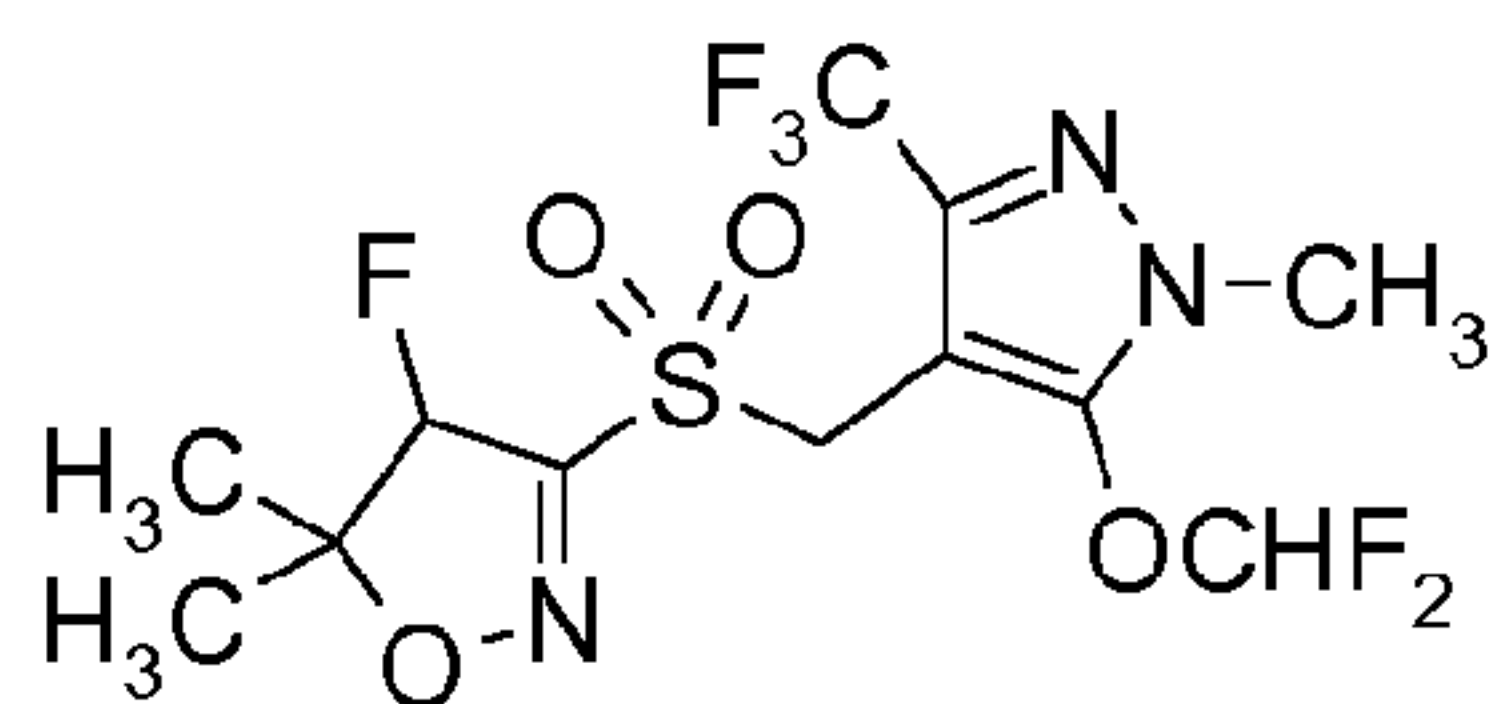
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b10) from the group of the VLCFA inhibitors:

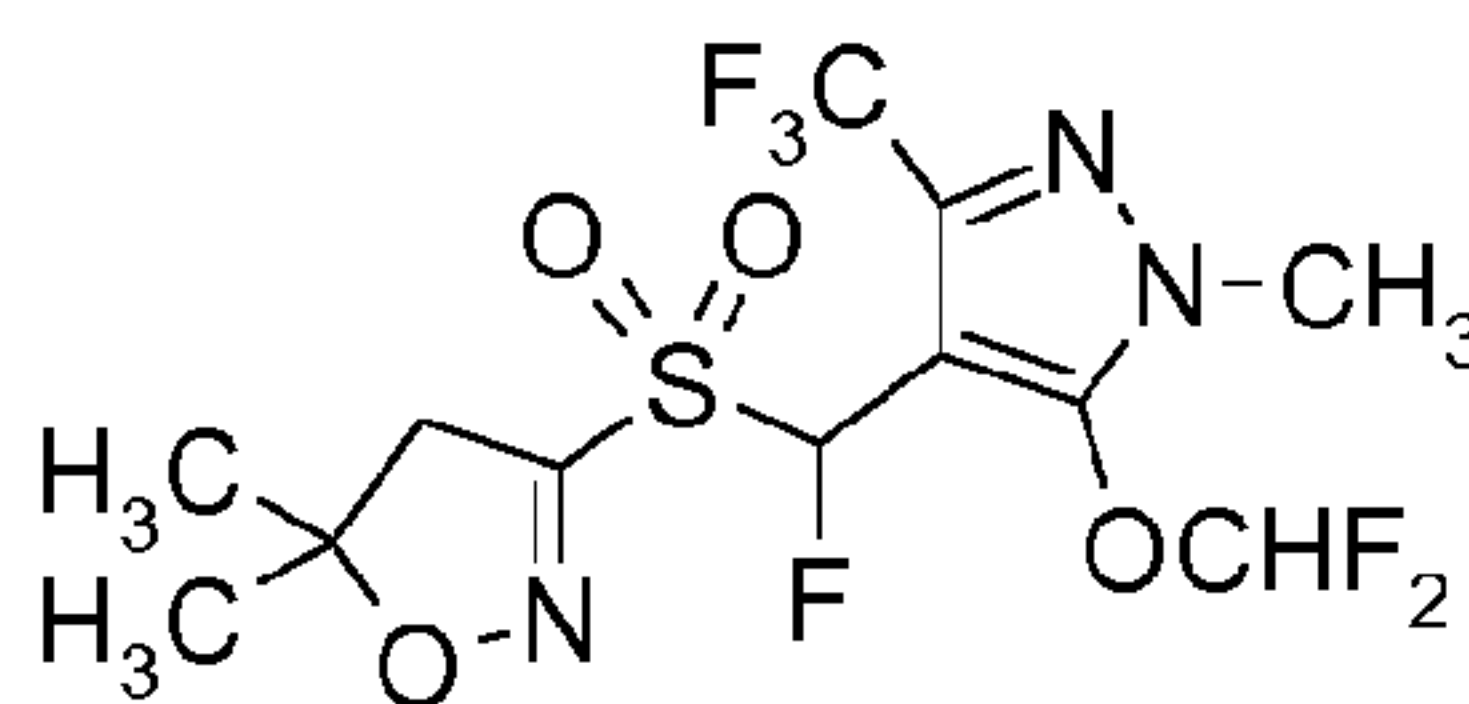
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chloroacetamides such as acetochlor, alachlor, butachlor, dimethachlor, dimethenamid, dimethenamid-P, metazachlor, metolachlor, metolachlor-S, pethoxamid, pretilachlor, propachlor, propisochlor and thenylchlor, oxyacetanilides such as flufenacet and mefenacet, acetanilides such as diphenamid, naproanilide, napropamide and napropamide-M, tetrazolinones such fentrazamide, and other herbicides such as anilofos, cafenstrole, fenoxasulfone, ipfencarbazone, piperophos, pyroxasulfone and isoxazoline compounds of the formulae II.1, II.2, II.3, II.4, II.5, II.6, II.7, II.8 and II.9

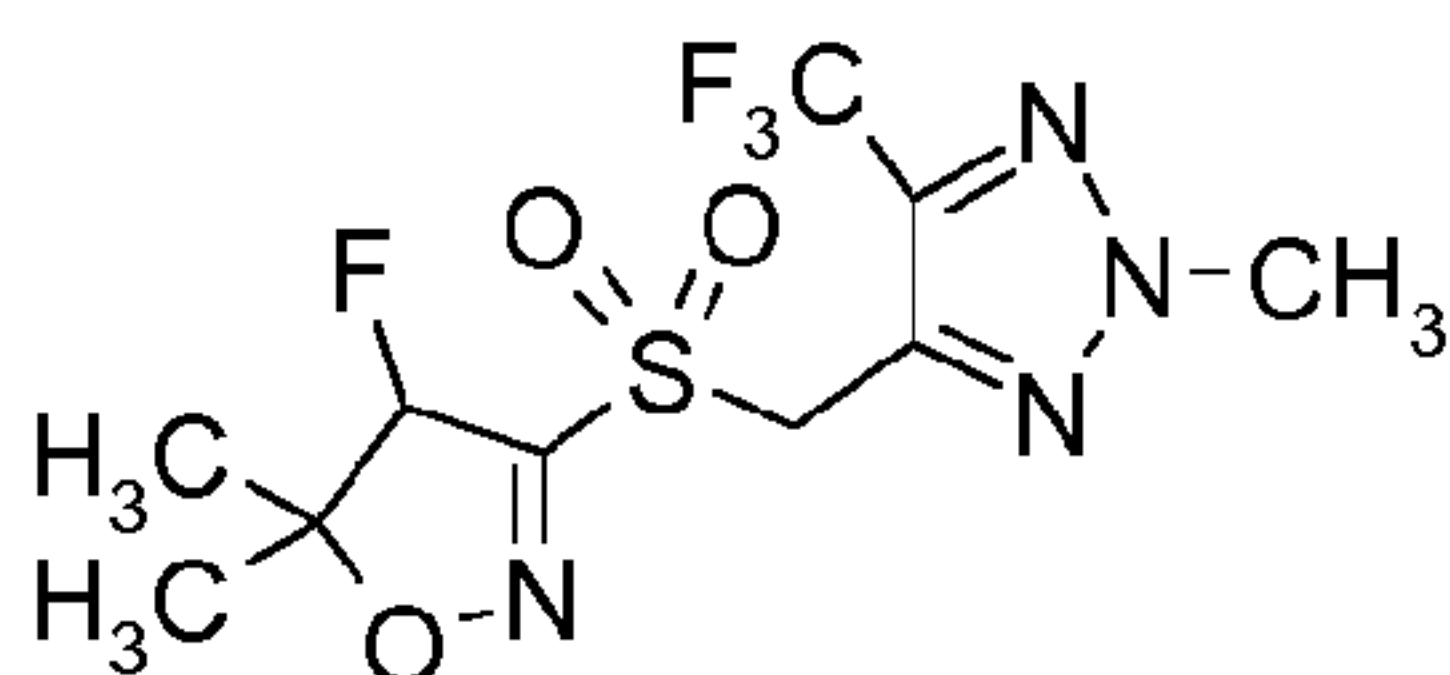
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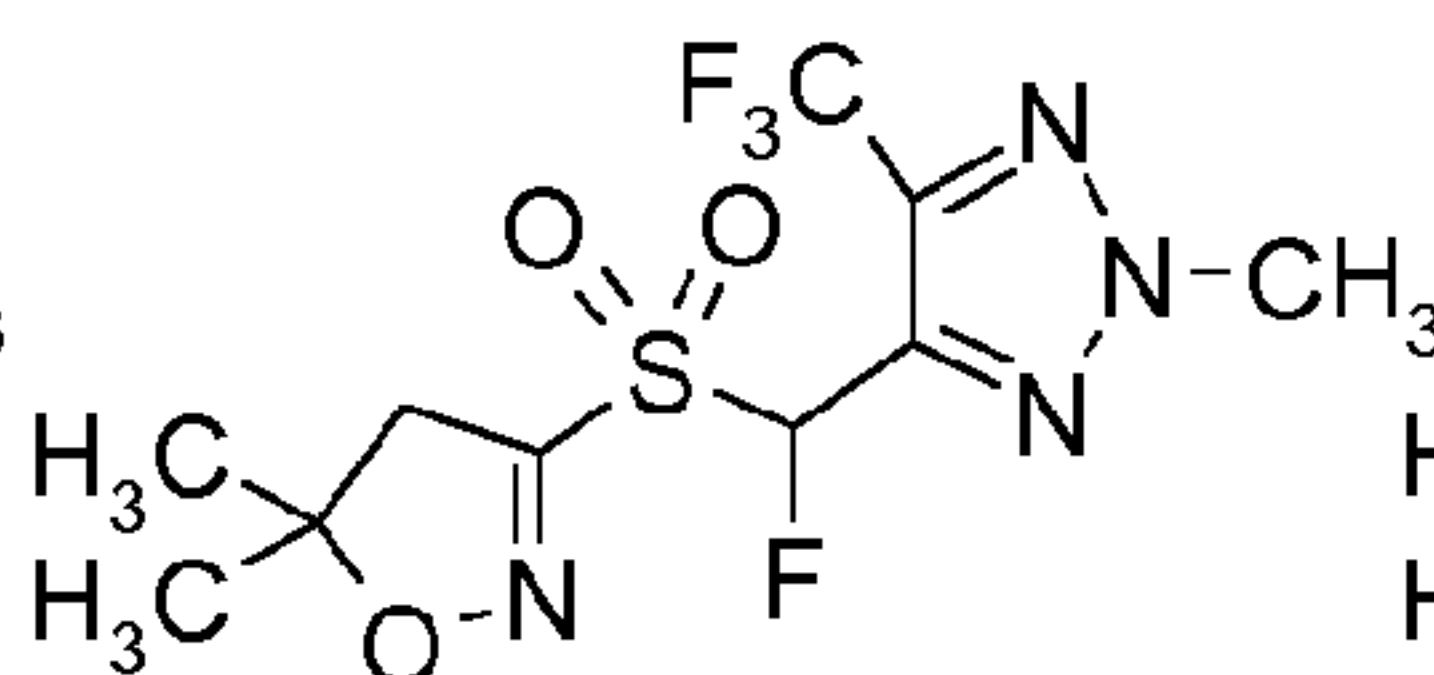
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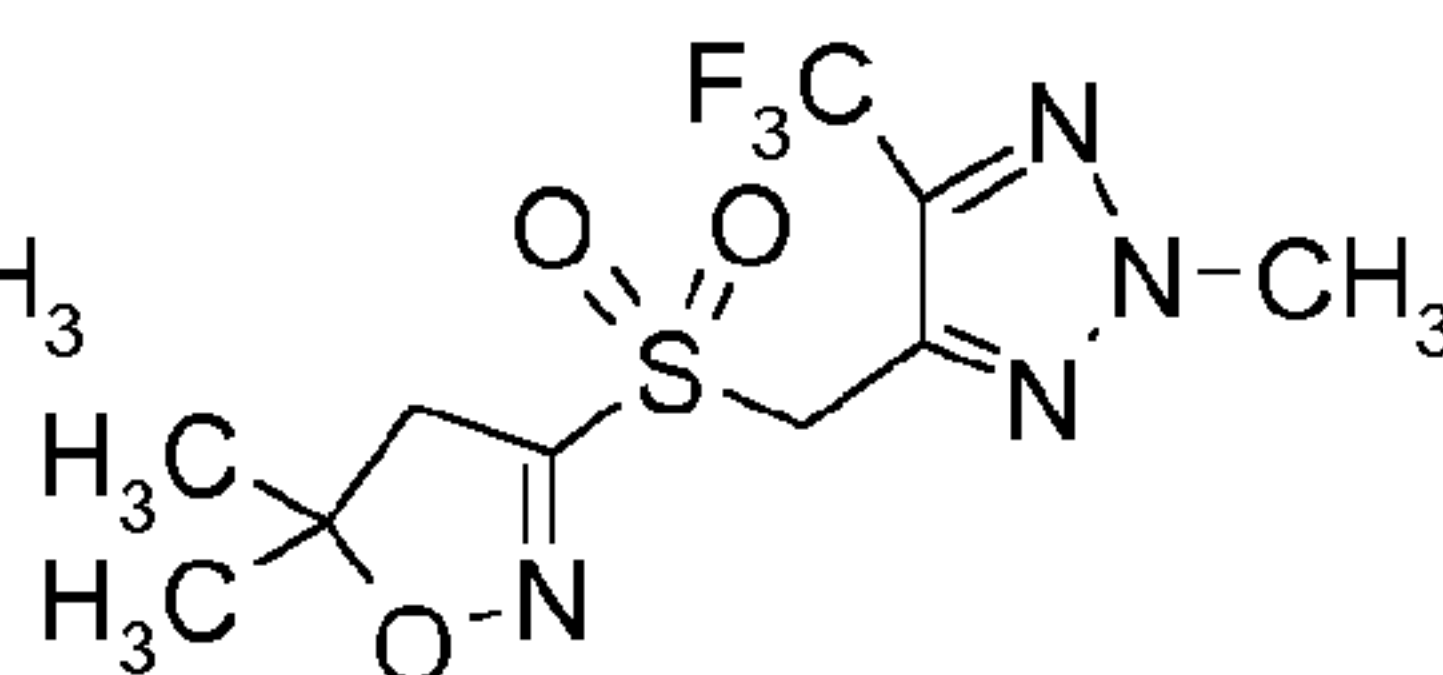
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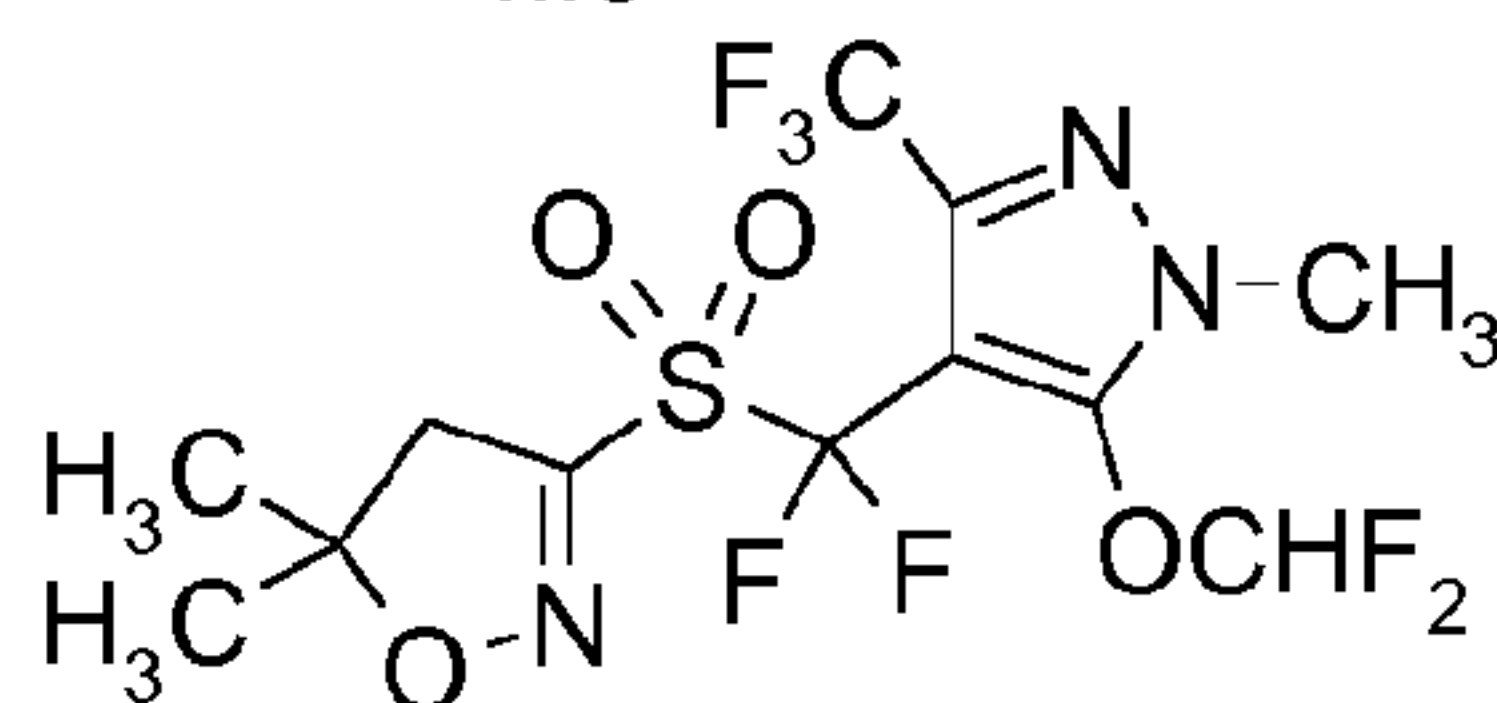
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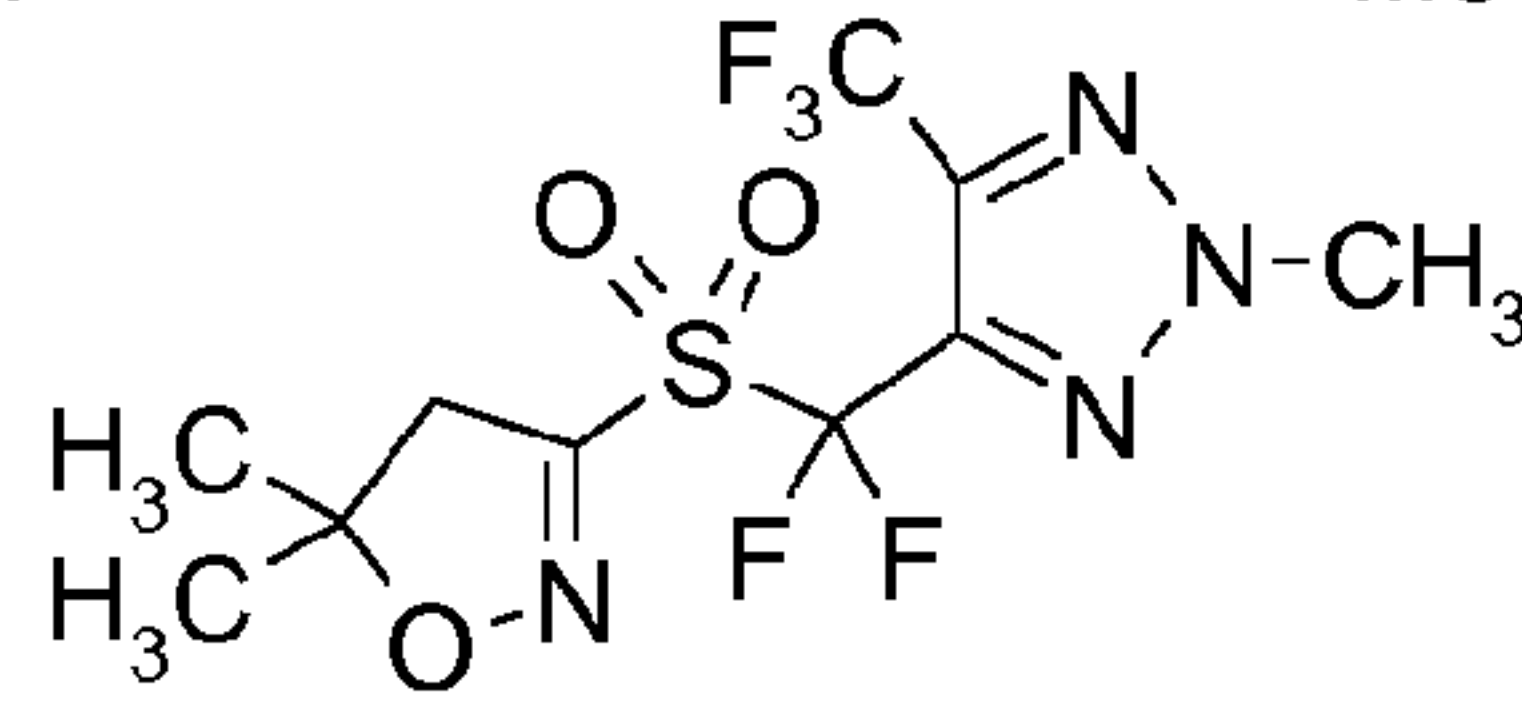
II.4



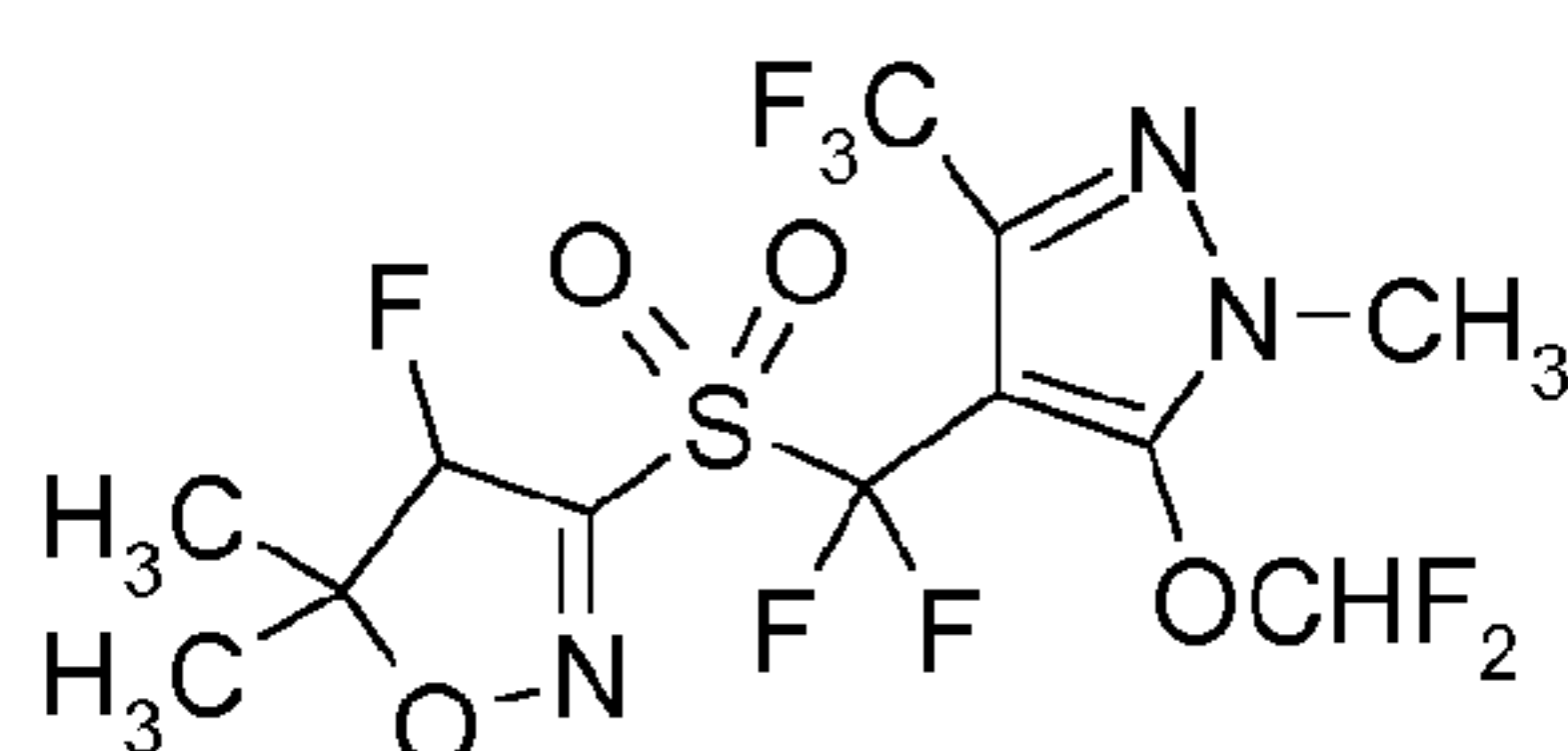
II.5



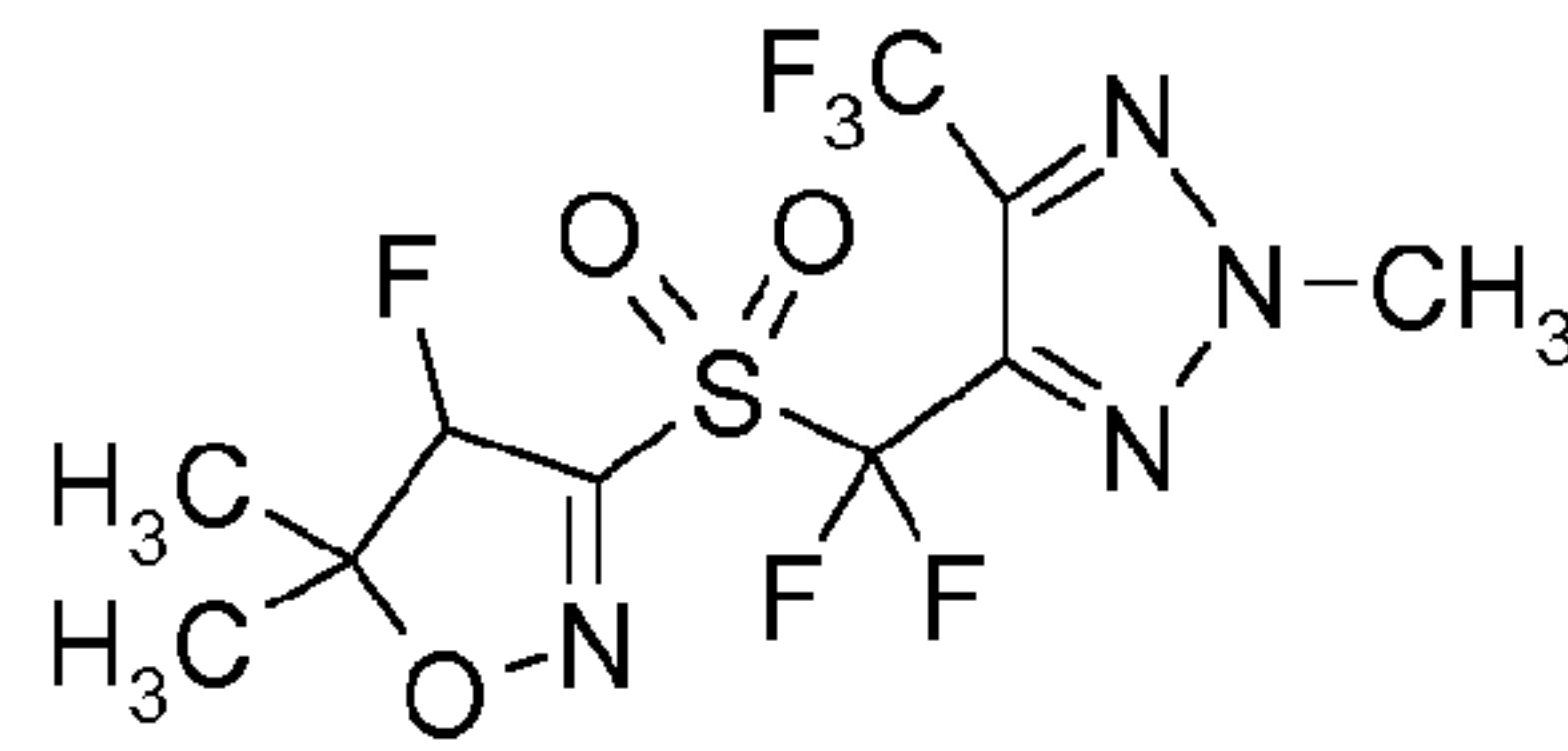
II.6



II.7



II.8



II.9

the isoxazoline compounds of the formula (I) are known in the art, e.g. from WO 2006/024820, WO 2006/037945, WO 2007/071900 and WO 2007/096576;

among the VLCFA inhibitors, preference is given to chloroacetamides and oxyacetamides;

b11) from the group of the cellulose biosynthesis inhibitors:

chlorthiamid, dichlobenil, flupoxam, isoxaben and 1-Cyclohexyl-5-pentafluorophenyl-14-[1,2,4,6]thiatriazin-3-ylamine;

b12) from the group of the decoupler herbicides:

dinoseb, dinoterb and DNOC and its salts;

b13) from the group of the auxinic herbicides:

2,4-D and its salts and esters such as clacyfos, 2,4-DB and its salts and esters, aminocyclopyrachlor and its salts and esters, aminopyralid and its salts such as aminopyralid-dimethylammonium, aminopyralid-tris(2-hydroxypropyl)ammonium and its

- esters, benazolin, benazolin-ethyl, chloramben and its salts and esters, clomeprop, clopyralid and its salts and esters, dicamba and its salts and esters, dichlorprop and its salts and esters, dichlorprop-P and its salts and esters, fluroxypyr, fluroxypyr-butometyl, fluroxypyr-meptyl, halauxifen and its salts and esters (CAS 943832-60-8); MCPA and its salts and esters, MCPA-thioethyl, MCPB and its salts and esters, mecoprop and its salts and esters, mecoprop-P and its salts and esters, picloram and its salts and esters, quinclorac, quinmerac, TBA (2,3,6) and its salts and esters and triclopyr and its salts and esters;
- 5 b14) from the group of the auxin transport inhibitors: diflufenzopyr, diflufenzopyr-sodium, naptalam and naptalam-sodium;
- b15) from the group of the other herbicides: bromobutide, chlorflurenol, chlorflurenol-methyl, cinmethylin, cumyluron, cyclopyrimorate (CAS 499223-49-3) and its salts and esters, dalapon, dazomet, difenzoquat, difenzoquat-metilsulfate, dimethipin, DSMA, dymron, 15 endothal and its salts, etobenzanid, flamprop, flamprop-isopropyl, flamprop-methyl, flamprop-M-isopropyl, flamprop-M-methyl, flurenol, flurenol-butyl, flurprimidol, fosamine, fosamine-ammonium, indanofan, indaziflam, maleic hydrazide, mefluidide, metam, methiozolin (CAS 403640-27-7), methyl azide, methyl bromide, methyl-dymron, methyl 20 iodide, MSMA, oleic acid, oxaziclomefone, pelargonic acid, pyributicarb, quinoclamine, triaziflam and tridiphan.

- Active compounds B and C having a carboxyl group can be employed in the form of the acid, in the form of an agriculturally suitable salt as mentioned above or else in the form of an agriculturally acceptable derivative in the compositions according to the invention.
- 25

- In the case of dicamba, suitable salts include those, where the counterion is an agriculturally acceptable cation. For example, suitable salts of dicamba are dicamba-sodium, dicamba-potassium, dicamba-methylammonium, dicamba-dimethylammonium, dicamba-isopropylammonium, dicamba-diglycolamine, dicamba-olamine, dicamba-diolamine, dicamba-trolamine, dicamba-N,N-bis-(3-aminopropyl)methylamine and dicamba-diethylenetriamine. Examples of a suitable ester are dicamba-methyl and dicamba-butotyl. Suitable salts of glyphosate are for example glyphosate-ammonium, glyphosate-diammonium, glyphosate-dimethylammonium, glyphosate-isopropylammonium, glyphosate-potassium, glyphosate-sodium, glyphosate-trimesium as well as the ethanolamine and diethanolamine salts, preferably glyphosate-diammonium, glyphosate-isopropylammonium and glyphosate-trimesium (sulfosate).
- 30
- 35

- A suitable salt of glufosinate is for example glufosinate-ammonium.
- 40 A suitable salt of glufosinate-P is for example glufosinate-P-ammonium.

Particularly preferred herbicides B are the herbicides B as defined above; in particular the herbicides B.1 - B.189 listed below in table B:

Table B:

	Herbicide B
A.1	clethodim
A.2	clodinafop-propargyl
A.3	cycloxydim
A.4	cyhalofop-butyl
A.5	fenoxaprop-ethyl
A.6	fenoxaprop-P-ethyl
A.7	metamifop
A.8	pinoxaden
A.9	profoxydim
A.10	sethoxydim
A.11	tepraloxydim
A.12	tralkoxydim
A.13	esprocarb
A.14	ethofumesate
A.15	molinate
A.16	prosulfocarb
A.17	thiobencarb
A.18	triallate
A.19	bensulfuron-methyl
A.20	bispyribac-sodium
A.21	cloransulam-methyl
A.22	chlorsulfuron
A.23	clorimuron
A.24	cyclosulfamuron
A.25	diclosulam
A.26	florasulam
A.27	flumetsulam
A.28	flupyrsulfuron-methyl-sodium
A.29	foramsulfuron
A.30	imazamox
A.31	imazamox-ammonium
A.32	imazapic
A.33	imazapic-ammonium
A.34	imazapic-isopropylammonium
A.35	imazapyr

	Herbicide B
A.36	imazapyr-ammonium
A.37	imazapyr-isopropylammonium
A.38	imazaquin
A.39	imazaquin-ammonium
A.40	imazethapyr
A.41	imazethapyr-ammonium
A.42	imazethapyr-isopropylammonium
A.43	imazosulfuron
A.44	iodosulfuron-methyl-sodium
A.45	iofensulfuron
A.46	iofensulfuron-sodium
A.47	mesosulfuron-methyl
A.48	metazosulfuron
A.49	metasulfuron-methyl
A.50	metosulam
A.51	nicosulfuron
A.52	penoxsulam
A.53	propoxycarbazon-sodium
A.54	pyrazosulfuron-ethyl
A.55	pyribenzoxim
A.56	pyriftalid
A.57	pyroxsulam
A.58	propyrisulfuron
A.59	rimsulfuron
A.60	sulfosulfuron
A.61	thiencarbazone-methyl
A.62	thifensulfuron-methyl
A.63	tribenuron-methyl
A.64	tritosulfuron
A.65	triafamone
A.66	ametryne
A.67	atrazine
A.68	bentazon
A.69	bromoxynil

	Herbicide B
A.70	bromoxynil-octanoate
A.71	bromoxynil-heptanoate
A.72	bromoxynil-potassium
A.73	diuron
A.74	fluometuron
A.75	hexazinone
A.76	isoproturon
A.77	linuron
A.78	metamitron
A.79	metribuzin
A.80	propanil
A.81	simazin
A.82	terbuthylazine
A.83	terbutryn
A.84	paraquat-dichloride
A.85	acifluorfen
A.86	butafenacil
A.87	carfentrazone-ethyl
A.88	flumioxazin
A.89	fomesafen
A.90	oxadiargyl
A.91	oxyfluorfen
A.92	saflufenacil
A.93	sulfentrazone
A.94	ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydro-pyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31-6)
A.95	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]-oxazin-6-yl)-1,3,5-triazinane-2,4-dione (CAS 1258836-72-4)
A.96	benzobicyclon
A.97	clomazone

	Herbicide B
A.98	diflufenican
A.99	flurochloridone
A.100	isoxaflutole
A.101	mesotrione
A.102	norflurazone
A.103	picolinafen
A.104	sulcotrione
A.105	tefuryltrione
A.106	tembotrione
A.107	topramezone
A.108	topramezone-sodium
A.109	bicyclopyrone
A.110	amitrole
A.111	fluometuron
A.112	fenquintrione
A.113	glyphosate
A.114	glyphosate-ammonium
A.115	glyphosate-dimethylammonium
A.116	glyphosate-isopropylammonium
A.117	glyphosate-trimesium (sulfosate)
A.118	glyphosate-potassium
A.119	glufosinate
A.120	glufosinate-ammonium
A.121	glufosinate-P
A.122	glufosinate-P-ammonium
A.123	pendimethalin
A.124	trifluralin
A.125	acetochlor
A.126	butachlor
A.127	cafenstrole
A.128	dimethenamid-P
A.129	fentrazamide
A.130	flufenacet
A.131	mefenacet
A.132	metazachlor

	Herbicide B
A.133	metolachlor
A.134	S-metolachlor
A.135	pretilachlor
A.136	fenoxasulfone
A.137	isoxaben
A.138	ipfencarbazone
A.139	pyroxasulfone
A.140	2,4-D
A.141	2,4-D-isobutyl
A.142	2,4-D-dimethylammonium
A.143	2,4-D-N,N,N-trimethylethanolammonium
A.144	aminopyralid
A.145	aminopyralid-methyl
A.146	aminopyralid-dimethyl-ammonium
A.147	aminopyralid-tris(2-hydroxypropyl)ammonium
A.148	clopyralid
A.149	clopyralid-methyl
A.150	clopyralid-olamine
A.151	dicamba
A.152	dicamba-butotyl
A.153	dicamba-diglycolamine
A.154	dicamba-dimethylammonium
A.155	dicamba-diolamine
A.156	dicamba-isopropylammonium
A.157	dicamba-potassium
A.158	dicamba-sodium
A.159	dicamba-trolamine
A.160	dicamba-N,N-bis-(3-aminopropyl)methylamine
A.161	dicamba-diethylenetriamine
A.162	fluroxypyr
A.163	fluroxypyr-meptyl
A.164	MCPA
A.165	MCPA-2-ethylhexyl
A.166	MCPA-dimethylammonium

	Herbicide B
A.167	quinclorac
A.168	quinclorac-dimethylammonium
A.169	quinmerac
A.170	quinmerac-dimethylammonium
A.171	aminocyclopyrachlor
A.172	aminocyclopyrachlor-potassium
A.173	aminocyclopyrachlor-methyl
A.174	diflufenzopyr
A.175	diflufenzopyr-sodium
A.176	dymron
A.177	indanofan
A.178	indaziflam
A.179	oxaziclomefone
A.180	triaziflam
A.181	II.1
A.182	II.2
A.183	II.3
A.184	II.4
A.185	II.5
A.186	II.6
A.187	II.7
A.188	II.8
A.189	II.9

Moreover, it may be useful to apply the phenylpyridines of formula (I) in combination with safeners. Safeners are chemical compounds which prevent or reduce damage on useful plants without having a major impact on the herbicidal action of the phenylpyridines of the formula (I) towards unwanted plants. They can be applied either before sowings (e.g. on seed treatments, shoots or seedlings) or in the pre-emergence application or post-emergence application of the useful plant.

The safeners and the phenylpyridines of formula (I) and optionally the herbicides B can be applied simultaneously or in succession.

In another embodiment of the present invention the compositions according to the present invention comprise at least one phenylpyridine of formula (I) and at least one safener C (component C).

Suitable safeners are e.g. (quinolin-8-oxy)acetic acids, 1-phenyl-5-haloalkyl-1H-1,2,4-triazol-3-carboxylic acids, 1-phenyl-4,5-dihydro-5-alkyl-1H-pyrazol-3,5-dicarboxylic acids, 4,5-dihydro-5,5-diaryl-3-isoxazol carboxylic acids, dichloroacetamides, alpha-oximinophenylacetoneitriles, acetophenonoximes, 4,6-dihalo-2-phenylpyrimidines, N-[[4-(aminocarbonyl)phenyl]sulfonyl]-2-benzoic amides, 1,8-naphthalic anhydride, 2-halo-4-(haloalkyl)-5-thiazol carboxylic acids, phosphorthiolates and N-alkyl-O-phenylcarbamates and their agriculturally acceptable salts and their agriculturally acceptable derivatives such amides, esters, and thioesters, provided they have an acid group.

Examples of preferred safeners C are benoxacor, cloquintocet, cyometrinil, cyprosulfamide, dichlormid, dicyclonon, dietholate, fenclorazole, fenclorim, flurazole, fluxofenim, furilazole, isoxadifen, mefenpyr, mephenate, naphthalic anhydride, oxabetrinil, 4-(dichloroacetyl)-1-oxa-4-azaspiro[4.5]decane (MON4660, CAS 71526-07-3), 2,2,5-trimethyl-3-(dichloroacetyl)-1,3-oxazolidine (R-29148, CAS 52836-31-4) and N-(2-Methoxybenzoyl)-4-[(methylaminocarbonyl)amino]benzenesulfonamide (CAS 129531-12-0).

Particularly preferred safeners C, which, as component C, are constituent of the composition according to the invention are the safeners C as defined above; in particular the safeners C.1 - C.17 listed below in table C:

Table C

	Safener C
C.1	benoxacor
C.2	cloquintocet
C.3	cloquintocet-mexyl
C.4	cyprosulfamide
C.5	dichlormid
C.6	fenchlorazole
C.7	fenchlorazole-ethyl
C.8	fencloirim
C.9	furilazole
C.10	isoxadifen
C.11	isoxadifen-ethyl
C.12	mefenpyr
C.13	mefenpyr-diethyl
C.14	naphtalic acid anhydride
C.15	4-(dichloroacetyl)-1-oxa-4-azaspiro[4.5]decane (MON4660, CAS 71526-07-3)
C.16	2,2,5-trimethyl-3-(dichloroacetyl)-1,3-oxazolidine (R-29148, CAS 52836-31-4)
C.17	N-(2-Methoxybenzoyl)-4-[(methylaminocarbonyl)amino]benzenesulfonamide (CAS 129531-12-0)

- The active compounds B of groups b1) to b15) and the active compounds C are known herbicides and safeners, see, for example, The Compendium of Pesticide Common Names (<http://www.alanwood.net/pesticides/>); Farm Chemicals Handbook 2000 volume 86, Meister Publishing Company, 2000; B. Hock, C. Fedtke, R. R. Schmidt, Herbizide [Herbicides], Georg Thieme Verlag, Stuttgart 1995; W. H. Ahrens, Herbicide Handbook, 7th edition, Weed Science Society of America, 1994; and K. K. Hatzios, Herbicide Handbook, Supplement for the 7th edition, Weed Science Society of America, 1998. 2,2,5-Trimethyl-3-(dichloroacetyl)-1,3-oxazolidine [CAS No. 52836-31-4] is also referred to as R-29148. 4-(Dichloroacetyl)-1-oxa-4-azaspiro[4.5]decane [CAS No. 71526-07-3] is also referred to as AD-67 and MON 4660.
- The assignment of the active compounds to the respective mechanisms of action is based on current knowledge. If several mechanisms of action apply to one active compound, this substance was only assigned to one mechanism of action.

According to a preferred embodiment of the invention, the composition comprises as herbicidal active compound B or component B at least one, preferably exactly one herbicide B.

5

According to another preferred embodiment of the invention, the composition comprises as herbicidal active compounds B or component B at least two, preferably exactly two herbicides B different from each other.

10 According to another preferred embodiment of the invention, the composition comprises as herbicidal active compounds B or component B at least three, preferably exactly three herbicides B different from each other.

15 According to another preferred embodiment of the invention, the composition comprises as herbicidal active compounds B or component B at least four, preferably exactly four herbicides B different from each other.

20 According to another preferred embodiment of the invention, the composition comprises as safening component C or component C at least one, preferably exactly one safener C.

25 According to another preferred embodiment of the invention, the composition comprises as component B at least one, preferably exactly one herbicide B, and as component C at least one, preferably exactly one, safener C.

According to another preferred embodiment of the invention, the composition comprises at least two, preferably exactly two, herbicides B different from each other, and as component C at least one, preferably exactly one, safener C.

30 According to another preferred embodiment of the invention, the composition comprises at least three, preferably exactly three, herbicides B different from each other, and as component C at least one, preferably exactly one, safener C.

35 According to another preferred embodiment of the invention, the composition comprises as component A at least one, preferably exactly one compound of formula (I), preferably of formula (I.a), especially preferred the compound (I.a.200), and as component B at least one, preferably exactly one, herbicide B.

40 According to another preferred embodiment of the invention, the composition comprises as component A at least one, preferably exactly one compound of

formula (I), preferably of formula (I.a), especially preferred the compound (I.a.200), and at least two, preferably exactly two, herbicides B different from each other.

5 According to another preferred embodiment of the invention, the composition comprises as component A at least one, preferably exactly one compound of formula (I), preferably of formula (I.a), especially preferred the compound (I.a.200), and at least three, preferably exactly three, herbicides B different from each other.

10 According to another preferred embodiment of the invention, the composition comprises as component A at least one, preferably exactly one compound of formula (I), preferably of formula (I.a), especially preferred the compound (I.a.200), and at least four, preferably exactly four, herbicides B different from each other.

15 According to another preferred embodiment of the invention, the composition comprises as component A at least one, preferably exactly one one compound of formula (I), preferably of formula (I.a), especially preferred the compound (I.a.200), and as component C at least one, preferably exactly one, safener C.

20 According to another preferred embodiment of the invention, the composition comprises as component A at least one, preferably exactly one compound of formula (I), preferably of formula (I.a), especially preferred the compound (I.a.200), as component B at least one, preferably exactly one, herbicide B, and as component C at least one, preferably exactly one safener C.

25 According to another preferred embodiment of the invention, the composition comprises as component A at least one, preferably exactly one compound of formula (I), preferably of formula (I.a), especially preferred the compound (I.a.200), at least two, preferably exactly two herbicides B different from each other, and as component C at least one, preferably exactly one, safener C.

30 According to another preferred embodiment of the invention, the composition comprises as component A at least one, preferably exactly one compound of formula (I), preferably of formula (I.a), especially preferred the compound (I.a.200), at least three, preferably exactly three herbicides B different from each other, and
35 as component C at least one, preferably exactly one, safener C.

According to another preferred embodiment of the invention, the composition comprises, in addition to a phenylpyridine of formula (I), especially an active
40 compound from the group consisting of (I.a.200), (I.a.207), (I.a.214), (I.a.228) and

(I.a.234), at least one and especially exactly one herbicidally active compound from group b4), in particular selected from the group consisting of flumioxazin, oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31-6; S-3100 , 3-[7-fluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[1,4]oxazin-6-yl]-1,5-dimethyl-6-thioxo-[1,3,5]triazinan-2,4-dione, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione (CAS 1258836-72-4), 2-(2,2,7-Trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1,4]oxazin-6-yl)-4,5,6,7-tetrahydro-isoindole-1,3-dione and 1-methyl-6-trifluoromethyl-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1,4]oxazin-6-yl)-1H-pyrimidine-2,4-dione.

According to another preferred embodiment of the invention, the composition comprises, in addition to a phenylpyridine of formula (I), especially an active compound from the group consisting of (I.a.200), (I.a.207), (I.a.214), (I.a.228) and (I.a.234), at least one and especially exactly one herbicidally active compound from group b6), in particular selected from the group consisting of glyphosate, glyphosate-isopropylammonium and glyphosate-trimesium (sulfosate).

According to another preferred embodiment of the invention, the composition comprises, in addition to a phenylpyridine of formula (I), especially an active compound from the group consisting of (I.a.200), (I.a.207), (I.a.214), (I.a.228) and (I.a.234), at least one and especially exactly one herbicidally active compound from group b7), in particular selected from the group consisting of glufosinate, glufosinate-P and glufosinate-ammonium.

According to another preferred embodiment of the invention, the composition comprises, in addition to a phenylpyridine of formula (I), especially an active compound from the group consisting of (I.a.200), (I.a.207), (I.a.214), (I.a.228) and (I.a.234), at least one and especially exactly one herbicidally active compound from group b10), in particular selected from the group consisting of acetochlor, cafenstrole, dimethenamid-P, fentrazamide, flufenacet, mefenacet, metazachlor, metolachlor, S-metolachlor, fenoxasulfone and pyroxasulfone. Likewise, preference is given to compositions comprising in addition to a phenylpyridine of formula (I), especially an active compound from the group consisting of (I.a.200), (I.a.207), (I.a.214), (I.a.228) and (I.a.234), at least one and especially exactly one herbicidally active compound from group b10), in particular selected from the group consisting of isoxazoline compounds of the formulae II.1, II.2, II.3, II.4, II.5, II.6, II.7, II.8 and II.9, as defined above.

According to another preferred embodiment of the invention, the composition comprises, in addition to a phenylpyridine of formula (I), especially an active compound from the group consisting of (I.a.200), (I.a.207), (I.a.214), (I.a.228) and
5 (I.a.234), at least one and especially exactly one herbicidally active compound from group b13), in particular selected from the group consisting of 2,4-D and its salts and esters, aminocyclopyrachlor and its salts and esters, aminopyralid and its salts such as aminopyralid-dimethylammonium, aminopyralid-tris(2-
hydroxypropyl)ammonium and its esters, clopyralid and its salts and esters,
10 dicamba and its salts and esters, fluroxypyr-meptyl, quinclorac and quinmerac.

Here and below, the term "binary compositions" includes compositions comprising one or more, for example 1, 2 or 3, active compounds of the formula (I) and either
15 one or more, for example 1, 2 or 3, herbicides B or one or more safeners C.

Correspondingly, the term "ternary compositions" includes compositions comprising one or more, for example 1, 2 or 3, active compounds of the formula (I), one or more, for example 1, 2 or 3, herbicides B and one or more, for example 1, 2 or 3,
20 safeners C.

In binary compositions comprising at least one compound of the formula (I) as component A and at least one herbicide B, the weight ratio of the active compounds A:B is generally in the range of from 1:1000 to 1000:1, preferably in the
25 range of from 1:500 to 500:1, in particular in the range of from 1:250 to 250:1 and particularly preferably in the range of from 1:75 to 75:1.

In binary compositions comprising at least one compound of the formula (I) as component A and at least one safener C, the weight ratio of the active compounds
30 A:C is generally in the range of from 1:1000 to 1000:1, preferably in the range of from 1:500 to 500:1, in particular in the range of from 1:250 to 250:1 and particularly preferably in the range of from 1:75 to 75:1.

In ternary compositions comprising at least one phenylpyridine of formula (I) as
35 component A, at least one herbicide B and at least one safener C, the relative proportions by weight of the components A:B are generally in the range of from 1:1000 to 1000:1, preferably in the range of from 1:500 to 500:1, in particular in the range of from 1:250 to 250:1 and particularly preferably in the range of from 1:75 to 75:1, the weight ratio of the components A:C is generally in the range of from
40 1:1000 to 1000:1, preferably in the range of from 1:500 to 500:1, in particular in the

range of from 1:250 to 250:1 and particularly preferably in the range of from 1:75 to 75:1, and the weight ratio of the components B:C is generally in the range of from 1:1000 to 1000:1, preferably in the range of from 1:500 to 500:1, in particular in the range of from 1:250 to 250:1 and particularly preferably in the range of from 1:75 to 75:1. The weight ratio of components A + B to component C is preferably in the range of from 1:500 to 500:1, in particular in the range of from 1:250 to 250:1 and particularly preferably in the range of from 1:75 to 75:1.

10 The weight ratios of the individual components in the preferred mixtures mentioned below are within the limits given herein, in particular within the preferred limits.

Particularly preferred are the compositions mentioned below comprising the phenylpyridines of formula (I) as defined and the substance(s) as defined in the respective row of table 1;
 15 especially preferred comprising as only herbicidal active compounds the phenylpyridines of formula (I) as defined and the substance(s) as defined in the respective row of table 1;
 most preferably comprising as only active compounds the phenylpyridines of formula (I) as defined and the substance(s) as defined in the respective row of table 1.
 20 1.

Particularly preferred are compositions 1.1 to 1.3419, comprising the phenylpyridine of formula (I.a.200) and the substance(s) as defined in the respective row of table 1:
 25

Table 1(compositions 1.1 to 1.3419):

comp. no.	herbi- cide B	safe- ner C	comp. no.	herbi- cide B	safe- ner C	comp. no.	herbi- cide B	safe- ner C
1.1	B.1	--	1.9	B.9	--	1.17	B.17	--
1.2	B.2	--	1.10	B.10	--	1.18	B.18	--
1.3	B.3	--	1.11	B.11	--	1.19	B.19	--
1.4	B.4	--	1.12	B.12	--	1.20	B.20	--
1.5	B.5	--	1.13	B.13	--	1.21	B.21	--
1.6	B.6	--	1.14	B.14	--	1.22	B.22	--
1.7	B.7	--	1.15	B.15	--	1.23	B.23	--
1.8	B.8	--	1.16	B.16	--	1.24	B.24	--

comp. no.	herbi- cide B	safe- ner C
1.25	B.25	--
1.26	B.26	--
1.27	B.27	--
1.28	B.28	--
1.29	B.29	--
1.30	B.30	--
1.31	B.31	--
1.32	B.32	--
1.33	B.33	--
1.34	B.34	--
1.35	B.35	--
1.36	B.36	--
1.37	B.37	--
1.38	B.38	--
1.39	B.39	--
1.40	B.40	--
1.41	B.41	--
1.42	B.42	--
1.43	B.43	--
1.44	B.44	--
1.45	B.45	--
1.46	B.46	--
1.47	B.47	--
1.48	B.48	--
1.49	B.49	--
1.50	B.50	--
1.51	B.51	--
1.52	B.52	--
1.53	B.53	--
1.54	B.54	--
1.55	B.55	--
1.56	B.56	--
1.57	B.57	--
1.58	B.58.	--
1.59	B.59	--
1.60	B.60	--

comp. no.	herbi- cide B	safe- ner C
1.61	B.61	--
1.62	B.62	--
1.63	B.63	--
1.64	B.64	--
1.65	B.65	--
1.66	B.66	--
1.67	B.67	--
1.68	B.68	--
1.69	B.69	--
1.70	B.70	--
1.71	B.71	--
1.72	B.72	--
1.73	B.73	--
1.74	B.74	--
1.75	B.75	--
1.76	B.76	--
1.77	B.77	--
1.78	B.78	--
1.79	B.79	--
1.80	B.80	--
1.81	B.81	--
1.82	B.82	--
1.83	B.83	--
1.84	B.84	--
1.85	B.85	--
1.86	B.86	--
1.87	B.87	--
1.88	B.88	--
1.89	B.89	--
1.90	B.90	--
1.91	B.91	--
1.92	B.92	--
1.93	B.93	--
1.94	B.94	--
1.95	B.95	--
1.96	B.96	--

comp. no.	herbi- cide B	safe- ner C
1.97	B.97	--
1.98	B.98	--
1.99	B.99	--
1.100	B.100	--
1.101	B.101	--
1.102	B.102	--
1.103	B.103	--
1.104	B.104	--
1.105	B.105	--
1.106	B.106	--
1.107	B.107	--
1.108	B.108	--
1.109	B.109	--
1.110	B.110	--
1.111	B.111	--
1.112	B.112	--
1.113	B.113	--
1.114	B.114	--
1.115	B.115	--
1.116	B.116	--
1.117	B.117	--
1.118	B.118	--
1.119	B.119	--
1.120	B.120	--
1.121	B.121	--
1.122	B.122	--
1.123	B.123	--
1.124	B.124	--
1.125	B.125	--
1.126	B.126	--
1.127	B.127	--
1.128	B.128	--
1.129	B.129	--
1.130	B.130	--
1.131	B.131	--
1.132	B.132	--

comp. no.	herbi- cide B	safe- ner C
1.133	B.133	--
1.134	B.134	--
1.135	B.135	--
1.136	B.136	--
1.137	B.137	--
1.138	B.138	--
1.139	B.139	--
1.140	B.140	--
1.141	B.141	--
1.142	B.142	--
1.143	B.143	--
1.144	B.144	--
1.145	B.145	--
1.146	B.146	--
1.147	B.147	--
1.148	B.148	--
1.149	B.149	--
1.150	B.150	--
1.151	B.151	--
1.152	B.152	--
1.153	B.153	--
1.154	B.154	--
1.155	B.155	--
1.156	B.156	--
1.157	B.157	--
1.158	B.158	--
1.159	B.159	--
1.160	B.160	--
1.161	B.161	--
1.162	B.162	--
1.163	B.163	--
1.164	B.164	--
1.165	B.165	--
1.166	B.166	--
1.167	B.167	--
1.168	B.168	--

comp. no.	herbi- cide B	safe- ner C
1.169	B.169	--
1.170	B.170	--
1.171	B.171	--
1.172	B.172	--
1.173	B.173	--
1.174	B.174	--
1.175	B.175	--
1.176	B.176	--
1.177	B.177	--
1.178	B.178	--
1.179	B.179	--
1.180	B.180	--
1.181	B.181	--
1.182	B.182	--
1.183	B.183	--
1.184	B.184	--
1.185	B.185	--
1.186	B.186	--
1.187	B.187	--
1.188	B.188	--
1.189	B.189	--
1.190	B.1	C.1
1.191	B.2	C.1
1.192	B.3	C.1
1.193	B.4	C.1
1.194	B.5	C.1
1.195	B.6	C.1
1.196	B.7	C.1
1.197	B.8	C.1
1.198	B.9	C.1
1.199	B.10	C.1
1.200	B.11	C.1
1.201	B.12	C.1
1.202	B.13	C.1
1.203	B.14	C.1
1.204	B.15	C.1

comp. no.	herbi- cide B	safe- ner C
1.205	B.16	C.1
1.206	B.17	C.1
1.207	B.18	C.1
1.208	B.19	C.1
1.209	B.20	C.1
1.210	B.21	C.1
1.211	B.22	C.1
1.212	B.23	C.1
1.213	B.24	C.1
1.214	B.25	C.1
1.215	B.26	C.1
1.216	B.27	C.1
1.217	B.28	C.1
1.218	B.29	C.1
1.219	B.30	C.1
1.220	B.31	C.1
1.221	B.32	C.1
1.222	B.33	C.1
1.223	B.34	C.1
1.224	B.35	C.1
1.225	B.36	C.1
1.226	B.37	C.1
1.227	B.38	C.1
1.228	B.39	C.1
1.229	B.40	C.1
1.230	B.41	C.1
1.231	B.42	C.1
1.232	B.43	C.1
1.233	B.44	C.1
1.234	B.45	C.1
1.235	B.46	C.1
1.236	B.47	C.1
1.237	B.48	C.1
1.238	B.49	C.1
1.239	B.50	C.1
1.240	B.51	C.1

WO 2018/019860

PCT/EP2017/068817

60

comp. no.	herbi- cide B	safe- ner C
1.241	B.52	C.1
1.242	B.53	C.1
1.243	B.54	C.1
1.244	B.55	C.1
1.245	B.56	C.1
1.246	B.57	C.1
1.247	B.58.	C.1
1.248	B.59	C.1
1.249	B.60	C.1
1.250	B.61	C.1
1.251	B.62	C.1
1.252	B.63	C.1
1.253	B.64	C.1
1.254	B.65	C.1
1.255	B.66	C.1
1.256	B.67	C.1
1.257	B.68	C.1
1.258	B.69	C.1
1.259	B.70	C.1
1.260	B.71	C.1
1.261	B.72	C.1
1.262	B.73	C.1
1.263	B.74	C.1
1.264	B.75	C.1
1.265	B.76	C.1
1.266	B.77	C.1
1.267	B.78	C.1
1.268	B.79	C.1
1.269	B.80	C.1
1.270	B.81	C.1
1.271	B.82	C.1
1.272	B.83	C.1
1.273	B.84	C.1
1.274	B.85	C.1
1.275	B.86	C.1
1.276	B.87	C.1

comp. no.	herbi- cide B	safe- ner C
1.277	B.88	C.1
1.278	B.89	C.1
1.279	B.90	C.1
1.280	B.91	C.1
1.281	B.92	C.1
1.282	B.93	C.1
1.283	B.94	C.1
1.284	B.95	C.1
1.285	B.96	C.1
1.286	B.97	C.1
1.287	B.98	C.1
1.288	B.99	C.1
1.289	B.100	C.1
1.290	B.101	C.1
1.291	B.102	C.1
1.292	B.103	C.1
1.293	B.104	C.1
1.294	B.105	C.1
1.295	B.106	C.1
1.296	B.107	C.1
1.297	B.108	C.1
1.298	B.109	C.1
1.299	B.110	C.1
1.300	B.111	C.1
1.301	B.112	C.1
1.302	B.113	C.1
1.303	B.114	C.1
1.304	B.115	C.1
1.305	B.116	C.1
1.306	B.117	C.1
1.307	B.118	C.1
1.308	B.119	C.1
1.309	B.120	C.1
1.310	B.121	C.1
1.311	B.122	C.1
1.312	B.123	C.1

comp. no.	herbi- cide B	safe- ner C
1.313	B.124	C.1
1.314	B.125	C.1
1.315	B.126	C.1
1.316	B.127	C.1
1.317	B.128	C.1
1.318	B.129	C.1
1.319	B.130	C.1
1.320	B.131	C.1
1.321	B.132	C.1
1.322	B.133	C.1
1.323	B.134	C.1
1.324	B.135	C.1
1.325	B.136	C.1
1.326	B.137	C.1
1.327	B.138	C.1
1.328	B.139	C.1
1.329	B.140	C.1
1.330	B.141	C.1
1.331	B.142	C.1
1.332	B.143	C.1
1.333	B.144	C.1
1.334	B.145	C.1
1.335	B.146	C.1
1.336	B.147	C.1
1.337	B.148	C.1
1.338	B.149	C.1
1.339	B.150	C.1
1.340	B.151	C.1
1.341	B.152	C.1
1.342	B.153	C.1
1.343	B.154	C.1
1.344	B.155	C.1
1.345	B.156	C.1
1.346	B.157	C.1
1.347	B.158	C.1
1.348	B.159	C.1

WO 2018/019860

PCT/EP2017/068817

61

comp. no.	herbi- cide B	safe- ner C
1.349	B.160	C.1
1.350	B.161	C.1
1.351	B.162	C.1
1.352	B.163	C.1
1.353	B.164	C.1
1.354	B.165	C.1
1.355	B.166	C.1
1.356	B.167	C.1
1.357	B.168	C.1
1.358	B.169	C.1
1.359	B.170	C.1
1.360	B.171	C.1
1.361	B.172	C.1
1.362	B.173	C.1
1.363	B.174	C.1
1.364	B.175	C.1
1.365	B.176	C.1
1.366	B.177	C.1
1.367	B.178	C.1
1.368	B.179	C.1
1.369	B.180	C.1
1.370	B.181	C.1
1.371	B.182	C.1
1.372	B.183	C.1
1.373	B.184	C.1
1.374	B.185	C.1
1.375	B.186	C.1
1.376	B.187	C.1
1.377	B.188	C.1
1.378	B.189	C.1
1.379	B.1	C.2
1.380	B.2	C.2
1.381	B.3	C.2
1.382	B.4	C.2
1.383	B.5	C.2
1.384	B.6	C.2

comp. no.	herbi- cide B	safe- ner C
1.385	B.7	C.2
1.386	B.8	C.2
1.387	B.9	C.2
1.388	B.10	C.2
1.389	B.11	C.2
1.390	B.12	C.2
1.391	B.13	C.2
1.392	B.14	C.2
1.393	B.15	C.2
1.394	B.16	C.2
1.395	B.17	C.2
1.396	B.18	C.2
1.397	B.19	C.2
1.398	B.20	C.2
1.399	B.21	C.2
1.400	B.22	C.2
1.401	B.23	C.2
1.402	B.24	C.2
1.403	B.25	C.2
1.404	B.26	C.2
1.405	B.27	C.2
1.406	B.28	C.2
1.407	B.29	C.2
1.408	B.30	C.2
1.409	B.31	C.2
1.410	B.32	C.2
1.411	B.33	C.2
1.412	B.34	C.2
1.413	B.35	C.2
1.414	B.36	C.2
1.415	B.37	C.2
1.416	B.38	C.2
1.417	B.39	C.2
1.418	B.40	C.2
1.419	B.41	C.2
1.420	B.42	C.2

comp. no.	herbi- cide B	safe- ner C
1.421	B.43	C.2
1.422	B.44	C.2
1.423	B.45	C.2
1.424	B.46	C.2
1.425	B.47	C.2
1.426	B.48	C.2
1.427	B.49	C.2
1.428	B.50	C.2
1.429	B.51	C.2
1.430	B.52	C.2
1.431	B.53	C.2
1.432	B.54	C.2
1.433	B.55	C.2
1.434	B.56	C.2
1.435	B.57	C.2
1.436	B.58.	C.2
1.437	B.59	C.2
1.438	B.60	C.2
1.439	B.61	C.2
1.440	B.62	C.2
1.441	B.63	C.2
1.442	B.64	C.2
1.443	B.65	C.2
1.444	B.66	C.2
1.445	B.67	C.2
1.446	B.68	C.2
1.447	B.69	C.2
1.448	B.70	C.2
1.449	B.71	C.2
1.450	B.72	C.2
1.451	B.73	C.2
1.452	B.74	C.2
1.453	B.75	C.2
1.454	B.76	C.2
1.455	B.77	C.2
1.456	B.78	C.2

comp. no.	herbi- cide B	safe- ner C
1.457	B.79	C.2
1.458	B.80	C.2
1.459	B.81	C.2
1.460	B.82	C.2
1.461	B.83	C.2
1.462	B.84	C.2
1.463	B.85	C.2
1.464	B.86	C.2
1.465	B.87	C.2
1.466	B.88	C.2
1.467	B.89	C.2
1.468	B.90	C.2
1.469	B.91	C.2
1.470	B.92	C.2
1.471	B.93	C.2
1.472	B.94	C.2
1.473	B.95	C.2
1.474	B.96	C.2
1.475	B.97	C.2
1.476	B.98	C.2
1.477	B.99	C.2
1.478	B.100	C.2
1.479	B.101	C.2
1.480	B.102	C.2
1.481	B.103	C.2
1.482	B.104	C.2
1.483	B.105	C.2
1.484	B.106	C.2
1.485	B.107	C.2
1.486	B.108	C.2
1.487	B.109	C.2
1.488	B.110	C.2
1.489	B.111	C.2
1.490	B.112	C.2
1.491	B.113	C.2
1.492	B.114	C.2

comp. no.	herbi- cide B	safe- ner C
1.493	B.115	C.2
1.494	B.116	C.2
1.495	B.117	C.2
1.496	B.118	C.2
1.497	B.119	C.2
1.498	B.120	C.2
1.499	B.121	C.2
1.500	B.122	C.2
1.501	B.123	C.2
1.502	B.124	C.2
1.503	B.125	C.2
1.504	B.126	C.2
1.505	B.127	C.2
1.506	B.128	C.2
1.507	B.129	C.2
1.508	B.130	C.2
1.509	B.131	C.2
1.510	B.132	C.2
1.511	B.133	C.2
1.512	B.134	C.2
1.513	B.135	C.2
1.514	B.136	C.2
1.515	B.137	C.2
1.516	B.138	C.2
1.517	B.139	C.2
1.518	B.140	C.2
1.519	B.141	C.2
1.520	B.142	C.2
1.521	B.143	C.2
1.522	B.144	C.2
1.523	B.145	C.2
1.524	B.146	C.2
1.525	B.147	C.2
1.526	B.148	C.2
1.527	B.149	C.2
1.528	B.150	C.2

comp. no.	herbi- cide B	safe- ner C
1.529	B.151	C.2
1.530	B.152	C.2
1.531	B.153	C.2
1.532	B.154	C.2
1.533	B.155	C.2
1.534	B.156	C.2
1.535	B.157	C.2
1.536	B.158	C.2
1.537	B.159	C.2
1.538	B.160	C.2
1.539	B.161	C.2
1.540	B.162	C.2
1.541	B.163	C.2
1.542	B.164	C.2
1.543	B.165	C.2
1.544	B.166	C.2
1.545	B.167	C.2
1.546	B.168	C.2
1.547	B.169	C.2
1.548	B.170	C.2
1.549	B.171	C.2
1.550	B.172	C.2
1.551	B.173	C.2
1.552	B.174	C.2
1.553	B.175	C.2
1.554	B.176	C.2
1.555	B.177	C.2
1.556	B.178	C.2
1.557	B.179	C.2
1.558	B.180	C.2
1.559	B.181	C.2
1.560	B.182	C.2
1.561	B.183	C.2
1.562	B.184	C.2
1.563	B.185	C.2
1.564	B.186	C.2

comp. no.	herbi- cide B	safe- ner C
1.565	B.187	C.2
1.566	B.188	C.2
1.567	B.189	C.2
1.568	B.1	C.3
1.569	B.2	C.3
1.570	B.3	C.3
1.571	B.4	C.3
1.572	B.5	C.3
1.573	B.6	C.3
1.574	B.7	C.3
1.575	B.8	C.3
1.576	B.9	C.3
1.577	B.10	C.3
1.578	B.11	C.3
1.579	B.12	C.3
1.580	B.13	C.3
1.581	B.14	C.3
1.582	B.15	C.3
1.583	B.16	C.3
1.584	B.17	C.3
1.585	B.18	C.3
1.586	B.19	C.3
1.587	B.20	C.3
1.588	B.21	C.3
1.589	B.22	C.3
1.590	B.23	C.3
1.591	B.24	C.3
1.592	B.25	C.3
1.593	B.26	C.3
1.594	B.27	C.3
1.595	B.28	C.3
1.596	B.29	C.3
1.597	B.30	C.3
1.598	B.31	C.3
1.599	B.32	C.3
1.600	B.33	C.3

comp. no.	herbi- cide B	safe- ner C
1.601	B.34	C.3
1.602	B.35	C.3
1.603	B.36	C.3
1.604	B.37	C.3
1.605	B.38	C.3
1.606	B.39	C.3
1.607	B.40	C.3
1.608	B.41	C.3
1.609	B.42	C.3
1.610	B.43	C.3
1.611	B.44	C.3
1.612	B.45	C.3
1.613	B.46	C.3
1.614	B.47	C.3
1.615	B.48	C.3
1.616	B.49	C.3
1.617	B.50	C.3
1.618	B.51	C.3
1.619	B.52	C.3
1.620	B.53	C.3
1.621	B.54	C.3
1.622	B.55	C.3
1.623	B.56	C.3
1.624	B.57	C.3
1.625	B.58.	C.3
1.626	B.59	C.3
1.627	B.60	C.3
1.628	B.61	C.3
1.629	B.62	C.3
1.630	B.63	C.3
1.631	B.64	C.3
1.632	B.65	C.3
1.633	B.66	C.3
1.634	B.67	C.3
1.635	B.68	C.3
1.636	B.69	C.3

comp. no.	herbi- cide B	safe- ner C
1.637	B.70	C.3
1.638	B.71	C.3
1.639	B.72	C.3
1.640	B.73	C.3
1.641	B.74	C.3
1.642	B.75	C.3
1.643	B.76	C.3
1.644	B.77	C.3
1.645	B.78	C.3
1.646	B.79	C.3
1.647	B.80	C.3
1.648	B.81	C.3
1.649	B.82	C.3
1.650	B.83	C.3
1.651	B.84	C.3
1.652	B.85	C.3
1.653	B.86	C.3
1.654	B.87	C.3
1.655	B.88	C.3
1.656	B.89	C.3
1.657	B.90	C.3
1.658	B.91	C.3
1.659	B.92	C.3
1.660	B.93	C.3
1.661	B.94	C.3
1.662	B.95	C.3
1.663	B.96	C.3
1.664	B.97	C.3
1.665	B.98	C.3
1.666	B.99	C.3
1.667	B.100	C.3
1.668	B.101	C.3
1.669	B.102	C.3
1.670	B.103	C.3
1.671	B.104	C.3
1.672	B.105	C.3

comp. no.	herbi- cide B	safe- ner C
1.673	B.106	C.3
1.674	B.107	C.3
1.675	B.108	C.3
1.676	B.109	C.3
1.677	B.110	C.3
1.678	B.111	C.3
1.679	B.112	C.3
1.680	B.113	C.3
1.681	B.114	C.3
1.682	B.115	C.3
1.683	B.116	C.3
1.684	B.117	C.3
1.685	B.118	C.3
1.686	B.119	C.3
1.687	B.120	C.3
1.688	B.121	C.3
1.689	B.122	C.3
1.690	B.123	C.3
1.691	B.124	C.3
1.692	B.125	C.3
1.693	B.126	C.3
1.694	B.127	C.3
1.695	B.128	C.3
1.696	B.129	C.3
1.697	B.130	C.3
1.698	B.131	C.3
1.699	B.132	C.3
1.700	B.133	C.3
1.701	B.134	C.3
1.702	B.135	C.3
1.703	B.136	C.3
1.704	B.137	C.3
1.705	B.138	C.3
1.706	B.139	C.3
1.707	B.140	C.3
1.708	B.141	C.3

comp. no.	herbi- cide B	safe- ner C
1.709	B.142	C.3
1.710	B.143	C.3
1.711	B.144	C.3
1.712	B.145	C.3
1.713	B.146	C.3
1.714	B.147	C.3
1.715	B.148	C.3
1.716	B.149	C.3
1.717	B.150	C.3
1.718	B.151	C.3
1.719	B.152	C.3
1.720	B.153	C.3
1.721	B.154	C.3
1.722	B.155	C.3
1.723	B.156	C.3
1.724	B.157	C.3
1.725	B.158	C.3
1.726	B.159	C.3
1.727	B.160	C.3
1.728	B.161	C.3
1.729	B.162	C.3
1.730	B.163	C.3
1.731	B.164	C.3
1.732	B.165	C.3
1.733	B.166	C.3
1.734	B.167	C.3
1.735	B.168	C.3
1.736	B.169	C.3
1.737	B.170	C.3
1.738	B.171	C.3
1.739	B.172	C.3
1.740	B.173	C.3
1.741	B.174	C.3
1.742	B.175	C.3
1.743	B.176	C.3
1.744	B.177	C.3

comp. no.	herbi- cide B	safe- ner C
1.745	B.178	C.3
1.746	B.179	C.3
1.747	B.180	C.3
1.748	B.181	C.3
1.749	B.182	C.3
1.750	B.183	C.3
1.751	B.184	C.3
1.752	B.185	C.3
1.753	B.186	C.3
1.754	B.187	C.3
1.755	B.188	C.3
1.756	B.189	C.3
1.757	B.1	C.4
1.758	B.2	C.4
1.759	B.3	C.4
1.760	B.4	C.4
1.761	B.5	C.4
1.762	B.6	C.4
1.763	B.7	C.4
1.764	B.8	C.4
1.765	B.9	C.4
1.766	B.10	C.4
1.767	B.11	C.4
1.768	B.12	C.4
1.769	B.13	C.4
1.770	B.14	C.4
1.771	B.15	C.4
1.772	B.16	C.4
1.773	B.17	C.4
1.774	B.18	C.4
1.775	B.19	C.4
1.776	B.20	C.4
1.777	B.21	C.4
1.778	B.22	C.4
1.779	B.23	C.4
1.780	B.24	C.4

WO 2018/019860

PCT/EP2017/068817

65

comp. no.	herbi- cide B	safe- ner C
1.781	B.25	C.4
1.782	B.26	C.4
1.783	B.27	C.4
1.784	B.28	C.4
1.785	B.29	C.4
1.786	B.30	C.4
1.787	B.31	C.4
1.788	B.32	C.4
1.789	B.33	C.4
1.790	B.34	C.4
1.791	B.35	C.4
1.792	B.36	C.4
1.793	B.37	C.4
1.794	B.38	C.4
1.795	B.39	C.4
1.796	B.40	C.4
1.797	B.41	C.4
1.798	B.42	C.4
1.799	B.43	C.4
1.800	B.44	C.4
1.801	B.45	C.4
1.802	B.46	C.4
1.803	B.47	C.4
1.804	B.48	C.4
1.805	B.49	C.4
1.806	B.50	C.4
1.807	B.51	C.4
1.808	B.52	C.4
1.809	B.53	C.4
1.810	B.54	C.4
1.811	B.55	C.4
1.812	B.56	C.4
1.813	B.57	C.4
1.814	B.58.	C.4
1.815	B.59	C.4
1.816	B.60	C.4

comp. no.	herbi- cide B	safe- ner C
1.817	B.61	C.4
1.818	B.62	C.4
1.819	B.63	C.4
1.820	B.64	C.4
1.821	B.65	C.4
1.822	B.66	C.4
1.823	B.67	C.4
1.824	B.68	C.4
1.825	B.69	C.4
1.826	B.70	C.4
1.827	B.71	C.4
1.828	B.72	C.4
1.829	B.73	C.4
1.830	B.74	C.4
1.831	B.75	C.4
1.832	B.76	C.4
1.833	B.77	C.4
1.834	B.78	C.4
1.835	B.79	C.4
1.836	B.80	C.4
1.837	B.81	C.4
1.838	B.82	C.4
1.839	B.83	C.4
1.840	B.84	C.4
1.841	B.85	C.4
1.842	B.86	C.4
1.843	B.87	C.4
1.844	B.88	C.4
1.845	B.89	C.4
1.846	B.90	C.4
1.847	B.91	C.4
1.848	B.92	C.4
1.849	B.93	C.4
1.850	B.94	C.4
1.851	B.95	C.4
1.852	B.96	C.4

comp. no.	herbi- cide B	safe- ner C
1.853	B.97	C.4
1.854	B.98	C.4
1.855	B.99	C.4
1.856	B.100	C.4
1.857	B.101	C.4
1.858	B.102	C.4
1.859	B.103	C.4
1.860	B.104	C.4
1.861	B.105	C.4
1.862	B.106	C.4
1.863	B.107	C.4
1.864	B.108	C.4
1.865	B.109	C.4
1.866	B.110	C.4
1.867	B.111	C.4
1.868	B.112	C.4
1.869	B.113	C.4
1.870	B.114	C.4
1.871	B.115	C.4
1.872	B.116	C.4
1.873	B.117	C.4
1.874	B.118	C.4
1.875	B.119	C.4
1.876	B.120	C.4
1.877	B.121	C.4
1.878	B.122	C.4
1.879	B.123	C.4
1.880	B.124	C.4
1.881	B.125	C.4
1.882	B.126	C.4
1.883	B.127	C.4
1.884	B.128	C.4
1.885	B.129	C.4
1.886	B.130	C.4
1.887	B.131	C.4
1.888	B.132	C.4

WO 2018/019860

PCT/EP2017/068817

66

comp. no.	herbi- cide B	safe- ner C
1.889	B.133	C.4
1.890	B.134	C.4
1.891	B.135	C.4
1.892	B.136	C.4
1.893	B.137	C.4
1.894	B.138	C.4
1.895	B.139	C.4
1.896	B.140	C.4
1.897	B.141	C.4
1.898	B.142	C.4
1.899	B.143	C.4
1.900	B.144	C.4
1.901	B.145	C.4
1.902	B.146	C.4
1.903	B.147	C.4
1.904	B.148	C.4
1.905	B.149	C.4
1.906	B.150	C.4
1.907	B.151	C.4
1.908	B.152	C.4
1.909	B.153	C.4
1.910	B.154	C.4
1.911	B.155	C.4
1.912	B.156	C.4
1.913	B.157	C.4
1.914	B.158	C.4
1.915	B.159	C.4
1.916	B.160	C.4
1.917	B.161	C.4
1.918	B.162	C.4
1.919	B.163	C.4
1.920	B.164	C.4
1.921	B.165	C.4
1.922	B.166	C.4
1.923	B.167	C.4
1.924	B.168	C.4

comp. no.	herbi- cide B	safe- ner C
1.925	B.169	C.4
1.926	B.170	C.4
1.927	B.171	C.4
1.928	B.172	C.4
1.929	B.173	C.4
1.930	B.174	C.4
1.931	B.175	C.4
1.932	B.176	C.4
1.933	B.177	C.4
1.934	B.178	C.4
1.935	B.179	C.4
1.936	B.180	C.4
1.937	B.181	C.4
1.938	B.182	C.4
1.939	B.183	C.4
1.940	B.184	C.4
1.941	B.185	C.4
1.942	B.186	C.4
1.943	B.187	C.4
1.944	B.188	C.4
1.945	B.189	C.4
1.946	B.1	C.5
1.947	B.2	C.5
1.948	B.3	C.5
1.949	B.4	C.5
1.950	B.5	C.5
1.951	B.6	C.5
1.952	B.7	C.5
1.953	B.8	C.5
1.954	B.9	C.5
1.955	B.10	C.5
1.956	B.11	C.5
1.957	B.12	C.5
1.958	B.13	C.5
1.959	B.14	C.5
1.960	B.15	C.5

comp. no.	herbi- cide B	safe- ner C
1.961	B.16	C.5
1.962	B.17	C.5
1.963	B.18	C.5
1.964	B.19	C.5
1.965	B.20	C.5
1.966	B.21	C.5
1.967	B.22	C.5
1.968	B.23	C.5
1.969	B.24	C.5
1.970	B.25	C.5
1.971	B.26	C.5
1.972	B.27	C.5
1.973	B.28	C.5
1.974	B.29	C.5
1.975	B.30	C.5
1.976	B.31	C.5
1.977	B.32	C.5
1.978	B.33	C.5
1.979	B.34	C.5
1.980	B.35	C.5
1.981	B.36	C.5
1.982	B.37	C.5
1.983	B.38	C.5
1.984	B.39	C.5
1.985	B.40	C.5
1.986	B.41	C.5
1.987	B.42	C.5
1.988	B.43	C.5
1.989	B.44	C.5
1.990	B.45	C.5
1.991	B.46	C.5
1.992	B.47	C.5
1.993	B.48	C.5
1.994	B.49	C.5
1.995	B.50	C.5
1.996	B.51	C.5

comp. no.	herbi- cide B	safe- ner C
1.997	B.52	C.5
1.998	B.53	C.5
1.999	B.54	C.5
1.1000	B.55	C.5
1.1001	B.56	C.5
1.1002	B.57	C.5
1.1003	B.58.	C.5
1.1004	B.59	C.5
1.1005	B.60	C.5
1.1006	B.61	C.5
1.1007	B.62	C.5
1.1008	B.63	C.5
1.1009	B.64	C.5
1.1010	B.65	C.5
1.1011	B.66	C.5
1.1012	B.67	C.5
1.1013	B.68	C.5
1.1014	B.69	C.5
1.1015	B.70	C.5
1.1016	B.71	C.5
1.1017	B.72	C.5
1.1018	B.73	C.5
1.1019	B.74	C.5
1.1020	B.75	C.5
1.1021	B.76	C.5
1.1022	B.77	C.5
1.1023	B.78	C.5
1.1024	B.79	C.5
1.1025	B.80	C.5
1.1026	B.81	C.5
1.1027	B.82	C.5
1.1028	B.83	C.5
1.1029	B.84	C.5
1.1030	B.85	C.5
1.1031	B.86	C.5
1.1032	B.87	C.5

comp. no.	herbi- cide B	safe- ner C
1.1033	B.88	C.5
1.1034	B.89	C.5
1.1035	B.90	C.5
1.1036	B.91	C.5
1.1037	B.92	C.5
1.1038	B.93	C.5
1.1039	B.94	C.5
1.1040	B.95	C.5
1.1041	B.96	C.5
1.1042	B.97	C.5
1.1043	B.98	C.5
1.1044	B.99	C.5
1.1045	B.100	C.5
1.1046	B.101	C.5
1.1047	B.102	C.5
1.1048	B.103	C.5
1.1049	B.104	C.5
1.1050	B.105	C.5
1.1051	B.106	C.5
1.1052	B.107	C.5
1.1053	B.108	C.5
1.1054	B.109	C.5
1.1055	B.110	C.5
1.1056	B.111	C.5
1.1057	B.112	C.5
1.1058	B.113	C.5
1.1059	B.114	C.5
1.1060	B.115	C.5
1.1061	B.116	C.5
1.1062	B.117	C.5
1.1063	B.118	C.5
1.1064	B.119	C.5
1.1065	B.120	C.5
1.1066	B.121	C.5
1.1067	B.122	C.5
1.1068	B.123	C.5

comp. no.	herbi- cide B	safe- ner C
1.1069	B.124	C.5
1.1070	B.125	C.5
1.1071	B.126	C.5
1.1072	B.127	C.5
1.1073	B.128	C.5
1.1074	B.129	C.5
1.1075	B.130	C.5
1.1076	B.131	C.5
1.1077	B.132	C.5
1.1078	B.133	C.5
1.1079	B.134	C.5
1.1080	B.135	C.5
1.1081	B.136	C.5
1.1082	B.137	C.5
1.1083	B.138	C.5
1.1084	B.139	C.5
1.1085	B.140	C.5
1.1086	B.141	C.5
1.1087	B.142	C.5
1.1088	B.143	C.5
1.1089	B.144	C.5
1.1090	B.145	C.5
1.1091	B.146	C.5
1.1092	B.147	C.5
1.1093	B.148	C.5
1.1094	B.149	C.5
1.1095	B.150	C.5
1.1096	B.151	C.5
1.1097	B.152	C.5
1.1098	B.153	C.5
1.1099	B.154	C.5
1.1100	B.155	C.5
1.1101	B.156	C.5
1.1102	B.157	C.5
1.1103	B.158	C.5
1.1104	B.159	C.5

comp. no.	herbi- cide B	safe- ner C
1.1105	B.160	C.5
1.1106	B.161	C.5
1.1107	B.162	C.5
1.1108	B.163	C.5
1.1109	B.164	C.5
1.1110	B.165	C.5
1.1111	B.166	C.5
1.1112	B.167	C.5
1.1113	B.168	C.5
1.1114	B.169	C.5
1.1115	B.170	C.5
1.1116	B.171	C.5
1.1117	B.172	C.5
1.1118	B.173	C.5
1.1119	B.174	C.5
1.1120	B.175	C.5
1.1121	B.176	C.5
1.1122	B.177	C.5
1.1123	B.178	C.5
1.1124	B.179	C.5
1.1125	B.180	C.5
1.1126	B.181	C.5
1.1127	B.182	C.5
1.1128	B.183	C.5
1.1129	B.184	C.5
1.1130	B.185	C.5
1.1131	B.186	C.5
1.1132	B.187	C.5
1.1133	B.188	C.5
1.1134	B.189	C.5
1.1135	B.1	C.6
1.1136	B.2	C.6
1.1137	B.3	C.6
1.1138	B.4	C.6
1.1139	B.5	C.6
1.1140	B.6	C.6

comp. no.	herbi- cide B	safe- ner C
1.1141	B.7	C.6
1.1142	B.8	C.6
1.1143	B.9	C.6
1.1144	B.10	C.6
1.1145	B.11	C.6
1.1146	B.12	C.6
1.1147	B.13	C.6
1.1148	B.14	C.6
1.1149	B.15	C.6
1.1150	B.16	C.6
1.1151	B.17	C.6
1.1152	B.18	C.6
1.1153	B.19	C.6
1.1154	B.20	C.6
1.1155	B.21	C.6
1.1156	B.22	C.6
1.1157	B.23	C.6
1.1158	B.24	C.6
1.1159	B.25	C.6
1.1160	B.26	C.6
1.1161	B.27	C.6
1.1162	B.28	C.6
1.1163	B.29	C.6
1.1164	B.30	C.6
1.1165	B.31	C.6
1.1166	B.32	C.6
1.1167	B.33	C.6
1.1168	B.34	C.6
1.1169	B.35	C.6
1.1170	B.36	C.6
1.1171	B.37	C.6
1.1172	B.38	C.6
1.1173	B.39	C.6
1.1174	B.40	C.6
1.1175	B.41	C.6
1.1176	B.42	C.6

comp. no.	herbi- cide B	safe- ner C
1.1177	B.43	C.6
1.1178	B.44	C.6
1.1179	B.45	C.6
1.1180	B.46	C.6
1.1181	B.47	C.6
1.1182	B.48	C.6
1.1183	B.49	C.6
1.1184	B.50	C.6
1.1185	B.51	C.6
1.1186	B.52	C.6
1.1187	B.53	C.6
1.1188	B.54	C.6
1.1189	B.55	C.6
1.1190	B.56	C.6
1.1191	B.57	C.6
1.1192	B.58.	C.6
1.1193	B.59	C.6
1.1194	B.60	C.6
1.1195	B.61	C.6
1.1196	B.62	C.6
1.1197	B.63	C.6
1.1198	B.64	C.6
1.1199	B.65	C.6
1.1200	B.66	C.6
1.1201	B.67	C.6
1.1202	B.68	C.6
1.1203	B.69	C.6
1.1204	B.70	C.6
1.1205	B.71	C.6
1.1206	B.72	C.6
1.1207	B.73	C.6
1.1208	B.74	C.6
1.1209	B.75	C.6
1.1210	B.76	C.6
1.1211	B.77	C.6
1.1212	B.78	C.6

comp. no.	herbi- cide B	safe- ner C
1.1213	B.79	C.6
1.1214	B.80	C.6
1.1215	B.81	C.6
1.1216	B.82	C.6
1.1217	B.83	C.6
1.1218	B.84	C.6
1.1219	B.85	C.6
1.1220	B.86	C.6
1.1221	B.87	C.6
1.1222	B.88	C.6
1.1223	B.89	C.6
1.1224	B.90	C.6
1.1225	B.91	C.6
1.1226	B.92	C.6
1.1227	B.93	C.6
1.1228	B.94	C.6
1.1229	B.95	C.6
1.1230	B.96	C.6
1.1231	B.97	C.6
1.1232	B.98	C.6
1.1233	B.99	C.6
1.1234	B.100	C.6
1.1235	B.101	C.6
1.1236	B.102	C.6
1.1237	B.103	C.6
1.1238	B.104	C.6
1.1239	B.105	C.6
1.1240	B.106	C.6
1.1241	B.107	C.6
1.1242	B.108	C.6
1.1243	B.109	C.6
1.1244	B.110	C.6
1.1245	B.111	C.6
1.1246	B.112	C.6
1.1247	B.113	C.6
1.1248	B.114	C.6

comp. no.	herbi- cide B	safe- ner C
1.1249	B.115	C.6
1.1250	B.116	C.6
1.1251	B.117	C.6
1.1252	B.118	C.6
1.1253	B.119	C.6
1.1254	B.120	C.6
1.1255	B.121	C.6
1.1256	B.122	C.6
1.1257	B.123	C.6
1.1258	B.124	C.6
1.1259	B.125	C.6
1.1260	B.126	C.6
1.1261	B.127	C.6
1.1262	B.128	C.6
1.1263	B.129	C.6
1.1264	B.130	C.6
1.1265	B.131	C.6
1.1266	B.132	C.6
1.1267	B.133	C.6
1.1268	B.134	C.6
1.1269	B.135	C.6
1.1270	B.136	C.6
1.1271	B.137	C.6
1.1272	B.138	C.6
1.1273	B.139	C.6
1.1274	B.140	C.6
1.1275	B.141	C.6
1.1276	B.142	C.6
1.1277	B.143	C.6
1.1278	B.144	C.6
1.1279	B.145	C.6
1.1280	B.146	C.6
1.1281	B.147	C.6
1.1282	B.148	C.6
1.1283	B.149	C.6
1.1284	B.150	C.6

comp. no.	herbi- cide B	safe- ner C
1.1285	B.151	C.6
1.1286	B.152	C.6
1.1287	B.153	C.6
1.1288	B.154	C.6
1.1289	B.155	C.6
1.1290	B.156	C.6
1.1291	B.157	C.6
1.1292	B.158	C.6
1.1293	B.159	C.6
1.1294	B.160	C.6
1.1295	B.161	C.6
1.1296	B.162	C.6
1.1297	B.163	C.6
1.1298	B.164	C.6
1.1299	B.165	C.6
1.1300	B.166	C.6
1.1301	B.167	C.6
1.1302	B.168	C.6
1.1303	B.169	C.6
1.1304	B.170	C.6
1.1305	B.171	C.6
1.1306	B.172	C.6
1.1307	B.173	C.6
1.1308	B.174	C.6
1.1309	B.175	C.6
1.1310	B.176	C.6
1.1311	B.177	C.6
1.1312	B.178	C.6
1.1313	B.179	C.6
1.1314	B.180	C.6
1.1315	B.181	C.6
1.1316	B.182	C.6
1.1317	B.183	C.6
1.1318	B.184	C.6
1.1319	B.185	C.6
1.1320	B.186	C.6

comp. no.	herbi- cide B	safe- ner C
1.1321	B.187	C.6
1.1322	B.188	C.6
1.1323	B.189	C.6
1.1324	B.1	C.7
1.1325	B.2	C.7
1.1326	B.3	C.7
1.1327	B.4	C.7
1.1328	B.5	C.7
1.1329	B.6	C.7
1.1330	B.7	C.7
1.1331	B.8	C.7
1.1332	B.9	C.7
1.1333	B.10	C.7
1.1334	B.11	C.7
1.1335	B.12	C.7
1.1336	B.13	C.7
1.1337	B.14	C.7
1.1338	B.15	C.7
1.1339	B.16	C.7
1.1340	B.17	C.7
1.1341	B.18	C.7
1.1342	B.19	C.7
1.1343	B.20	C.7
1.1344	B.21	C.7
1.1345	B.22	C.7
1.1346	B.23	C.7
1.1347	B.24	C.7
1.1348	B.25	C.7
1.1349	B.26	C.7
1.1350	B.27	C.7
1.1351	B.28	C.7
1.1352	B.29	C.7
1.1353	B.30	C.7
1.1354	B.31	C.7
1.1355	B.32	C.7
1.1356	B.33	C.7

comp. no.	herbi- cide B	safe- ner C
1.1357	B.34	C.7
1.1358	B.35	C.7
1.1359	B.36	C.7
1.1360	B.37	C.7
1.1361	B.38	C.7
1.1362	B.39	C.7
1.1363	B.40	C.7
1.1364	B.41	C.7
1.1365	B.42	C.7
1.1366	B.43	C.7
1.1367	B.44	C.7
1.1368	B.45	C.7
1.1369	B.46	C.7
1.1370	B.47	C.7
1.1371	B.48	C.7
1.1372	B.49	C.7
1.1373	B.50	C.7
1.1374	B.51	C.7
1.1375	B.52	C.7
1.1376	B.53	C.7
1.1377	B.54	C.7
1.1378	B.55	C.7
1.1379	B.56	C.7
1.1380	B.57	C.7
1.1381	B.58.	C.7
1.1382	B.59	C.7
1.1383	B.60	C.7
1.1384	B.61	C.7
1.1385	B.62	C.7
1.1386	B.63	C.7
1.1387	B.64	C.7
1.1388	B.65	C.7
1.1389	B.66	C.7
1.1390	B.67	C.7
1.1391	B.68	C.7
1.1392	B.69	C.7

comp. no.	herbi- cide B	safe- ner C
1.1393	B.70	C.7
1.1394	B.71	C.7
1.1395	B.72	C.7
1.1396	B.73	C.7
1.1397	B.74	C.7
1.1398	B.75	C.7
1.1399	B.76	C.7
1.1400	B.77	C.7
1.1401	B.78	C.7
1.1402	B.79	C.7
1.1403	B.80	C.7
1.1404	B.81	C.7
1.1405	B.82	C.7
1.1406	B.83	C.7
1.1407	B.84	C.7
1.1408	B.85	C.7
1.1409	B.86	C.7
1.1410	B.87	C.7
1.1411	B.88	C.7
1.1412	B.89	C.7
1.1413	B.90	C.7
1.1414	B.91	C.7
1.1415	B.92	C.7
1.1416	B.93	C.7
1.1417	B.94	C.7
1.1418	B.95	C.7
1.1419	B.96	C.7
1.1420	B.97	C.7
1.1421	B.98	C.7
1.1422	B.99	C.7
1.1423	B.100	C.7
1.1424	B.101	C.7
1.1425	B.102	C.7
1.1426	B.103	C.7
1.1427	B.104	C.7
1.1428	B.105	C.7

comp. no.	herbi- cide B	safe- ner C
1.1429	B.106	C.7
1.1430	B.107	C.7
1.1431	B.108	C.7
1.1432	B.109	C.7
1.1433	B.110	C.7
1.1434	B.111	C.7
1.1435	B.112	C.7
1.1436	B.113	C.7
1.1437	B.114	C.7
1.1438	B.115	C.7
1.1439	B.116	C.7
1.1440	B.117	C.7
1.1441	B.118	C.7
1.1442	B.119	C.7
1.1443	B.120	C.7
1.1444	B.121	C.7
1.1445	B.122	C.7
1.1446	B.123	C.7
1.1447	B.124	C.7
1.1448	B.125	C.7
1.1449	B.126	C.7
1.1450	B.127	C.7
1.1451	B.128	C.7
1.1452	B.129	C.7
1.1453	B.130	C.7
1.1454	B.131	C.7
1.1455	B.132	C.7
1.1456	B.133	C.7
1.1457	B.134	C.7
1.1458	B.135	C.7
1.1459	B.136	C.7
1.1460	B.137	C.7
1.1461	B.138	C.7
1.1462	B.139	C.7
1.1463	B.140	C.7
1.1464	B.141	C.7

comp. no.	herbi- cide B	safe- ner C
1.1465	B.142	C.7
1.1466	B.143	C.7
1.1467	B.144	C.7
1.1468	B.145	C.7
1.1469	B.146	C.7
1.1470	B.147	C.7
1.1471	B.148	C.7
1.1472	B.149	C.7
1.1473	B.150	C.7
1.1474	B.151	C.7
1.1475	B.152	C.7
1.1476	B.153	C.7
1.1477	B.154	C.7
1.1478	B.155	C.7
1.1479	B.156	C.7
1.1480	B.157	C.7
1.1481	B.158	C.7
1.1482	B.159	C.7
1.1483	B.160	C.7
1.1484	B.161	C.7
1.1485	B.162	C.7
1.1486	B.163	C.7
1.1487	B.164	C.7
1.1488	B.165	C.7
1.1489	B.166	C.7
1.1490	B.167	C.7
1.1491	B.168	C.7
1.1492	B.169	C.7
1.1493	B.170	C.7
1.1494	B.171	C.7
1.1495	B.172	C.7
1.1496	B.173	C.7
1.1497	B.174	C.7
1.1498	B.175	C.7
1.1499	B.176	C.7
1.1500	B.177	C.7

comp. no.	herbi- cide B	safe- ner C
1.1501	B.178	C.7
1.1502	B.179	C.7
1.1503	B.180	C.7
1.1504	B.181	C.7
1.1505	B.182	C.7
1.1506	B.183	C.7
1.1507	B.184	C.7
1.1508	B.185	C.7
1.1509	B.186	C.7
1.1510	B.187	C.7
1.1511	B.188	C.7
1.1512	B.189	C.7
1.1513	B.1	C.8
1.1514	B.2	C.8
1.1515	B.3	C.8
1.1516	B.4	C.8
1.1517	B.5	C.8
1.1518	B.6	C.8
1.1519	B.7	C.8
1.1520	B.8	C.8
1.1521	B.9	C.8
1.1522	B.10	C.8
1.1523	B.11	C.8
1.1524	B.12	C.8
1.1525	B.13	C.8
1.1526	B.14	C.8
1.1527	B.15	C.8
1.1528	B.16	C.8
1.1529	B.17	C.8
1.1530	B.18	C.8
1.1531	B.19	C.8
1.1532	B.20	C.8
1.1533	B.21	C.8
1.1534	B.22	C.8
1.1535	B.23	C.8
1.1536	B.24	C.8

comp. no.	herbi- cide B	safe- ner C
1.1537	B.25	C.8
1.1538	B.26	C.8
1.1539	B.27	C.8
1.1540	B.28	C.8
1.1541	B.29	C.8
1.1542	B.30	C.8
1.1543	B.31	C.8
1.1544	B.32	C.8
1.1545	B.33	C.8
1.1546	B.34	C.8
1.1547	B.35	C.8
1.1548	B.36	C.8
1.1549	B.37	C.8
1.1550	B.38	C.8
1.1551	B.39	C.8
1.1552	B.40	C.8
1.1553	B.41	C.8
1.1554	B.42	C.8
1.1555	B.43	C.8
1.1556	B.44	C.8
1.1557	B.45	C.8
1.1558	B.46	C.8
1.1559	B.47	C.8
1.1560	B.48	C.8
1.1561	B.49	C.8
1.1562	B.50	C.8
1.1563	B.51	C.8
1.1564	B.52	C.8
1.1565	B.53	C.8
1.1566	B.54	C.8
1.1567	B.55	C.8
1.1568	B.56	C.8
1.1569	B.57	C.8
1.1570	B.58.	C.8
1.1571	B.59	C.8
1.1572	B.60	C.8

comp. no.	herbi- cide B	safe- ner C
1.1573	B.61	C.8
1.1574	B.62	C.8
1.1575	B.63	C.8
1.1576	B.64	C.8
1.1577	B.65	C.8
1.1578	B.66	C.8
1.1579	B.67	C.8
1.1580	B.68	C.8
1.1581	B.69	C.8
1.1582	B.70	C.8
1.1583	B.71	C.8
1.1584	B.72	C.8
1.1585	B.73	C.8
1.1586	B.74	C.8
1.1587	B.75	C.8
1.1588	B.76	C.8
1.1589	B.77	C.8
1.1590	B.78	C.8
1.1591	B.79	C.8
1.1592	B.80	C.8
1.1593	B.81	C.8
1.1594	B.82	C.8
1.1595	B.83	C.8
1.1596	B.84	C.8
1.1597	B.85	C.8
1.1598	B.86	C.8
1.1599	B.87	C.8
1.1600	B.88	C.8
1.1601	B.89	C.8
1.1602	B.90	C.8
1.1603	B.91	C.8
1.1604	B.92	C.8
1.1605	B.93	C.8
1.1606	B.94	C.8
1.1607	B.95	C.8
1.1608	B.96	C.8

comp. no.	herbi- cide B	safe- ner C
1.1609	B.97	C.8
1.1610	B.98	C.8
1.1611	B.99	C.8
1.1612	B.100	C.8
1.1613	B.101	C.8
1.1614	B.102	C.8
1.1615	B.103	C.8
1.1616	B.104	C.8
1.1617	B.105	C.8
1.1618	B.106	C.8
1.1619	B.107	C.8
1.1620	B.108	C.8
1.1621	B.109	C.8
1.1622	B.110	C.8
1.1623	B.111	C.8
1.1624	B.112	C.8
1.1625	B.113	C.8
1.1626	B.114	C.8
1.1627	B.115	C.8
1.1628	B.116	C.8
1.1629	B.117	C.8
1.1630	B.118	C.8
1.1631	B.119	C.8
1.1632	B.120	C.8
1.1633	B.121	C.8
1.1634	B.122	C.8
1.1635	B.123	C.8
1.1636	B.124	C.8
1.1637	B.125	C.8
1.1638	B.126	C.8
1.1639	B.127	C.8
1.1640	B.128	C.8
1.1641	B.129	C.8
1.1642	B.130	C.8
1.1643	B.131	C.8
1.1644	B.132	C.8

comp. no.	herbi- cide B	safe- ner C
1.1645	B.133	C.8
1.1646	B.134	C.8
1.1647	B.135	C.8
1.1648	B.136	C.8
1.1649	B.137	C.8
1.1650	B.138	C.8
1.1651	B.139	C.8
1.1652	B.140	C.8
1.1653	B.141	C.8
1.1654	B.142	C.8
1.1655	B.143	C.8
1.1656	B.144	C.8
1.1657	B.145	C.8
1.1658	B.146	C.8
1.1659	B.147	C.8
1.1660	B.148	C.8
1.1661	B.149	C.8
1.1662	B.150	C.8
1.1663	B.151	C.8
1.1664	B.152	C.8
1.1665	B.153	C.8
1.1666	B.154	C.8
1.1667	B.155	C.8
1.1668	B.156	C.8
1.1669	B.157	C.8
1.1670	B.158	C.8
1.1671	B.159	C.8
1.1672	B.160	C.8
1.1673	B.161	C.8
1.1674	B.162	C.8
1.1675	B.163	C.8
1.1676	B.164	C.8
1.1677	B.165	C.8
1.1678	B.166	C.8
1.1679	B.167	C.8
1.1680	B.168	C.8

comp. no.	herbi- cide B	safe- ner C
1.1681	B.169	C.8
1.1682	B.170	C.8
1.1683	B.171	C.8
1.1684	B.172	C.8
1.1685	B.173	C.8
1.1686	B.174	C.8
1.1687	B.175	C.8
1.1688	B.176	C.8
1.1689	B.177	C.8
1.1690	B.178	C.8
1.1691	B.179	C.8
1.1692	B.180	C.8
1.1693	B.181	C.8
1.1694	B.182	C.8
1.1695	B.183	C.8
1.1696	B.184	C.8
1.1697	B.185	C.8
1.1698	B.186	C.8
1.1699	B.187	C.8
1.1700	B.188	C.8
1.1701	B.189	C.8
1.1702	B.1	C.9
1.1703	B.2	C.9
1.1704	B.3	C.9
1.1705	B.4	C.9
1.1706	B.5	C.9
1.1707	B.6	C.9
1.1708	B.7	C.9
1.1709	B.8	C.9
1.1710	B.9	C.9
1.1711	B.10	C.9
1.1712	B.11	C.9
1.1713	B.12	C.9
1.1714	B.13	C.9
1.1715	B.14	C.9
1.1716	B.15	C.9

comp. no.	herbi- cide B	safe- ner C
1.1717	B.16	C.9
1.1718	B.17	C.9
1.1719	B.18	C.9
1.1720	B.19	C.9
1.1721	B.20	C.9
1.1722	B.21	C.9
1.1723	B.22	C.9
1.1724	B.23	C.9
1.1725	B.24	C.9
1.1726	B.25	C.9
1.1727	B.26	C.9
1.1728	B.27	C.9
1.1729	B.28	C.9
1.1730	B.29	C.9
1.1731	B.30	C.9
1.1732	B.31	C.9
1.1733	B.32	C.9
1.1734	B.33	C.9
1.1735	B.34	C.9
1.1736	B.35	C.9
1.1737	B.36	C.9
1.1738	B.37	C.9
1.1739	B.38	C.9
1.1740	B.39	C.9
1.1741	B.40	C.9
1.1742	B.41	C.9
1.1743	B.42	C.9
1.1744	B.43	C.9
1.1745	B.44	C.9
1.1746	B.45	C.9
1.1747	B.46	C.9
1.1748	B.47	C.9
1.1749	B.48	C.9
1.1750	B.49	C.9
1.1751	B.50	C.9
1.1752	B.51	C.9

comp. no.	herbi- cide B	safe- ner C
1.1753	B.52	C.9
1.1754	B.53	C.9
1.1755	B.54	C.9
1.1756	B.55	C.9
1.1757	B.56	C.9
1.1758	B.57	C.9
1.1759	B.58.	C.9
1.1760	B.59	C.9
1.1761	B.60	C.9
1.1762	B.61	C.9
1.1763	B.62	C.9
1.1764	B.63	C.9
1.1765	B.64	C.9
1.1766	B.65	C.9
1.1767	B.66	C.9
1.1768	B.67	C.9
1.1769	B.68	C.9
1.1770	B.69	C.9
1.1771	B.70	C.9
1.1772	B.71	C.9
1.1773	B.72	C.9
1.1774	B.73	C.9
1.1775	B.74	C.9
1.1776	B.75	C.9
1.1777	B.76	C.9
1.1778	B.77	C.9
1.1779	B.78	C.9
1.1780	B.79	C.9
1.1781	B.80	C.9
1.1782	B.81	C.9
1.1783	B.82	C.9
1.1784	B.83	C.9
1.1785	B.84	C.9
1.1786	B.85	C.9
1.1787	B.86	C.9
1.1788	B.87	C.9

comp. no.	herbi- cide B	safe- ner C
1.1789	B.88	C.9
1.1790	B.89	C.9
1.1791	B.90	C.9
1.1792	B.91	C.9
1.1793	B.92	C.9
1.1794	B.93	C.9
1.1795	B.94	C.9
1.1796	B.95	C.9
1.1797	B.96	C.9
1.1798	B.97	C.9
1.1799	B.98	C.9
1.1800	B.99	C.9
1.1801	B.100	C.9
1.1802	B.101	C.9
1.1803	B.102	C.9
1.1804	B.103	C.9
1.1805	B.104	C.9
1.1806	B.105	C.9
1.1807	B.106	C.9
1.1808	B.107	C.9
1.1809	B.108	C.9
1.1810	B.109	C.9
1.1811	B.110	C.9
1.1812	B.111	C.9
1.1813	B.112	C.9
1.1814	B.113	C.9
1.1815	B.114	C.9
1.1816	B.115	C.9
1.1817	B.116	C.9
1.1818	B.117	C.9
1.1819	B.118	C.9
1.1820	B.119	C.9
1.1821	B.120	C.9
1.1822	B.121	C.9
1.1823	B.122	C.9
1.1824	B.123	C.9

comp. no.	herbi- cide B	safe- ner C
1.1825	B.124	C.9
1.1826	B.125	C.9
1.1827	B.126	C.9
1.1828	B.127	C.9
1.1829	B.128	C.9
1.1830	B.129	C.9
1.1831	B.130	C.9
1.1832	B.131	C.9
1.1833	B.132	C.9
1.1834	B.133	C.9
1.1835	B.134	C.9
1.1836	B.135	C.9
1.1837	B.136	C.9
1.1838	B.137	C.9
1.1839	B.138	C.9
1.1840	B.139	C.9
1.1841	B.140	C.9
1.1842	B.141	C.9
1.1843	B.142	C.9
1.1844	B.143	C.9
1.1845	B.144	C.9
1.1846	B.145	C.9
1.1847	B.146	C.9
1.1848	B.147	C.9
1.1849	B.148	C.9
1.1850	B.149	C.9
1.1851	B.150	C.9
1.1852	B.151	C.9
1.1853	B.152	C.9
1.1854	B.153	C.9
1.1855	B.154	C.9
1.1856	B.155	C.9
1.1857	B.156	C.9
1.1858	B.157	C.9
1.1859	B.158	C.9
1.1860	B.159	C.9

WO 2018/019860

PCT/EP2017/068817

75

comp. no.	herbi- cide B	safe- ner C
1.1861	B.160	C.9
1.1862	B.161	C.9
1.1863	B.162	C.9
1.1864	B.163	C.9
1.1865	B.164	C.9
1.1866	B.165	C.9
1.1867	B.166	C.9
1.1868	B.167	C.9
1.1869	B.168	C.9
1.1870	B.169	C.9
1.1871	B.170	C.9
1.1872	B.171	C.9
1.1873	B.172	C.9
1.1874	B.173	C.9
1.1875	B.174	C.9
1.1876	B.175	C.9
1.1877	B.176	C.9
1.1878	B.177	C.9
1.1879	B.178	C.9
1.1880	B.179	C.9
1.1881	B.180	C.9
1.1882	B.181	C.9
1.1883	B.182	C.9
1.1884	B.183	C.9
1.1885	B.184	C.9
1.1886	B.185	C.9
1.1887	B.186	C.9
1.1888	B.187	C.9
1.1889	B.188	C.9
1.1890	B.189	C.9
1.1891	B.1	C.10
1.1892	B.2	C.10
1.1893	B.3	C.10
1.1894	B.4	C.10
1.1895	B.5	C.10
1.1896	B.6	C.10

comp. no.	herbi- cide B	safe- ner C
1.1897	B.7	C.10
1.1898	B.8	C.10
1.1899	B.9	C.10
1.1900	B.10	C.10
1.1901	B.11	C.10
1.1902	B.12	C.10
1.1903	B.13	C.10
1.1904	B.14	C.10
1.1905	B.15	C.10
1.1906	B.16	C.10
1.1907	B.17	C.10
1.1908	B.18	C.10
1.1909	B.19	C.10
1.1910	B.20	C.10
1.1911	B.21	C.10
1.1912	B.22	C.10
1.1913	B.23	C.10
1.1914	B.24	C.10
1.1915	B.25	C.10
1.1916	B.26	C.10
1.1917	B.27	C.10
1.1918	B.28	C.10
1.1919	B.29	C.10
1.1920	B.30	C.10
1.1921	B.31	C.10
1.1922	B.32	C.10
1.1923	B.33	C.10
1.1924	B.34	C.10
1.1925	B.35	C.10
1.1926	B.36	C.10
1.1927	B.37	C.10
1.1928	B.38	C.10
1.1929	B.39	C.10
1.1930	B.40	C.10
1.1931	B.41	C.10
1.1932	B.42	C.10

comp. no.	herbi- cide B	safe- ner C
1.1933	B.43	C.10
1.1934	B.44	C.10
1.1935	B.45	C.10
1.1936	B.46	C.10
1.1937	B.47	C.10
1.1938	B.48	C.10
1.1939	B.49	C.10
1.1940	B.50	C.10
1.1941	B.51	C.10
1.1942	B.52	C.10
1.1943	B.53	C.10
1.1944	B.54	C.10
1.1945	B.55	C.10
1.1946	B.56	C.10
1.1947	B.57	C.10
1.1948	B.58.	C.10
1.1949	B.59	C.10
1.1950	B.60	C.10
1.1951	B.61	C.10
1.1952	B.62	C.10
1.1953	B.63	C.10
1.1954	B.64	C.10
1.1955	B.65	C.10
1.1956	B.66	C.10
1.1957	B.67	C.10
1.1958	B.68	C.10
1.1959	B.69	C.10
1.1960	B.70	C.10
1.1961	B.71	C.10
1.1962	B.72	C.10
1.1963	B.73	C.10
1.1964	B.74	C.10
1.1965	B.75	C.10
1.1966	B.76	C.10
1.1967	B.77	C.10
1.1968	B.78	C.10

WO 2018/019860

PCT/EP2017/068817

76

comp. no.	herbi- cide B	safe- ner C
1.1969	B.79	C.10
1.1970	B.80	C.10
1.1971	B.81	C.10
1.1972	B.82	C.10
1.1973	B.83	C.10
1.1974	B.84	C.10
1.1975	B.85	C.10
1.1976	B.86	C.10
1.1977	B.87	C.10
1.1978	B.88	C.10
1.1979	B.89	C.10
1.1980	B.90	C.10
1.1981	B.91	C.10
1.1982	B.92	C.10
1.1983	B.93	C.10
1.1984	B.94	C.10
1.1985	B.95	C.10
1.1986	B.96	C.10
1.1987	B.97	C.10
1.1988	B.98	C.10
1.1989	B.99	C.10
1.1990	B.100	C.10
1.1991	B.101	C.10
1.1992	B.102	C.10
1.1993	B.103	C.10
1.1994	B.104	C.10
1.1995	B.105	C.10
1.1996	B.106	C.10
1.1997	B.107	C.10
1.1998	B.108	C.10
1.1999	B.109	C.10
1.2000	B.110	C.10
1.2001	B.111	C.10
1.2002	B.112	C.10
1.2003	B.113	C.10
1.2004	B.114	C.10

comp. no.	herbi- cide B	safe- ner C
1.2005	B.115	C.10
1.2006	B.116	C.10
1.2007	B.117	C.10
1.2008	B.118	C.10
1.2009	B.119	C.10
1.2010	B.120	C.10
1.2011	B.121	C.10
1.2012	B.122	C.10
1.2013	B.123	C.10
1.2014	B.124	C.10
1.2015	B.125	C.10
1.2016	B.126	C.10
1.2017	B.127	C.10
1.2018	B.128	C.10
1.2019	B.129	C.10
1.2020	B.130	C.10
1.2021	B.131	C.10
1.2022	B.132	C.10
1.2023	B.133	C.10
1.2024	B.134	C.10
1.2025	B.135	C.10
1.2026	B.136	C.10
1.2027	B.137	C.10
1.2028	B.138	C.10
1.2029	B.139	C.10
1.2030	B.140	C.10
1.2031	B.141	C.10
1.2032	B.142	C.10
1.2033	B.143	C.10
1.2034	B.144	C.10
1.2035	B.145	C.10
1.2036	B.146	C.10
1.2037	B.147	C.10
1.2038	B.148	C.10
1.2039	B.149	C.10
1.2040	B.150	C.10

comp. no.	herbi- cide B	safe- ner C
1.2041	B.151	C.10
1.2042	B.152	C.10
1.2043	B.153	C.10
1.2044	B.154	C.10
1.2045	B.155	C.10
1.2046	B.156	C.10
1.2047	B.157	C.10
1.2048	B.158	C.10
1.2049	B.159	C.10
1.2050	B.160	C.10
1.2051	B.161	C.10
1.2052	B.162	C.10
1.2053	B.163	C.10
1.2054	B.164	C.10
1.2055	B.165	C.10
1.2056	B.166	C.10
1.2057	B.167	C.10
1.2058	B.168	C.10
1.2059	B.169	C.10
1.2060	B.170	C.10
1.2061	B.171	C.10
1.2062	B.172	C.10
1.2063	B.173	C.10
1.2064	B.174	C.10
1.2065	B.175	C.10
1.2066	B.176	C.10
1.2067	B.177	C.10
1.2068	B.178	C.10
1.2069	B.179	C.10
1.2070	B.180	C.10
1.2071	B.181	C.10
1.2072	B.182	C.10
1.2073	B.183	C.10
1.2074	B.184	C.10
1.2075	B.185	C.10
1.2076	B.186	C.10

comp. no.	herbi- cide B	safe- ner C
1.2077	B.187	C.10
1.2078	B.188	C.10
1.2079	B.189	C.10
1.2080	B.1	C.11
1.2081	B.2	C.11
1.2082	B.3	C.11
1.2083	B.4	C.11
1.2084	B.5	C.11
1.2085	B.6	C.11
1.2086	B.7	C.11
1.2087	B.8	C.11
1.2088	B.9	C.11
1.2089	B.10	C.11
1.2090	B.11	C.11
1.2091	B.12	C.11
1.2092	B.13	C.11
1.2093	B.14	C.11
1.2094	B.15	C.11
1.2095	B.16	C.11
1.2096	B.17	C.11
1.2097	B.18	C.11
1.2098	B.19	C.11
1.2099	B.20	C.11
1.2100	B.21	C.11
1.2101	B.22	C.11
1.2102	B.23	C.11
1.2103	B.24	C.11
1.2104	B.25	C.11
1.2105	B.26	C.11
1.2106	B.27	C.11
1.2107	B.28	C.11
1.2108	B.29	C.11
1.2109	B.30	C.11
1.2110	B.31	C.11
1.2111	B.32	C.11
1.2112	B.33	C.11

comp. no.	herbi- cide B	safe- ner C
1.2113	B.34	C.11
1.2114	B.35	C.11
1.2115	B.36	C.11
1.2116	B.37	C.11
1.2117	B.38	C.11
1.2118	B.39	C.11
1.2119	B.40	C.11
1.2120	B.41	C.11
1.2121	B.42	C.11
1.2122	B.43	C.11
1.2123	B.44	C.11
1.2124	B.45	C.11
1.2125	B.46	C.11
1.2126	B.47	C.11
1.2127	B.48	C.11
1.2128	B.49	C.11
1.2129	B.50	C.11
1.2130	B.51	C.11
1.2131	B.52	C.11
1.2132	B.53	C.11
1.2133	B.54	C.11
1.2134	B.55	C.11
1.2135	B.56	C.11
1.2136	B.57	C.11
1.2137	B.58.	C.11
1.2138	B.59	C.11
1.2139	B.60	C.11
1.2140	B.61	C.11
1.2141	B.62	C.11
1.2142	B.63	C.11
1.2143	B.64	C.11
1.2144	B.65	C.11
1.2145	B.66	C.11
1.2146	B.67	C.11
1.2147	B.68	C.11
1.2148	B.69	C.11

comp. no.	herbi- cide B	safe- ner C
1.2149	B.70	C.11
1.2150	B.71	C.11
1.2151	B.72	C.11
1.2152	B.73	C.11
1.2153	B.74	C.11
1.2154	B.75	C.11
1.2155	B.76	C.11
1.2156	B.77	C.11
1.2157	B.78	C.11
1.2158	B.79	C.11
1.2159	B.80	C.11
1.2160	B.81	C.11
1.2161	B.82	C.11
1.2162	B.83	C.11
1.2163	B.84	C.11
1.2164	B.85	C.11
1.2165	B.86	C.11
1.2166	B.87	C.11
1.2167	B.88	C.11
1.2168	B.89	C.11
1.2169	B.90	C.11
1.2170	B.91	C.11
1.2171	B.92	C.11
1.2172	B.93	C.11
1.2173	B.94	C.11
1.2174	B.95	C.11
1.2175	B.96	C.11
1.2176	B.97	C.11
1.2177	B.98	C.11
1.2178	B.99	C.11
1.2179	B.100	C.11
1.2180	B.101	C.11
1.2181	B.102	C.11
1.2182	B.103	C.11
1.2183	B.104	C.11
1.2184	B.105	C.11

comp. no.	herbi- cide B	safe- ner C
1.2185	B.106	C.11
1.2186	B.107	C.11
1.2187	B.108	C.11
1.2188	B.109	C.11
1.2189	B.110	C.11
1.2190	B.111	C.11
1.2191	B.112	C.11
1.2192	B.113	C.11
1.2193	B.114	C.11
1.2194	B.115	C.11
1.2195	B.116	C.11
1.2196	B.117	C.11
1.2197	B.118	C.11
1.2198	B.119	C.11
1.2199	B.120	C.11
1.2200	B.121	C.11
1.2201	B.122	C.11
1.2202	B.123	C.11
1.2203	B.124	C.11
1.2204	B.125	C.11
1.2205	B.126	C.11
1.2206	B.127	C.11
1.2207	B.128	C.11
1.2208	B.129	C.11
1.2209	B.130	C.11
1.2210	B.131	C.11
1.2211	B.132	C.11
1.2212	B.133	C.11
1.2213	B.134	C.11
1.2214	B.135	C.11
1.2215	B.136	C.11
1.2216	B.137	C.11
1.2217	B.138	C.11
1.2218	B.139	C.11
1.2219	B.140	C.11
1.2220	B.141	C.11

comp. no.	herbi- cide B	safe- ner C
1.2221	B.142	C.11
1.2222	B.143	C.11
1.2223	B.144	C.11
1.2224	B.145	C.11
1.2225	B.146	C.11
1.2226	B.147	C.11
1.2227	B.148	C.11
1.2228	B.149	C.11
1.2229	B.150	C.11
1.2230	B.151	C.11
1.2231	B.152	C.11
1.2232	B.153	C.11
1.2233	B.154	C.11
1.2234	B.155	C.11
1.2235	B.156	C.11
1.2236	B.157	C.11
1.2237	B.158	C.11
1.2238	B.159	C.11
1.2239	B.160	C.11
1.2240	B.161	C.11
1.2241	B.162	C.11
1.2242	B.163	C.11
1.2243	B.164	C.11
1.2244	B.165	C.11
1.2245	B.166	C.11
1.2246	B.167	C.11
1.2247	B.168	C.11
1.2248	B.169	C.11
1.2249	B.170	C.11
1.2250	B.171	C.11
1.2251	B.172	C.11
1.2252	B.173	C.11
1.2253	B.174	C.11
1.2254	B.175	C.11
1.2255	B.176	C.11
1.2256	B.177	C.11

comp. no.	herbi- cide B	safe- ner C
1.2257	B.178	C.11
1.2258	B.179	C.11
1.2259	B.180	C.11
1.2260	B.181	C.11
1.2261	B.182	C.11
1.2262	B.183	C.11
1.2263	B.184	C.11
1.2264	B.185	C.11
1.2265	B.186	C.11
1.2266	B.187	C.11
1.2267	B.188	C.11
1.2268	B.189	C.11
1.2269	B.1	C.12
1.2270	B.2	C.12
1.2271	B.3	C.12
1.2272	B.4	C.12
1.2273	B.5	C.12
1.2274	B.6	C.12
1.2275	B.7	C.12
1.2276	B.8	C.12
1.2277	B.9	C.12
1.2278	B.10	C.12
1.2279	B.11	C.12
1.2280	B.12	C.12
1.2281	B.13	C.12
1.2282	B.14	C.12
1.2283	B.15	C.12
1.2284	B.16	C.12
1.2285	B.17	C.12
1.2286	B.18	C.12
1.2287	B.19	C.12
1.2288	B.20	C.12
1.2289	B.21	C.12
1.2290	B.22	C.12
1.2291	B.23	C.12
1.2292	B.24	C.12

comp. no.	herbi- cide B	safe- ner C
1.2293	B.25	C.12
1.2294	B.26	C.12
1.2295	B.27	C.12
1.2296	B.28	C.12
1.2297	B.29	C.12
1.2298	B.30	C.12
1.2299	B.31	C.12
1.2300	B.32	C.12
1.2301	B.33	C.12
1.2302	B.34	C.12
1.2303	B.35	C.12
1.2304	B.36	C.12
1.2305	B.37	C.12
1.2306	B.38	C.12
1.2307	B.39	C.12
1.2308	B.40	C.12
1.2309	B.41	C.12
1.2310	B.42	C.12
1.2311	B.43	C.12
1.2312	B.44	C.12
1.2313	B.45	C.12
1.2314	B.46	C.12
1.2315	B.47	C.12
1.2316	B.48	C.12
1.2317	B.49	C.12
1.2318	B.50	C.12
1.2319	B.51	C.12
1.2320	B.52	C.12
1.2321	B.53	C.12
1.2322	B.54	C.12
1.2323	B.55	C.12
1.2324	B.56	C.12
1.2325	B.57	C.12
1.2326	B.58.	C.12
1.2327	B.59	C.12
1.2328	B.60	C.12

comp. no.	herbi- cide B	safe- ner C
1.2329	B.61	C.12
1.2330	B.62	C.12
1.2331	B.63	C.12
1.2332	B.64	C.12
1.2333	B.65	C.12
1.2334	B.66	C.12
1.2335	B.67	C.12
1.2336	B.68	C.12
1.2337	B.69	C.12
1.2338	B.70	C.12
1.2339	B.71	C.12
1.2340	B.72	C.12
1.2341	B.73	C.12
1.2342	B.74	C.12
1.2343	B.75	C.12
1.2344	B.76	C.12
1.2345	B.77	C.12
1.2346	B.78	C.12
1.2347	B.79	C.12
1.2348	B.80	C.12
1.2349	B.81	C.12
1.2350	B.82	C.12
1.2351	B.83	C.12
1.2352	B.84	C.12
1.2353	B.85	C.12
1.2354	B.86	C.12
1.2355	B.87	C.12
1.2356	B.88	C.12
1.2357	B.89	C.12
1.2358	B.90	C.12
1.2359	B.91	C.12
1.2360	B.92	C.12
1.2361	B.93	C.12
1.2362	B.94	C.12
1.2363	B.95	C.12
1.2364	B.96	C.12

comp. no.	herbi- cide B	safe- ner C
1.2365	B.97	C.12
1.2366	B.98	C.12
1.2367	B.99	C.12
1.2368	B.100	C.12
1.2369	B.101	C.12
1.2370	B.102	C.12
1.2371	B.103	C.12
1.2372	B.104	C.12
1.2373	B.105	C.12
1.2374	B.106	C.12
1.2375	B.107	C.12
1.2376	B.108	C.12
1.2377	B.109	C.12
1.2378	B.110	C.12
1.2379	B.111	C.12
1.2380	B.112	C.12
1.2381	B.113	C.12
1.2382	B.114	C.12
1.2383	B.115	C.12
1.2384	B.116	C.12
1.2385	B.117	C.12
1.2386	B.118	C.12
1.2387	B.119	C.12
1.2388	B.120	C.12
1.2389	B.121	C.12
1.2390	B.122	C.12
1.2391	B.123	C.12
1.2392	B.124	C.12
1.2393	B.125	C.12
1.2394	B.126	C.12
1.2395	B.127	C.12
1.2396	B.128	C.12
1.2397	B.129	C.12
1.2398	B.130	C.12
1.2399	B.131	C.12
1.2400	B.132	C.12

comp. no.	herbi- cide B	safe- ner C
1.2401	B.133	C.12
1.2402	B.134	C.12
1.2403	B.135	C.12
1.2404	B.136	C.12
1.2405	B.137	C.12
1.2406	B.138	C.12
1.2407	B.139	C.12
1.2408	B.140	C.12
1.2409	B.141	C.12
1.2410	B.142	C.12
1.2411	B.143	C.12
1.2412	B.144	C.12
1.2413	B.145	C.12
1.2414	B.146	C.12
1.2415	B.147	C.12
1.2416	B.148	C.12
1.2417	B.149	C.12
1.2418	B.150	C.12
1.2419	B.151	C.12
1.2420	B.152	C.12
1.2421	B.153	C.12
1.2422	B.154	C.12
1.2423	B.155	C.12
1.2424	B.156	C.12
1.2425	B.157	C.12
1.2426	B.158	C.12
1.2427	B.159	C.12
1.2428	B.160	C.12
1.2429	B.161	C.12
1.2430	B.162	C.12
1.2431	B.163	C.12
1.2432	B.164	C.12
1.2433	B.165	C.12
1.2434	B.166	C.12
1.2435	B.167	C.12
1.2436	B.168	C.12

comp. no.	herbi- cide B	safe- ner C
1.2437	B.169	C.12
1.2438	B.170	C.12
1.2439	B.171	C.12
1.2440	B.172	C.12
1.2441	B.173	C.12
1.2442	B.174	C.12
1.2443	B.175	C.12
1.2444	B.176	C.12
1.2445	B.177	C.12
1.2446	B.178	C.12
1.2447	B.179	C.12
1.2448	B.180	C.12
1.2449	B.181	C.12
1.2450	B.182	C.12
1.2451	B.183	C.12
1.2452	B.184	C.12
1.2453	B.185	C.12
1.2454	B.186	C.12
1.2455	B.187	C.12
1.2456	B.188	C.12
1.2457	B.189	C.12
1.2458	B.1	C.13
1.2459	B.2	C.13
1.2460	B.3	C.13
1.2461	B.4	C.13
1.2462	B.5	C.13
1.2463	B.6	C.13
1.2464	B.7	C.13
1.2465	B.8	C.13
1.2466	B.9	C.13
1.2467	B.10	C.13
1.2468	B.11	C.13
1.2469	B.12	C.13
1.2470	B.13	C.13
1.2471	B.14	C.13
1.2472	B.15	C.13

comp. no.	herbi- cide B	safe- ner C
1.2473	B.16	C.13
1.2474	B.17	C.13
1.2475	B.18	C.13
1.2476	B.19	C.13
1.2477	B.20	C.13
1.2478	B.21	C.13
1.2479	B.22	C.13
1.2480	B.23	C.13
1.2481	B.24	C.13
1.2482	B.25	C.13
1.2483	B.26	C.13
1.2484	B.27	C.13
1.2485	B.28	C.13
1.2486	B.29	C.13
1.2487	B.30	C.13
1.2488	B.31	C.13
1.2489	B.32	C.13
1.2490	B.33	C.13
1.2491	B.34	C.13
1.2492	B.35	C.13
1.2493	B.36	C.13
1.2494	B.37	C.13
1.2495	B.38	C.13
1.2496	B.39	C.13
1.2497	B.40	C.13
1.2498	B.41	C.13
1.2499	B.42	C.13
1.2500	B.43	C.13
1.2501	B.44	C.13
1.2502	B.45	C.13
1.2503	B.46	C.13
1.2504	B.47	C.13
1.2505	B.48	C.13
1.2506	B.49	C.13
1.2507	B.50	C.13
1.2508	B.51	C.13

comp. no.	herbi- cide B	safe- ner C
1.2509	B.52	C.13
1.2510	B.53	C.13
1.2511	B.54	C.13
1.2512	B.55	C.13
1.2513	B.56	C.13
1.2514	B.57	C.13
1.2515	B.58.	C.13
1.2516	B.59	C.13
1.2517	B.60	C.13
1.2518	B.61	C.13
1.2519	B.62	C.13
1.2520	B.63	C.13
1.2521	B.64	C.13
1.2522	B.65	C.13
1.2523	B.66	C.13
1.2524	B.67	C.13
1.2525	B.68	C.13
1.2526	B.69	C.13
1.2527	B.70	C.13
1.2528	B.71	C.13
1.2529	B.72	C.13
1.2530	B.73	C.13
1.2531	B.74	C.13
1.2532	B.75	C.13
1.2533	B.76	C.13
1.2534	B.77	C.13
1.2535	B.78	C.13
1.2536	B.79	C.13
1.2537	B.80	C.13
1.2538	B.81	C.13
1.2539	B.82	C.13
1.2540	B.83	C.13
1.2541	B.84	C.13
1.2542	B.85	C.13
1.2543	B.86	C.13
1.2544	B.87	C.13

comp. no.	herbi- cide B	safe- ner C
1.2545	B.88	C.13
1.2546	B.89	C.13
1.2547	B.90	C.13
1.2548	B.91	C.13
1.2549	B.92	C.13
1.2550	B.93	C.13
1.2551	B.94	C.13
1.2552	B.95	C.13
1.2553	B.96	C.13
1.2554	B.97	C.13
1.2555	B.98	C.13
1.2556	B.99	C.13
1.2557	B.100	C.13
1.2558	B.101	C.13
1.2559	B.102	C.13
1.2560	B.103	C.13
1.2561	B.104	C.13
1.2562	B.105	C.13
1.2563	B.106	C.13
1.2564	B.107	C.13
1.2565	B.108	C.13
1.2566	B.109	C.13
1.2567	B.110	C.13
1.2568	B.111	C.13
1.2569	B.112	C.13
1.2570	B.113	C.13
1.2571	B.114	C.13
1.2572	B.115	C.13
1.2573	B.116	C.13
1.2574	B.117	C.13
1.2575	B.118	C.13
1.2576	B.119	C.13
1.2577	B.120	C.13
1.2578	B.121	C.13
1.2579	B.122	C.13
1.2580	B.123	C.13

comp. no.	herbi- cide B	safe- ner C
1.2581	B.124	C.13
1.2582	B.125	C.13
1.2583	B.126	C.13
1.2584	B.127	C.13
1.2585	B.128	C.13
1.2586	B.129	C.13
1.2587	B.130	C.13
1.2588	B.131	C.13
1.2589	B.132	C.13
1.2590	B.133	C.13
1.2591	B.134	C.13
1.2592	B.135	C.13
1.2593	B.136	C.13
1.2594	B.137	C.13
1.2595	B.138	C.13
1.2596	B.139	C.13
1.2597	B.140	C.13
1.2598	B.141	C.13
1.2599	B.142	C.13
1.2600	B.143	C.13
1.2601	B.144	C.13
1.2602	B.145	C.13
1.2603	B.146	C.13
1.2604	B.147	C.13
1.2605	B.148	C.13
1.2606	B.149	C.13
1.2607	B.150	C.13
1.2608	B.151	C.13
1.2609	B.152	C.13
1.2610	B.153	C.13
1.2611	B.154	C.13
1.2612	B.155	C.13
1.2613	B.156	C.13
1.2614	B.157	C.13
1.2615	B.158	C.13
1.2616	B.159	C.13

comp. no.	herbi- cide B	safe- ner C
1.2617	B.160	C.13
1.2618	B.161	C.13
1.2619	B.162	C.13
1.2620	B.163	C.13
1.2621	B.164	C.13
1.2622	B.165	C.13
1.2623	B.166	C.13
1.2624	B.167	C.13
1.2625	B.168	C.13
1.2626	B.169	C.13
1.2627	B.170	C.13
1.2628	B.171	C.13
1.2629	B.172	C.13
1.2630	B.173	C.13
1.2631	B.174	C.13
1.2632	B.175	C.13
1.2633	B.176	C.13
1.2634	B.177	C.13
1.2635	B.178	C.13
1.2636	B.179	C.13
1.2637	B.180	C.13
1.2638	B.181	C.13
1.2639	B.182	C.13
1.2640	B.183	C.13
1.2641	B.184	C.13
1.2642	B.185	C.13
1.2643	B.186	C.13
1.2644	B.187	C.13
1.2645	B.188	C.13
1.2646	B.189	C.13
1.2647	B.1	C.14
1.2648	B.2	C.14
1.2649	B.3	C.14
1.2650	B.4	C.14
1.2651	B.5	C.14
1.2652	B.6	C.14

comp. no.	herbi- cide B	safe- ner C
1.2653	B.7	C.14
1.2654	B.8	C.14
1.2655	B.9	C.14
1.2656	B.10	C.14
1.2657	B.11	C.14
1.2658	B.12	C.14
1.2659	B.13	C.14
1.2660	B.14	C.14
1.2661	B.15	C.14
1.2662	B.16	C.14
1.2663	B.17	C.14
1.2664	B.18	C.14
1.2665	B.19	C.14
1.2666	B.20	C.14
1.2667	B.21	C.14
1.2668	B.22	C.14
1.2669	B.23	C.14
1.2670	B.24	C.14
1.2671	B.25	C.14
1.2672	B.26	C.14
1.2673	B.27	C.14
1.2674	B.28	C.14
1.2675	B.29	C.14
1.2676	B.30	C.14
1.2677	B.31	C.14
1.2678	B.32	C.14
1.2679	B.33	C.14
1.2680	B.34	C.14
1.2681	B.35	C.14
1.2682	B.36	C.14
1.2683	B.37	C.14
1.2684	B.38	C.14
1.2685	B.39	C.14
1.2686	B.40	C.14
1.2687	B.41	C.14
1.2688	B.42	C.14

comp. no.	herbi- cide B	safe- ner C
1.2689	B.43	C.14
1.2690	B.44	C.14
1.2691	B.45	C.14
1.2692	B.46	C.14
1.2693	B.47	C.14
1.2694	B.48	C.14
1.2695	B.49	C.14
1.2696	B.50	C.14
1.2697	B.51	C.14
1.2698	B.52	C.14
1.2699	B.53	C.14
1.2700	B.54	C.14
1.2701	B.55	C.14
1.2702	B.56	C.14
1.2703	B.57	C.14
1.2704	B.58.	C.14
1.2705	B.59	C.14
1.2706	B.60	C.14
1.2707	B.61	C.14
1.2708	B.62	C.14
1.2709	B.63	C.14
1.2710	B.64	C.14
1.2711	B.65	C.14
1.2712	B.66	C.14
1.2713	B.67	C.14
1.2714	B.68	C.14
1.2715	B.69	C.14
1.2716	B.70	C.14
1.2717	B.71	C.14
1.2718	B.72	C.14
1.2719	B.73	C.14
1.2720	B.74	C.14
1.2721	B.75	C.14
1.2722	B.76	C.14
1.2723	B.77	C.14
1.2724	B.78	C.14

comp. no.	herbi- cide B	safe- ner C
1.2725	B.79	C.14
1.2726	B.80	C.14
1.2727	B.81	C.14
1.2728	B.82	C.14
1.2729	B.83	C.14
1.2730	B.84	C.14
1.2731	B.85	C.14
1.2732	B.86	C.14
1.2733	B.87	C.14
1.2734	B.88	C.14
1.2735	B.89	C.14
1.2736	B.90	C.14
1.2737	B.91	C.14
1.2738	B.92	C.14
1.2739	B.93	C.14
1.2740	B.94	C.14
1.2741	B.95	C.14
1.2742	B.96	C.14
1.2743	B.97	C.14
1.2744	B.98	C.14
1.2745	B.99	C.14
1.2746	B.100	C.14
1.2747	B.101	C.14
1.2748	B.102	C.14
1.2749	B.103	C.14
1.2750	B.104	C.14
1.2751	B.105	C.14
1.2752	B.106	C.14
1.2753	B.107	C.14
1.2754	B.108	C.14
1.2755	B.109	C.14
1.2756	B.110	C.14
1.2757	B.111	C.14
1.2758	B.112	C.14
1.2759	B.113	C.14
1.2760	B.114	C.14

comp. no.	herbi- cide B	safe- ner C
1.2761	B.115	C.14
1.2762	B.116	C.14
1.2763	B.117	C.14
1.2764	B.118	C.14
1.2765	B.119	C.14
1.2766	B.120	C.14
1.2767	B.121	C.14
1.2768	B.122	C.14
1.2769	B.123	C.14
1.2770	B.124	C.14
1.2771	B.125	C.14
1.2772	B.126	C.14
1.2773	B.127	C.14
1.2774	B.128	C.14
1.2775	B.129	C.14
1.2776	B.130	C.14
1.2777	B.131	C.14
1.2778	B.132	C.14
1.2779	B.133	C.14
1.2780	B.134	C.14
1.2781	B.135	C.14
1.2782	B.136	C.14
1.2783	B.137	C.14
1.2784	B.138	C.14
1.2785	B.139	C.14
1.2786	B.140	C.14
1.2787	B.141	C.14
1.2788	B.142	C.14
1.2789	B.143	C.14
1.2790	B.144	C.14
1.2791	B.145	C.14
1.2792	B.146	C.14
1.2793	B.147	C.14
1.2794	B.148	C.14
1.2795	B.149	C.14
1.2796	B.150	C.14

comp. no.	herbi- cide B	safe- ner C
1.2797	B.151	C.14
1.2798	B.152	C.14
1.2799	B.153	C.14
1.2800	B.154	C.14
1.2801	B.155	C.14
1.2802	B.156	C.14
1.2803	B.157	C.14
1.2804	B.158	C.14
1.2805	B.159	C.14
1.2806	B.160	C.14
1.2807	B.161	C.14
1.2808	B.162	C.14
1.2809	B.163	C.14
1.2810	B.164	C.14
1.2811	B.165	C.14
1.2812	B.166	C.14
1.2813	B.167	C.14
1.2814	B.168	C.14
1.2815	B.169	C.14
1.2816	B.170	C.14
1.2817	B.171	C.14
1.2818	B.172	C.14
1.2819	B.173	C.14
1.2820	B.174	C.14
1.2821	B.175	C.14
1.2822	B.176	C.14
1.2823	B.177	C.14
1.2824	B.178	C.14
1.2825	B.179	C.14
1.2826	B.180	C.14
1.2827	B.181	C.14
1.2828	B.182	C.14
1.2829	B.183	C.14
1.2830	B.184	C.14
1.2831	B.185	C.14
1.2832	B.186	C.14

comp. no.	herbi- cide B	safe- ner C
1.2833	B.187	C.14
1.2834	B.188	C.14
1.2835	B.189	C.14
1.2836	B.1	C.15
1.2837	B.2	C.15
1.2838	B.3	C.15
1.2839	B.4	C.15
1.2840	B.5	C.15
1.2841	B.6	C.15
1.2842	B.7	C.15
1.2843	B.8	C.15
1.2844	B.9	C.15
1.2845	B.10	C.15
1.2846	B.11	C.15
1.2847	B.12	C.15
1.2848	B.13	C.15
1.2849	B.14	C.15
1.2850	B.15	C.15
1.2851	B.16	C.15
1.2852	B.17	C.15
1.2853	B.18	C.15
1.2854	B.19	C.15
1.2855	B.20	C.15
1.2856	B.21	C.15
1.2857	B.22	C.15
1.2858	B.23	C.15
1.2859	B.24	C.15
1.2860	B.25	C.15
1.2861	B.26	C.15
1.2862	B.27	C.15
1.2863	B.28	C.15
1.2864	B.29	C.15
1.2865	B.30	C.15
1.2866	B.31	C.15
1.2867	B.32	C.15
1.2868	B.33	C.15

comp. no.	herbi- cide B	safe- ner C
1.2869	B.34	C.15
1.2870	B.35	C.15
1.2871	B.36	C.15
1.2872	B.37	C.15
1.2873	B.38	C.15
1.2874	B.39	C.15
1.2875	B.40	C.15
1.2876	B.41	C.15
1.2877	B.42	C.15
1.2878	B.43	C.15
1.2879	B.44	C.15
1.2880	B.45	C.15
1.2881	B.46	C.15
1.2882	B.47	C.15
1.2883	B.48	C.15
1.2884	B.49	C.15
1.2885	B.50	C.15
1.2886	B.51	C.15
1.2887	B.52	C.15
1.2888	B.53	C.15
1.2889	B.54	C.15
1.2890	B.55	C.15
1.2891	B.56	C.15
1.2892	B.57	C.15
1.2893	B.58.	C.15
1.2894	B.59	C.15
1.2895	B.60	C.15
1.2896	B.61	C.15
1.2897	B.62	C.15
1.2898	B.63	C.15
1.2899	B.64	C.15
1.2900	B.65	C.15
1.2901	B.66	C.15
1.2902	B.67	C.15
1.2903	B.68	C.15
1.2904	B.69	C.15

comp. no.	herbi- cide B	safe- ner C
1.2905	B.70	C.15
1.2906	B.71	C.15
1.2907	B.72	C.15
1.2908	B.73	C.15
1.2909	B.74	C.15
1.2910	B.75	C.15
1.2911	B.76	C.15
1.2912	B.77	C.15
1.2913	B.78	C.15
1.2914	B.79	C.15
1.2915	B.80	C.15
1.2916	B.81	C.15
1.2917	B.82	C.15
1.2918	B.83	C.15
1.2919	B.84	C.15
1.2920	B.85	C.15
1.2921	B.86	C.15
1.2922	B.87	C.15
1.2923	B.88	C.15
1.2924	B.89	C.15
1.2925	B.90	C.15
1.2926	B.91	C.15
1.2927	B.92	C.15
1.2928	B.93	C.15
1.2929	B.94	C.15
1.2930	B.95	C.15
1.2931	B.96	C.15
1.2932	B.97	C.15
1.2933	B.98	C.15
1.2934	B.99	C.15
1.2935	B.100	C.15
1.2936	B.101	C.15
1.2937	B.102	C.15
1.2938	B.103	C.15
1.2939	B.104	C.15
1.2940	B.105	C.15

comp. no.	herbi- cide B	safe- ner C
1.2941	B.106	C.15
1.2942	B.107	C.15
1.2943	B.108	C.15
1.2944	B.109	C.15
1.2945	B.110	C.15
1.2946	B.111	C.15
1.2947	B.112	C.15
1.2948	B.113	C.15
1.2949	B.114	C.15
1.2950	B.115	C.15
1.2951	B.116	C.15
1.2952	B.117	C.15
1.2953	B.118	C.15
1.2954	B.119	C.15
1.2955	B.120	C.15
1.2956	B.121	C.15
1.2957	B.122	C.15
1.2958	B.123	C.15
1.2959	B.124	C.15
1.2960	B.125	C.15
1.2961	B.126	C.15
1.2962	B.127	C.15
1.2963	B.128	C.15
1.2964	B.129	C.15
1.2965	B.130	C.15
1.2966	B.131	C.15
1.2967	B.132	C.15
1.2968	B.133	C.15
1.2969	B.134	C.15
1.2970	B.135	C.15
1.2971	B.136	C.15
1.2972	B.137	C.15
1.2973	B.138	C.15
1.2974	B.139	C.15
1.2975	B.140	C.15
1.2976	B.141	C.15

comp. no.	herbi- cide B	safe- ner C
1.2977	B.142	C.15
1.2978	B.143	C.15
1.2979	B.144	C.15
1.2980	B.145	C.15
1.2981	B.146	C.15
1.2982	B.147	C.15
1.2983	B.148	C.15
1.2984	B.149	C.15
1.2985	B.150	C.15
1.2986	B.151	C.15
1.2987	B.152	C.15
1.2988	B.153	C.15
1.2989	B.154	C.15
1.2990	B.155	C.15
1.2991	B.156	C.15
1.2992	B.157	C.15
1.2993	B.158	C.15
1.2994	B.159	C.15
1.2995	B.160	C.15
1.2996	B.161	C.15
1.2997	B.162	C.15
1.2998	B.163	C.15
1.2999	B.164	C.15
1.3000	B.165	C.15
1.3001	B.166	C.15
1.3002	B.167	C.15
1.3003	B.168	C.15
1.3004	B.169	C.15
1.3005	B.170	C.15
1.3006	B.171	C.15
1.3007	B.172	C.15
1.3008	B.173	C.15
1.3009	B.174	C.15
1.3010	B.175	C.15
1.3011	B.176	C.15
1.3012	B.177	C.15

comp. no.	herbi- cide B	safe- ner C
1.3013	B.178	C.15
1.3014	B.179	C.15
1.3015	B.180	C.15
1.3016	B.181	C.15
1.3017	B.182	C.15
1.3018	B.183	C.15
1.3019	B.184	C.15
1.3020	B.185	C.15
1.3021	B.186	C.15
1.3022	B.187	C.15
1.3023	B.188	C.15
1.3024	B.189	C.15
1.3025	B.1	C.16
1.3026	B.2	C.16
1.3027	B.3	C.16
1.3028	B.4	C.16
1.3029	B.5	C.16
1.3030	B.6	C.16
1.3031	B.7	C.16
1.3032	B.8	C.16
1.3033	B.9	C.16
1.3034	B.10	C.16
1.3035	B.11	C.16
1.3036	B.12	C.16
1.3037	B.13	C.16
1.3038	B.14	C.16
1.3039	B.15	C.16
1.3040	B.16	C.16
1.3041	B.17	C.16
1.3042	B.18	C.16
1.3043	B.19	C.16
1.3044	B.20	C.16
1.3045	B.21	C.16
1.3046	B.22	C.16
1.3047	B.23	C.16
1.3048	B.24	C.16

WO 2018/019860

PCT/EP2017/068817

86

comp. no.	herbi- cide B	safe- ner C
1.3049	B.25	C.16
1.3050	B.26	C.16
1.3051	B.27	C.16
1.3052	B.28	C.16
1.3053	B.29	C.16
1.3054	B.30	C.16
1.3055	B.31	C.16
1.3056	B.32	C.16
1.3057	B.33	C.16
1.3058	B.34	C.16
1.3059	B.35	C.16
1.3060	B.36	C.16
1.3061	B.37	C.16
1.3062	B.38	C.16
1.3063	B.39	C.16
1.3064	B.40	C.16
1.3065	B.41	C.16
1.3066	B.42	C.16
1.3067	B.43	C.16
1.3068	B.44	C.16
1.3069	B.45	C.16
1.3070	B.46	C.16
1.3071	B.47	C.16
1.3072	B.48	C.16
1.3073	B.49	C.16
1.3074	B.50	C.16
1.3075	B.51	C.16
1.3076	B.52	C.16
1.3077	B.53	C.16
1.3078	B.54	C.16
1.3079	B.55	C.16
1.3080	B.56	C.16
1.3081	B.57	C.16
1.3082	B.58.	C.16
1.3083	B.59	C.16
1.3084	B.60	C.16

comp. no.	herbi- cide B	safe- ner C
1.3085	B.61	C.16
1.3086	B.62	C.16
1.3087	B.63	C.16
1.3088	B.64	C.16
1.3089	B.65	C.16
1.3090	B.66	C.16
1.3091	B.67	C.16
1.3092	B.68	C.16
1.3093	B.69	C.16
1.3094	B.70	C.16
1.3095	B.71	C.16
1.3096	B.72	C.16
1.3097	B.73	C.16
1.3098	B.74	C.16
1.3099	B.75	C.16
1.3100	B.76	C.16
1.3101	B.77	C.16
1.3102	B.78	C.16
1.3103	B.79	C.16
1.3104	B.80	C.16
1.3105	B.81	C.16
1.3106	B.82	C.16
1.3107	B.83	C.16
1.3108	B.84	C.16
1.3109	B.85	C.16
1.3110	B.86	C.16
1.3111	B.87	C.16
1.3112	B.88	C.16
1.3113	B.89	C.16
1.3114	B.90	C.16
1.3115	B.91	C.16
1.3116	B.92	C.16
1.3117	B.93	C.16
1.3118	B.94	C.16
1.3119	B.95	C.16
1.3120	B.96	C.16

comp. no.	herbi- cide B	safe- ner C
1.3121	B.97	C.16
1.3122	B.98	C.16
1.3123	B.99	C.16
1.3124	B.100	C.16
1.3125	B.101	C.16
1.3126	B.102	C.16
1.3127	B.103	C.16
1.3128	B.104	C.16
1.3129	B.105	C.16
1.3130	B.106	C.16
1.3131	B.107	C.16
1.3132	B.108	C.16
1.3133	B.109	C.16
1.3134	B.110	C.16
1.3135	B.111	C.16
1.3136	B.112	C.16
1.3137	B.113	C.16
1.3138	B.114	C.16
1.3139	B.115	C.16
1.3140	B.116	C.16
1.3141	B.117	C.16
1.3142	B.118	C.16
1.3143	B.119	C.16
1.3144	B.120	C.16
1.3145	B.121	C.16
1.3146	B.122	C.16
1.3147	B.123	C.16
1.3148	B.124	C.16
1.3149	B.125	C.16
1.3150	B.126	C.16
1.3151	B.127	C.16
1.3152	B.128	C.16
1.3153	B.129	C.16
1.3154	B.130	C.16
1.3155	B.131	C.16
1.3156	B.132	C.16

comp. no.	herbi- cide B	safe- ner C
1.3157	B.133	C.16
1.3158	B.134	C.16
1.3159	B.135	C.16
1.3160	B.136	C.16
1.3161	B.137	C.16
1.3162	B.138	C.16
1.3163	B.139	C.16
1.3164	B.140	C.16
1.3165	B.141	C.16
1.3166	B.142	C.16
1.3167	B.143	C.16
1.3168	B.144	C.16
1.3169	B.145	C.16
1.3170	B.146	C.16
1.3171	B.147	C.16
1.3172	B.148	C.16
1.3173	B.149	C.16
1.3174	B.150	C.16
1.3175	B.151	C.16
1.3176	B.152	C.16
1.3177	B.153	C.16
1.3178	B.154	C.16
1.3179	B.155	C.16
1.3180	B.156	C.16
1.3181	B.157	C.16
1.3182	B.158	C.16
1.3183	B.159	C.16
1.3184	B.160	C.16
1.3185	B.161	C.16
1.3186	B.162	C.16
1.3187	B.163	C.16
1.3188	B.164	C.16
1.3189	B.165	C.16
1.3190	B.166	C.16
1.3191	B.167	C.16
1.3192	B.168	C.16

comp. no.	herbi- cide B	safe- ner C
1.3193	B.169	C.16
1.3194	B.170	C.16
1.3195	B.171	C.16
1.3196	B.172	C.16
1.3197	B.173	C.16
1.3198	B.174	C.16
1.3199	B.175	C.16
1.3200	B.176	C.16
1.3201	B.177	C.16
1.3202	B.178	C.16
1.3203	B.179	C.16
1.3204	B.180	C.16
1.3205	B.181	C.16
1.3206	B.182	C.16
1.3207	B.183	C.16
1.3208	B.184	C.16
1.3209	B.185	C.16
1.3210	B.186	C.16
1.3211	B.187	C.16
1.3212	B.188	C.16
1.3213	B.189	C.16
1.3214	B.1	C.17
1.3215	B.2	C.17
1.3216	B.3	C.17
1.3217	B.4	C.17
1.3218	B.5	C.17
1.3219	B.6	C.17
1.3220	B.7	C.17
1.3221	B.8	C.17
1.3222	B.9	C.17
1.3223	B.10	C.17
1.3224	B.11	C.17
1.3225	B.12	C.17
1.3226	B.13	C.17
1.3227	B.14	C.17
1.3228	B.15	C.17

comp. no.	herbi- cide B	safe- ner C
1.3229	B.16	C.17
1.3230	B.17	C.17
1.3231	B.18	C.17
1.3232	B.19	C.17
1.3233	B.20	C.17
1.3234	B.21	C.17
1.3235	B.22	C.17
1.3236	B.23	C.17
1.3237	B.24	C.17
1.3238	B.25	C.17
1.3239	B.26	C.17
1.3240	B.27	C.17
1.3241	B.28	C.17
1.3242	B.29	C.17
1.3243	B.30	C.17
1.3244	B.31	C.17
1.3245	B.32	C.17
1.3246	B.33	C.17
1.3247	B.34	C.17
1.3248	B.35	C.17
1.3249	B.36	C.17
1.3250	B.37	C.17
1.3251	B.38	C.17
1.3252	B.39	C.17
1.3253	B.40	C.17
1.3254	B.41	C.17
1.3255	B.42	C.17
1.3256	B.43	C.17
1.3257	B.44	C.17
1.3258	B.45	C.17
1.3259	B.46	C.17
1.3260	B.47	C.17
1.3261	B.48	C.17
1.3262	B.49	C.17
1.3263	B.50	C.17
1.3264	B.51	C.17

comp. no.	herbi- cide B	safe- ner C
1.3265	B.52	C.17
1.3266	B.53	C.17
1.3267	B.54	C.17
1.3268	B.55	C.17
1.3269	B.56	C.17
1.3270	B.57	C.17
1.3271	B.58.	C.17
1.3272	B.59	C.17
1.3273	B.60	C.17
1.3274	B.61	C.17
1.3275	B.62	C.17
1.3276	B.63	C.17
1.3277	B.64	C.17
1.3278	B.65	C.17
1.3279	B.66	C.17
1.3280	B.67	C.17
1.3281	B.68	C.17
1.3282	B.69	C.17
1.3283	B.70	C.17
1.3284	B.71	C.17
1.3285	B.72	C.17
1.3286	B.73	C.17
1.3287	B.74	C.17
1.3288	B.75	C.17
1.3289	B.76	C.17
1.3290	B.77	C.17
1.3291	B.78	C.17
1.3292	B.79	C.17
1.3293	B.80	C.17
1.3294	B.81	C.17
1.3295	B.82	C.17
1.3296	B.83	C.17
1.3297	B.84	C.17
1.3298	B.85	C.17
1.3299	B.86	C.17
1.3300	B.87	C.17

comp. no.	herbi- cide B	safe- ner C
1.3301	B.88	C.17
1.3302	B.89	C.17
1.3303	B.90	C.17
1.3304	B.91	C.17
1.3305	B.92	C.17
1.3306	B.93	C.17
1.3307	B.94	C.17
1.3308	B.95	C.17
1.3309	B.96	C.17
1.3310	B.97	C.17
1.3311	B.98	C.17
1.3312	B.99	C.17
1.3313	B.100	C.17
1.3314	B.101	C.17
1.3315	B.102	C.17
1.3316	B.103	C.17
1.3317	B.104	C.17
1.3318	B.105	C.17
1.3319	B.106	C.17
1.3320	B.107	C.17
1.3321	B.108	C.17
1.3322	B.109	C.17
1.3323	B.110	C.17
1.3324	B.111	C.17
1.3325	B.112	C.17
1.3326	B.113	C.17
1.3327	B.114	C.17
1.3328	B.115	C.17
1.3329	B.116	C.17
1.3330	B.117	C.17
1.3331	B.118	C.17
1.3332	B.119	C.17
1.3333	B.120	C.17
1.3334	B.121	C.17
1.3335	B.122	C.17
1.3336	B.123	C.17

comp. no.	herbi- cide B	safe- ner C
1.3337	B.124	C.17
1.3338	B.125	C.17
1.3339	B.126	C.17
1.3340	B.127	C.17
1.3341	B.128	C.17
1.3342	B.129	C.17
1.3343	B.130	C.17
1.3344	B.131	C.17
1.3345	B.132	C.17
1.3346	B.133	C.17
1.3347	B.134	C.17
1.3348	B.135	C.17
1.3349	B.136	C.17
1.3350	B.137	C.17
1.3351	B.138	C.17
1.3352	B.139	C.17
1.3353	B.140	C.17
1.3354	B.141	C.17
1.3355	B.142	C.17
1.3356	B.143	C.17
1.3357	B.144	C.17
1.3358	B.145	C.17
1.3359	B.146	C.17
1.3360	B.147	C.17
1.3361	B.148	C.17
1.3362	B.149	C.17
1.3363	B.150	C.17
1.3364	B.151	C.17
1.3365	B.152	C.17
1.3366	B.153	C.17
1.3367	B.154	C.17
1.3368	B.155	C.17
1.3369	B.156	C.17
1.3370	B.157	C.17
1.3371	B.158	C.17
1.3372	B.159	C.17

comp. no.	herbi- cide B	safe- ner C
1.3373	B.160	C.17
1.3374	B.161	C.17
1.3375	B.162	C.17
1.3376	B.163	C.17
1.3377	B.164	C.17
1.3378	B.165	C.17
1.3379	B.166	C.17
1.3380	B.167	C.17
1.3381	B.168	C.17
1.3382	B.169	C.17
1.3383	B.170	C.17
1.3384	B.171	C.17
1.3385	B.172	C.17
1.3386	B.173	C.17
1.3387	B.174	C.17
1.3388	B.175	C.17
1.3389	B.176	C.17
1.3390	B.177	C.17
1.3391	B.178	C.17
1.3392	B.179	C.17
1.3393	B.180	C.17
1.3394	B.181	C.17
1.3395	B.182	C.17
1.3396	B.183	C.17
1.3397	B.184	C.17
1.3398	B.185	C.17
1.3399	B.186	C.17
1.3400	B.187	C.17
1.3401	B.188	C.17
1.3402	B.189	C.17
1.3403	--	C.1
1.3404	--	C.2
1.3405	--	C.3
1.3406	--	C.4
1.3407	--	C.5
1.3408	--	C.6

comp. no.	herbi- cide B	safe- ner C
1.3409	--	C.7
1.3410	--	C.8
1.3411	--	C.9
1.3412	--	C.10
1.3413	--	C.11
1.3414	--	C.12
1.3415	--	C.13
1.3416	--	C.14
1.3417	--	C.15
1.3418	--	C.16
1.3419	--	C.17

The specific number for each single composition is deductible as follows:

Composition 1.777 for example comprises the phenylpyridine of formula (I.a.200),
cloransulam-methyl (B.21) and cyprosulfamide (C.4) (*see table 1, entry 1.777; as well as*
5 *table B, entry B.21 and table C, entry C.4*).

Composition 2.777 for example comprises the phenylpyridine of formula (I.a.207) (*see the*
definition for compositions 2.1 to 2.3419 below), cloransulam-methyl (B.21) and
cyprosulfamide (C.4) (*see table 1, entry 1.777; as well as table B, entry B.21 and table C,*
10 *entry C.4*).

Composition 7.777 for example comprises saflufenacil (B.92) (*see the definition for*
compositions 7.1 to 7.3383 below), and the compound (I.a.200), cloransulam-methyl (B.21)
and cyprosulfamide (C.4) (*see table 1, entry 1.777; as well as table B, entry B.21 and table*
15 *C, entry C.4*).

Also especially preferred are compositions 2.1. to 2.3419 which differ from the
corresponding compositions 1.1 to 1.3419 only in that they comprise as the active
20 compound A (I.a.207).

Also especially preferred are compositions 3.1. to 3.3419 which differ from the
corresponding compositions 1.1 to 1.3419 only in that they comprise as the active
compound A (I.a.214).
25

Also especially preferred are compositions 4.1. to 4.3419 which differ from the
corresponding compositions 1.1 to 1.3419 only in that they comprise as the active
compound A (I.a.228).

Also especially preferred are compositions 5.1. to 5.3419 which differ from the
corresponding compositions 1.1 to 1.3419 only in that they comprise as the active
compound A (I.a.234).
30

Also especially preferred are compositions 6.1. to 6.3419 which differ from the
corresponding compositions 1.1 to 1.3419 only in that they additionally comprise B.88 as
further herbicide B.
35

Also especially preferred are compositions 7.1. to 7.3419 which differ from the
corresponding compositions 1.1 to 1.3419 only in that they additionally comprise B.92 as
further herbicide B.
40

Also especially preferred are compositions 8.1. to 8.3419 which differ from the corresponding compositions 1.1 to 1.3419 only in that they additionally comprise B.95 as further herbicide B.

- 5 Also especially preferred are compositions 9.1. to 9.3419 which differ from the corresponding compositions 1.1 to 1.3419 only in that they additionally comprise B.116 as further herbicide B.

- 10 Also especially preferred are compositions 10.1. to 10.3419 which differ from the corresponding compositions 1.1 to 1.3419 only in that they additionally comprise B.125 as further herbicide B.

- 15 Also especially preferred are compositions 11.1. to 11.3419 which differ from the corresponding compositions 1.1 to 1.3419 only in that they additionally comprise B.151 as further herbicide B.

- 20 Also especially preferred are compositions 12.1. to 12.3419 which differ from the corresponding compositions 1.1 to 1.3419 only in that they additionally comprise B.88 and B.116 as further herbicides B.

- 25 Also especially preferred are compositions 13.1. to 13.3419 which differ from the corresponding compositions 1.1 to 1.3419 only in that they additionally comprise B.92 and B.116 as further herbicides B.

- Also especially preferred are compositions 14.1. to 14.3419 which differ from the corresponding compositions 1.1 to 1.3419 only in that they additionally comprise B.95 and B.116 as further herbicides B.

- 30 Also especially preferred are compositions 15.1. to 15.3419 which differ from the corresponding compositions 1.1 to 1.3419 only in that they additionally comprise B.116 and B.125 as further herbicides B.

- 35 Also especially preferred are compositions 16.1. to 16.3419 which differ from the corresponding compositions 1.1 to 1.3419 only in that they additionally comprise B.116 and B.151 as further herbicides B.

- 40 Also especially preferred are compositions 17.1. to 17.3419 which differ from the corresponding compositions 1.1 to 1.3419 only in that they additionally comprise B.88 , B.92 and B.116 as further herbicides B.

Also especially preferred are compositions 18.1. to 18.3419 which differ from the corresponding compositions 1.1 to 1.3419 only in that they additionally comprise B.95, B.92 and B.116 as further herbicides B.

5 Also especially preferred are compositions 19.1. to 19.3419 which differ from the corresponding compositions 1.1 to 1.3419 only in that they additionally comprise B.92, B.116 and B.125 as further herbicides B.

10 Also especially preferred are compositions 20.1. to 20.3419 which differ from the corresponding compositions 1.1 to 1.3419 only in that they additionally comprise B.92, B.116 and B.151 as further herbicides B.

15 It is generally preferred to use the compounds of the invention in combination with herbicides that are selective for the crop being treated and which complement the spectrum of weeds controlled by these compounds at the application rate employed. It is further generally preferred to apply the compounds of the invention and other complementary herbicides at the same time, either as a combination formulation or as a tank mix.

20 It is recognized that the polynucleotide molecules and polypeptides of the invention encompass polypeptides comprising an amino acid sequence that is sufficiently identical to the amino acid sequences set forth in SEQ ID Nos: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 25 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 30 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 35 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 40 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541,

542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, or 565,. The term "sufficiently identical" is used herein to refer to a first amino acid or nucleotide sequence that contains a sufficient or minimum number of identical or equivalent (e.g., with a similar side chain) amino acid residues or nucleotides to a second amino acid or nucleotide sequence such that the first and second amino acid or nucleotide sequences have a common structural domain and/or common functional activity.

Generally, "sequence identity" refers to the extent to which two optimally aligned DNA or amino acid sequences are invariant throughout a window of alignment of components, e.g., nucleotides or amino acids. An "identity fraction" for aligned segments of a test sequence and a reference sequence is the number of identical components that are shared by the two aligned sequences divided by the total number of components in reference sequence segment, i.e., the entire reference sequence or a smaller defined part of the reference sequence. "Percent identity" is the identity fraction times 100. Optimal alignment of sequences for aligning a comparison window are well known to those skilled in the art and may be conducted by tools such as the local homology algorithm of Smith and Waterman, the homology alignment algorithm of Needleman and Wunsch, the search for similarity method of Pearson and Lipman, and preferably by computerized implementations of these algorithms such as GAP, BESTFIT, FASTA, and TFASTA available as part of the GCG. Wisconsin Package. (Accelrys Inc. Burlington, Mass.)

Polynucleotides and Oligonucleotides

By an "isolated polynucleotide", including DNA, RNA, or a combination of these, single or double stranded, in the sense or antisense orientation or a combination of both, dsRNA or otherwise, we mean a polynucleotide which is at least partially separated from the polynucleotide sequences with which it is associated or linked in its native state. That means other nucleic acid molecules are present in an amount less than 5% based on weight of the amount of the desired nucleic acid, preferably less than 2% by weight, more preferably less than 1% by weight, most preferably less than 0.5% by weight. Preferably, an "isolated" nucleic acid is free of some of the sequences that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated herbicide resistance and/or tolerance related protein encoding nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be free from some of the other cellular material with which it is naturally associated, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. Preferably, the isolated polynucleotide is at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other components with which they are naturally

associated. As the skilled addressee would be aware, an isolated polynucleotide can be an exogenous polynucleotide present in, for example, a transgenic organism which does not naturally comprise the polynucleotide. Furthermore, the terms "polynucleotide(s)", "nucleic acid sequence(s)", "nucleotide sequence(s)", "nucleic acid(s)", "nucleic acid molecule" are used interchangeably herein and refer to nucleotides, either ribonucleotides or deoxyribonucleotides or a combination of both, in a polymeric unbranched form of any length.

The term "mutated PPO nucleic acid" refers to a PPO nucleic acid having a sequence that is mutated from a wild-type PPO nucleic acid, such as e.g. SEQ ID NO: 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 624, or 626, or homologues, paralogues and orthologues thereof; and that confers increased phenylpyridine herbicide tolerance to a plant in which it is expressed. Furthermore, the term "mutated protoporphyrinogen oxidase (mutated PPO)" refers to the replacement of an amino acid of the wild-type primary sequences SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, or a variant, a derivative, a homologue, an orthologue, or paralogue thereof, with another amino acid. The expression "mutated amino acid" will be used below to designate the amino acid which is replaced by another amino acid, thereby designating the site of the mutation in the primary sequence of the protein.

In a preferred embodiment, the PPO nucleotide sequence encoding a mutated PPO comprises the sequence of SEQ ID NO: 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 624, or 626, or a variant or derivative thereof.

Furthermore, it will be understood by the person skilled in the art that the PPO nucleotide sequences encompass homologues, paralogues and orthologues of SEQ ID NO: 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 624, or 626, as defined hereinafter.

The term "variant" with respect to a sequence (e.g., a polypeptide or nucleic acid sequence such as – for example – a transcription regulating nucleotide sequence of the invention) is intended to mean substantially similar sequences. For nucleotide sequences comprising an open reading frame, variants include those sequences that, because of the degeneracy of the genetic code, encode the identical amino acid sequence of the native protein. Naturally occurring allelic variants such as these can be identified with the use of well-known molecular biology techniques, as, for example, with polymerase chain reaction (PCR) and hybridization techniques. Variant nucleotide sequences also include synthetically derived

nucleotide sequences, such as those generated, for example, by using site-directed mutagenesis and for open reading frames, encode the native protein, as well as those that encode a polypeptide having amino acid substitutions relative to the native protein, e.g. the mutated PPO according to the present invention as disclosed herein.

5

Generally, nucleotide sequence variants of the invention will have at least 30, 40, 50, 60, to 70%, e.g., preferably 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, to 79%, generally at least 80%, e.g., 81%-84%, at least 85%, e.g., 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, to 98% and 99% nucleotide "sequence identity" to the nucleotide
 10 sequence encoding a polypeptide of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107,
 15 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321,
 20 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416,
 25 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508,
 30 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, or 565.

35 The % identity of a polynucleotide is determined by GAP (Needleman and Wunsch, 1970) analysis (GCG program) with a gap creation penalty=5, and a gap extension penalty=0.3. Unless stated otherwise, the query sequence is at least 45 nucleotides in length, and the GAP analysis aligns the two sequences over a region of at least 45 nucleotides. Preferably,
 40 the query sequence is at least 150 nucleotides in length, and the GAP analysis aligns the two sequences over a region of at least 150 nucleotides. More preferably, the query sequence is at least 300 nucleotides in length and the GAP analysis aligns the two sequences over a region of at least 300 nucleotides. Even more preferably, the GAP analysis aligns the two sequences over their entire length.

Polypeptides

By "substantially purified polypeptide" or "purified" a polypeptide is meant that has been
5 separated from one or more lipids, nucleic acids, other polypeptides, or other contaminating
molecules with which it is associated in its native state. It is preferred that the substantially
purified polypeptide is at least 60% free, more preferably at least 75% free, and more
preferably at least 90% free from other components with which it is naturally associated. As
the skilled addressee will appreciate, the purified polypeptide can be a recombinantly
10 produced polypeptide. The terms "polypeptide" and "protein" are generally used
interchangeably and refer to a single polypeptide chain which may or may not be modified
by addition of non-amino acid groups. It would be understood that such polypeptide chains
may associate with other polypeptides or proteins or other molecules such as co-factors.
The terms "proteins" and "polypeptides" as used herein also include variants, mutants,
15 modifications, analogous and/or derivatives of the polypeptides of the invention as
described herein.

The % identity of a polypeptide is determined by GAP (Needleman and Wunsch, 1970)
analysis (GCG program) with a gap creation penalty=5, and a gap extension penalty=0.3.
20 The query sequence is at least 25 amino acids in length, and the GAP analysis aligns the
two sequences over a region of at least 25 amino acids. More preferably, the query
sequence is at least 50 amino acids in length, and the GAP analysis aligns the two
sequences over a region of at least 50 amino acids. More preferably, the query sequence is
at least 100 amino acids in length and the GAP analysis aligns the two sequences over a
25 region of at least 100 amino acids. Even more preferably, the query sequence is at least
250 amino acids in length and the GAP analysis aligns the two sequences over a region of
at least 250 amino acids. Even more preferably, the GAP analysis aligns the two sequences
over their entire length.

30 With regard to a defined polypeptide, it will be appreciated that % identity figures higher
than those provided above will encompass preferred embodiments. Thus, where applicable,
in light of the minimum % identity figures, it is preferred that the PPO polypeptide of the
invention comprises an amino acid sequence which is at least 40%, more preferably at least
45%, more preferably at least 50%, more preferably at least 55%, more preferably at least
35 60%, more preferably at least 65%, more preferably at least 70%, more preferably at least
75%, more preferably at least 80%, more preferably at least 85%, more preferably at least
90%, more preferably at least 91%, more preferably at least 92%, more preferably at least
93%, more preferably at least 94%, more preferably at least 95%, more preferably at least
96%, more preferably at least 97%, more preferably at least 98%, more preferably at least
40 99%, more preferably at least 99.1%, more preferably at least 99.2%, more preferably at
least 99.3%, more preferably at least 99.4%, more preferably at least 99.5%, more
preferably at least 99.6%, more preferably at least 99.7%, more preferably at least 99.8%,

and even more preferably at least 99.9% identical to SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, or 565.

25

By "variant" polypeptide is intended a polypeptide derived from the protein of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464,

465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, or 565, by deletion (so-called truncation) or addition of one or more amino acids to the N-terminal and/or C-terminal end of the native protein; deletion or addition of one or more amino acids at one or more sites in the native protein; or substitution of one or more amino acids at one or more sites in the native protein.

Such variants may result from, for example, genetic polymorphism or from human manipulation. Methods for such manipulations are generally known in the art.

“Derivatives” of a protein encompass peptides, oligopeptides, polypeptides, proteins and enzymes having amino acid substitutions, deletions and/or insertions relative to the unmodified protein in question and having similar biological and functional activity as the unmodified protein from which they are derived.

“Homologues” of a protein encompass peptides, oligopeptides, polypeptides, proteins and enzymes having amino acid substitutions, deletions and/or insertions relative to the unmodified protein in question and having similar biological and functional activity as the unmodified protein from which they are derived.

A deletion refers to removal of one or more amino acids from a protein.

An insertion refers to one or more amino acid residues being introduced into a predetermined site in a protein. Insertions may comprise N-terminal and/or C-terminal fusions as well as intra-sequence insertions of single or multiple amino acids. Generally, insertions within the amino acid sequence will be smaller than N- or C-terminal fusions, of the order of about 1 to 10 residues. Examples of N- or C-terminal fusion proteins or peptides include the binding domain or activation domain of a transcriptional activator as used in the yeast two-hybrid system, phage coat proteins, (histidine)-6-tag, glutathione S-transferase-tag, protein A, maltose-binding protein, dihydrofolate reductase, Tag•100 epitope, c-myc epitope, FLAG®-epitope, lacZ, CMP (calmodulin-binding peptide), HA epitope, protein C epitope and VSV epitope.

A substitution refers to replacement of amino acids of the protein with other amino acids having similar properties (such as similar hydrophobicity, hydrophilicity, antigenicity, propensity to form or break α -helical structures or β -sheet structures). Amino acid substitutions are typically of single residues, but may be clustered depending upon functional constraints placed upon the polypeptide and may range from 1 to 10 amino acids; insertions will usually be of the order of about 1 to 10 amino acid residues. The amino acid substitutions are preferably conservative amino acid substitutions. Conservative substitution

tables are well known in the art (see for example Creighton (1984) Proteins. W.H. Freeman and Company (Eds)).

Table 1: Examples of conserved amino acid substitutions

Residue	Conservative Substitutions	Residue	Conservative Substitutions
Ala	Ser	Leu	Ile; Val
Arg	Lys	Lys	Arg; Gln
Asn	Gln; His	Met	Leu; Ile
Asp	Glu	Phe	Met; Leu; Tyr
Gln	Asn	Ser	Thr; Gly
Cys	Ser	Thr	Ser; Val
Glu	Asp	Trp	Tyr
Gly	Pro	Tyr	Trp; Phe
His	Asn; Gln	Val	Ile; Leu
Ile	Leu, Val		

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Amino acid substitutions, deletions and/or insertions may readily be made using peptide synthetic techniques well known in the art, such as solid phase peptide synthesis and the like, or by recombinant DNA manipulation. Methods for the manipulation of DNA sequences to produce substitution, insertion or deletion variants of a protein are well known in the art.

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For example, techniques for making substitution mutations at predetermined sites in DNA are well known to those skilled in the art and include M13 mutagenesis, T7-Gen in vitro mutagenesis (USB, Cleveland, OH), QuickChange Site Directed mutagenesis (Stratagene, San Diego, CA), PCR-mediated site-directed mutagenesis or other site-directed mutagenesis protocols.

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“Derivatives” further include peptides, oligopeptides, polypeptides which may, compared to the amino acid sequence of the naturally-occurring form of the protein, such as the protein of interest, comprise substitutions of amino acids with non-naturally occurring amino acid residues, or additions of non-naturally occurring amino acid residues. “Derivatives” of a

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protein also encompass peptides, oligopeptides, polypeptides which comprise naturally occurring altered (glycosylated, acylated, prenylated, phosphorylated, myristoylated, sulphated etc.) or non-naturally altered amino acid residues compared to the amino acid sequence of a naturally-occurring form of the polypeptide. A derivative may also comprise one or more non-amino acid substituents or additions compared to the amino acid

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sequence from which it is derived, for example a reporter molecule or other ligand, covalently or non-covalently bound to the amino acid sequence, such as a reporter molecule which is bound to facilitate its detection, and non-naturally occurring amino acid residues relative to the amino acid sequence of a naturally-occurring protein. Furthermore,

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“derivatives” also include fusions of the naturally-occurring form of the protein with tagging peptides such as FLAG, HIS6 or thioredoxin (for a review of tagging peptides, see Terpe,

Appl. Microbiol. Biotechnol. 60, 523-533, 2003).

“Orthologues” and “paralogues” encompass evolutionary concepts used to describe the ancestral relationships of genes. Paralogues are genes within the same species that have originated through duplication of an ancestral gene; orthologues are genes from different organisms that have originated through speciation, and are also derived from a common ancestral gene.

It is well-known in the art that paralogues and orthologues may share distinct domains harboring suitable amino acid residues at given sites, such as binding pockets for particular substrates or binding motifs for interaction with other proteins.

The term “domain” refers to a set of amino acids conserved at specific positions along an alignment of sequences of evolutionarily related proteins. While amino acids at other positions can vary between homologues, amino acids that are highly conserved at specific positions indicate amino acids that are likely essential in the structure, stability or function of a protein. Identified by their high degree of conservation in aligned sequences of a family of protein homologues, they can be used as identifiers to determine if any polypeptide in question belongs to a previously identified polypeptide family.

The term “motif” or “consensus sequence” refers to a short conserved region in the sequence of evolutionarily related proteins. Motifs are frequently highly conserved parts of domains, but may also include only part of the domain, or be located outside of conserved domain (if all of the amino acids of the motif fall outside of a defined domain). Preferred motifs which are contained in the sequences of the PPO polypeptides according to the present invention are SQ[N/K/H]KRYI, TLGTLFSS, [F/Y]TTF[V/I]GG.

Specialist databases exist for the identification of domains, for example, SMART (Schultz et al. (1998) Proc. Natl. Acad. Sci. USA 95, 5857-5864; Letunic et al. (2002) Nucleic Acids Res 30, 242-244), InterPro (Mulder et al., (2003) Nucl. Acids. Res. 31, 315-318), Prosite (Bucher and Bairoch (1994), A generalized profile syntax for biomolecular sequences motifs and its function in automatic sequence interpretation. (In) ISMB-94; Proceedings 2nd International Conference on Intelligent Systems for Molecular Biology. Altman R., Brutlag D., Karp P., Lathrop R., Searls D., Eds., pp53-61, AAAI Press, Menlo Park; Hulo et al., Nucl. Acids. Res. 32:D134-D137, (2004)), or Pfam (Bateman et al., Nucleic Acids Research 30(1): 276-280 (2002)). A set of tools for in silico analysis of protein sequences is available on the ExPASy proteomics server (Swiss Institute of Bioinformatics (Gasteiger et al., ExPASy: the proteomics server for in-depth protein knowledge and analysis, Nucleic Acids Res. 31:3784-3788(2003)). Domains or motifs may also be identified using routine techniques, such as by sequence alignment.

Methods for the alignment of sequences for comparison are well known in the art, such

methods include GAP, BESTFIT, BLAST, FASTA and TFASTA. GAP uses the algorithm of Needleman and Wunsch ((1970) J Mol Biol 48: 443-453) to find the global (i.e. spanning the complete sequences) alignment of two sequences that maximizes the number of matches and minimizes the number of gaps. The BLAST algorithm (Altschul et al. (1990) J Mol Biol

215: 403-10) calculates percent sequence identity and performs a statistical analysis of the similarity between the two sequences. The software for performing BLAST analysis is publicly available through the National Centre for Biotechnology Information (NCBI).

Homologues may readily be identified using, for example, the ClustalW multiple sequence alignment algorithm (version 1.83), with the default pairwise alignment parameters, and a scoring method in percentage. Global percentages of similarity and identity may also be determined using one of the methods available in the MatGAT software package

(Campanella et al., BMC Bioinformatics. 2003 Jul 10;4:29. MatGAT: an application that generates similarity/identity matrices using protein or DNA sequences.). Minor manual editing may be performed to optimise alignment between conserved motifs, as would be apparent to a person skilled in the art. Furthermore, instead of using full-length sequences for the identification of homologues, specific domains may also be used. The sequence identity values may be determined over the entire nucleic acid or amino acid sequence or over selected domains or conserved motif(s), using the programs mentioned above using the default parameters. For local alignments, the Smith-Waterman algorithm is particularly useful (Smith TF, Waterman MS (1981) J. Mol. Biol 147(1);195-7).

The inventors of the present invention have found that by substituting one or more of the key amino acid residues, employing e.g. one of the above described methods to mutate the encoding nucleic acids, the phenylpyridine herbicide tolerance or resistance could be remarkably increased as compared to the activity of the wild type PPO enzymes with SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, or 117, . Preferred substitutions of mutated PPO are those that increase the herbicide tolerance of the plant, but leave the biological activity of the oxidase activity substantially unaffected.

Accordingly, in another object of the present invention the key amino acid residues of a PPO enzyme comprising SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, or 117, a variant, derivative, orthologue, paralogue or homologue thereof, is substituted by any other amino acid.

In one embodiment, the key amino acid residues of a PPO enzyme, a variant, derivative, orthologue, paralogue or homologue thereof, is substituted by a conserved amino acid as depicted in Table 1.

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It will be understood by the person skilled in the art that amino acids located in a close proximity to the positions of amino acids mentioned below may also be substituted. Thus, in another embodiment the variant of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 10 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 15 627, a variant, derivative, orthologue, paralogue or homologue thereof comprises a mutated PPO, wherein an amino acid ± 3 , ± 2 or ± 1 amino acid positions from a key amino acid is substituted by any other amino acid.

Based on techniques well-known in the art, a highly characteristic sequence pattern can be developed, by means of which further of mutated PPO candidates with the desired activity may be searched.

Searching for further mutated PPO candidates by applying a suitable sequence pattern would also be encompassed by the present invention. It will be understood by a skilled reader that the present sequence pattern is not limited by the exact distances between two adjacent amino acid residues of said pattern. Each of the distances between two neighbours in the above patterns may, for example, vary independently of each other by up to ± 10 , ± 5 , ± 3 , ± 2 or ± 1 amino acid positions without substantially affecting the desired activity.

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Furthermore, by applying the method of site directed mutagenesis, in particular saturation mutagenesis (see e.g. Schenk et al., Biospektrum 03/2006, pages 277-279), the inventors of the present invention have identified and generated specific amino acid substitutions and combinations thereof, which - when introduced into a plant by transforming and expressing the respective mutated PPO encoding nucleic acid - confer increased herbicide resistance or tolerance to a phenylpyridine herbicide to said plant.

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Thus, in a particularly preferred embodiment, the variant or derivative of the mutated PPO refers to a polypeptide comprising SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 40 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86,

103

87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, or 117, , comprising a single amino acid substitution at positions depicted in the following Table 2a. .

- 5 **Table 2a:** Single amino acid substitutions within SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, or 117

SEQ ID	Organism	Mutated site 1	Mutated site 2	Mutated site 3	Mutated site 4	Mutated site 5
1	Amaranthus tuberculatus	R128	G210	G211	L397	F420
2	Amaranthus tuberculatus	R128	G210	G211	L397	F420
3	Amaranthus tuberculatus	R128	G210	-	L396	F419
4	Amaranthus tuberculatus	R128	G210	-	L396	F419
5	Amaranthus hypochondriacus	R128	G210	G211	L398	F421
6	Amaranthus tuberculatus	R98	G180	G181	L368	F391
7	Spinacia oleracea	R127	G209	G210	L397	F420
8	Vitis vinifera	R100	G182	G183	L373	F396
9	Ricinus communis	R99	A181	G182	L372	F395
10	Theobroma cacao	R98	A180	G181	L370	F393
11	Glycine max	R98	A180	A181	L367	F390
12	Prunus persica	R96	A175	G176	L366	F389
13	Medicago truncatula	R98	A180	A181	L367	F390
14	Fragaria vesca subsp. vesca	R98	A177	G178	L368	F391
15	Citrus clementina	R98	A180	A181	L370	F393
16	Citrus clementina	R98	A180	A181	L370	F393
17	Cicer arietinum	R98	A180	A181	L367	F390
18	Cucumis sativus	R98	A180	G181	L368	F391
19	Cucumis sativus	R93	A175	G176	L363	F386
20	Nicotiana tabacum	R98	G178	G179	L369	F392
21	Solanum lycopersicum	R95	G175	G176	L366	F389
22	Arabidopsis thaliana	R101	A182	A183	L371	F394
23	Arabidopsis lyrata subsp. lyrata	R103	A186	A187	L375	F398
24	Arabidopsis thaliana	R101	A182	A183	L364	F387
25	Arabidopsis thaliana	R147	A228	A229	L410	F433

26	Ambrosia artemisiifolia	R74	G151	G152	L336	F359
27	Setaria italica	R128	A213	G214	L408	F431
28	Sorghum bicolor	R130	A215	G216	L410	F433
29	Arabidopsis thaliana	R101	A152	A153	L341	F364
30	Zea mays	R130	A215	G216	L410	F433
31	Zea mays	R130	A215	G216	L410	F433
32	LEMPA	R105	G188	G189	L381	F404
33	LEMPA	R150	A226	G227	L409	Y432
34	Populus trichocarpa	R100	A182	G183	L373	F396
35	Capsella rubella	R165	A248	A249	L433	F456
36	Brachypodium distachyon	R134	A219	G220	L414	F437
37	Oryza sativa Japonica Group	R95	G179	G180	L374	F397
38	Picea sitchensis	R100	G186	A187	L354	F377
39	Solanum tuberosum	R98	G178	G179	L369	F392
40	Oryza sativa Indica Group	R95	G190	G191	L385	F408
41	Oryza sativa Japonica Group	R95	G190	G191	L385	F408
42	Eutrema salsugineum	R96	A179	A180	L368	F391
43	Selaginella moellendorffii	R97	G175	S176	L377	F400
44	Selaginella moellendorffii	R97	G175	S176	L377	F400
45	Amaranthus tuberculatus	R128	G210	G211	-	-
46	Amaranthus tuberculatus	R128	G210	-	-	-
47	Zea mays	-	A67	G68	L262	F285
48	Aegilops tauschii	R30	A96	G97	L291	F314
49	Genlisea aurea	R89	G168	G169	-	-
50	Amborella trichopoda	-	-	-	L161	F184
51	Rhodothermus marinus	R87	A162	G163	L330	F353
52	Salinibacter ruber	R87	A161	G162	L330	F353
53	Salinibacter ruber M8	R87	A161	G162	L330	F353
54	Zea mays	-	-	-	L69	F92
55	Rhodothermus marinus	R87	A162	G163	L330	F353
56	Caldithrix abyssi	R86	A160	G161	L329	F352
57	Opitutus terrae PB90-1	R103	A178	G179	L345	M368
58	Verrucomicrobia bacterium	R91	A166	G167	L332	Y355
59	Ignavibacterium album	R88	A163	G164	L332	F355
60	Coralimargarita sp. CAG:312	R88	G163	A164	L331	Y354
61	Salisaeta longa	R88	A163	G164	L329	F352
62	Ambrosia artemisiifolia	R98	G175	G176	-	-

63	Melioribacter roseus P3M-2	R88	A163	G164	L333	F356
64	Halothiobacillus neapolitanus c2	R97	A170	G171	L343	F366
65	Chondrus crispus	Y98	S176	G177	L352	Y376
66	Rubritalea marina	R88	A163	G164	L339	M362
67	Acidobacteria bacterium	R88	A161	G162	L330	F353
68	Coralimargarita akajimensis DSM 45221	R88	A163	G164	L323	F346
69	Oscillochloris trichoides DG6	R90	S164	G165	L340	L363
70	Opitutaceae bacterium TAV1	R86	A161	G162	L352	L375
71	Amborella trichopoda	R87	A173	A174	L230	-
72	Opitutaceae bacterium TAV5	R105	A180	G181	L368	L391
73	Chloroflexus sp. Y-400-fl	R91	A166	G167	L335	L358
74	Leptospirillum sp. Group II '5-way CG'	R92	A167	S168	L335	F358
75	Leptospirillum ferriphilum ML-04	R92	A167	S168	L335	F358
76	Verrucomicrobia bacterium SCGC AAA300-O17	R89	A165	A166	L334	Y357
77	Chloroflexus aggregans DSM 9485	R92	A167	G168	L336	L359
78	Desulfurobacterium thermolithotrophum	R86	A161	G162	L333	M356
79	Desulfurobacterium sp. TC5-1	R90	A165	G166	L332	M355
80	Arthrospira platensis C1	R93	A176	G177	L352	Y375
81	Leptospirillum sp. Group II 'C75'	R92	A167	S168	L335	F358
82	Verrucomicrobiae bacterium DG1235	R87	A164	G165	L332	M355
83	Verrucomicrobia bacterium SCGC AAA300-K03	R89	A165	A166	L334	F357
84	Synechococcus sp. JA-3-3Ab	R101	A177	G178	L350	F373
85	Hymenobacter norwichensis	R86	A161	G162	A321	F344

86	Pontibacter sp. BAB1700	R85	G159	G160	S319	Y342
87	Leptospirillum ferrodiazotrophum	R92	A172	S173	L339	F362
88	Prevotella histicola F0411	C89	A164	G165	L328	F351
89	Flexithrix dorotheae	R84	A158	G159	A313	F336
90	Geobacter metallireducens GS-15	R93	A168	G169	L342	M365
91	Synechococcus sp. JA-2- 3B'a(2-13)	R93	A169	G170	L362	F385
92	Crinalium epipsammum PCC 9333	R85	A168	G169	L344	F367
93	Planctomyces maris	A99	T187	S188	F358	F381
94	Geobacter uraniireducens Rf4	R93	A170	G171	L344	M367
95	Acidithiobacillus ferrivorans	R87	A162	G163	L323	F346
96	Prevotella melaninogenica	C88	A163	G164	L327	F350
97	Thermovibrio ammonificans	R86	A160	G161	L333	M356
98	Brassica_rapa	R143	A219	G220	L402	Y425
99	Brassica_rapa	R112	A195	A196	L384	F407
100	Gossypium	R146	A222	G223	L405	Y428
101	Gossypium	R98	A180	G181	L370	F393
102	Conyza_canadensis	R142	A218	G219	L401	Y424
103	Conyza_canadensis	R102	G179	G180	L365	F388
104	Kochia_scobaria	R172	A248	G249	L431	F454
105	Lolium_rigidum	R138	A214	G215	L397	Y420
106	Lolium_rigidum	R97	A182	G183	L377	F400
107	Gossypium hirsutum PPO1	R146	A222	G223	L405	Y428
108	Beta vulgaris PPO1	R167	A243	G244	L426	Y449
109	Hordeum vulgare PPO1	R137	A213	G214	L396	Y419
110	Hordeum vulgare PPO2	R142	A227	G228	L422	F445
111	Triticum aestivum PPO1	R138	A214	G215	L397	Y420
112	Solanum lycopersicum PPO2	R95	G175	G176	L366	F389
113	Triticum aestivum PPO1_v2	R153	A229	G230	L412	Y435
114	Gossypium hirsutum PPO1_v2	R146	A222	G223	L405	Y428

115	Gossypium hirsutum PPO2	R98	A180	G181	L370	F393
116	Beta vulgaris PPO1_v2	R167	A243	G244	L426	Y449
117	Brassica napus_PPO2	R99	A182	A183	L371	F394

In a further particularly preferred embodiment, the variant or derivative of the mutated PPO refers to SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, or 117, comprising a single amino acid substitutions at the positions depicted in the following Table 2b.

It should be noted that Mutated site 1 of Table 2a) corresponds to Pos 1 of Table 2b); Mutated site 2 of Table 2a) corresponds to Pos 16 of Table 2b); Mutated site 3 of Table 2a) corresponds to Pos 17 of Table 2b); Mutated site 4 of Table 2a) corresponds to Pos 38 of Table 2b); Mutated site 5 of Table 2a) corresponds to Pos 42 of Table 2b).

Table 2b

ID	Pos 1	Pos 2	Pos 3	Pos 4	Pos 5		Pos 6	Pos 7	Pos 8	Pos 9	Pos 10	Pos 11	Pos 12	Pos 13	Pos 14	Pos 15	Pos 16	Pos 17	Pos 18	Pos 19	Pos 20
1	R128	Y129	A131	S149	I151	A154	P164	K169	E182	S183	E189	F196	D202	C209	G210	G211	L216	M218	H219	H220	
2	R128	Y129	A131	S149	I151	A154	P164	K169	E182	S183	E189	F196	D202	C209	G210	G211	L216	M218	H219	H220	
3	R128	Y129	A131	S149	I151	A154	P164	K169	E182	S183	E189	F196	D202	C209	G210	-	L215	M217	H218	H219	
4	R128	Y129	A131	S149	I151	A154	P164	K169	E182	S183	E189	F196	D202	C209	G210	-	L215	M217	Y218	H219	
5	R128	Y129	A131	S149	I151	A154	P164	K169	E182	S183	E189	F196	D202	C209	G210	G211	L216	V218	H219	H220	
6	R98	Y99	A101	S119	I121	A124	P134	K139	E152	S153	E159	F166	D172	C179	G180	G181	L186	M188	H189	H190	
7	R127	Y128	A130	S148	I150	A153	P163	K168	E181	S182	E188	F195	D201	S208	G209	G210	L215	M217	R218	H219	
8	R100	Y101	V103	S121	I123	A126	P136	K141	E154	S155	Q161	V168	D174	S181	G182	G183	L188	M190	H191	H192	
9	R99	Y100	V102	S120	I122	A125	P135	K140	E153	S154	Q160	V167	D173	S180	A181	G182	L187	V189	C190	H191	
10	R98	Y99	V101	S119	I121	A124	P134	K139	E152	S153	Q159	V166	D172	S179	A180	G181	L186	M188	R189	H190	
11	R98	Y99	V101	S119	L121	A124	P134	R139	E152	S153	E159	V166	D172	S179	A180	A181	L186	M188	R189	H190	
12	R96	Y97	V99	S117	F119	A122	P132	D137	E147	S148	Q154	V161	D167	S174	A175	G176	L181	M183	R184	H185	
13	R98	Y99	V101	S119	L121	A124	P134	R139	E152	S153	E159	V166	D172	S179	A180	A181	L186	I188	R189	H190	
14	R98	Y99	A101	S119	F121	T124	P134	K139	E149	S150	Q156	V163	D169	S176	A177	G178	L183	M185	P186	H187	
15	R98	Y99	V101	S119	F121	A124	P134	K139	E152	S153	Q159	V166	D172	S179	A180	A181	L186	M188	R189	H190	
16	R98	Y99	V101	S119	F121	A124	P134	K139	E152	S153	Q159	V166	D172	S179	A180	A181	L186	M188	R189	H190	
17	R98	Y99	V101	S119	L121	A124	P134	R139	E152	S153	E159	V166	D172	S179	A180	A181	L186	M188	R189	H190	
18	R98	Y99	V101	S119	F121	A124	P134	K139	E152	S153	Q159	V166	D172	S179	A180	G181	L186	M188	S189	H190	
19	R93	Y94	V96	S114	F116	A119	P129	K134	E147	S148	Q154	V161	D167	S174	A175	G176	L181	M183	S184	H185	
20	R98	Y99	A101	S119	F121	T124	P134	N139	E150	S151	Q157	V164	D170	C177	G178	G179	L184	M186	H187	H188	
21	R95	Y96	A98	S116	F118	T121	P131	N136	E147	S148	Q154	V161	D167	C174	G175	G176	L181	M183	H184	L185	
22	R101	Y102	V104	S122	V124	T127	P137	K142	E154	S155	Q161	V168	D174	S181	A182	A183	L188	M190	K191	H192	
23	R103	Y104	V106	S124	V126	T129	P139	K144	E158	S159	Q165	V172	D178	S185	A186	A187	L192	M194	K195	H196	
24	R101	Y102	V104	S122	V124	T127	P137	K142	E154	S155	Q161	V168	D174	S181	A182	A183	L188	M190	K191	H192	

25	R147	Y148	V150	S168	V170	T173	P183	K188	E200	S201	Q207	V214	D220	S227	A228	A229	L234	M236	K237	H238
26	R74	Y75	V77	S95	F97	T100	P110	K115	E123	S124	Q130	V137	D143	S150	G151	G152	L157	M159	R160	H161
27	R128	Y129	V131	S149	V151	T154	P164	K169	E185	S186	E192	V199	D205	S212	A213	G214	L219	I221	R222	H223
28	R130	Y131	V133	S151	V153	T156	P166	K171	E187	S188	E194	V201	D207	S214	A215	G216	L221	I223	C224	H225
29	R101	Y102	V104	-	-	-	-	-	E124	S125	Q131	V138	D144	S151	A152	A153	L158	M160	K161	H162
30	R130	Y131	V133	S151	V153	T156	P166	K171	E187	S188	E194	V201	D207	S214	A215	G216	L221	I223	R224	H225
31	R130	Y131	V133	S151	V153	T156	P166	K171	E187	S188	E194	V201	D207	S214	A215	G216	L221	I223	R224	H225
32	R105	Y106	V108	S126	L128	T131	P141	R146	E160	S161	Q167	V174	D180	S187	G188	G189	L194	M196	P197	H198
33	R150	F151	L153	F171	L173	I176	A186	P191	E201	E202	-	V212	E218	Y225	A226	G227	L232	M234	K235	A236
34	R100	Y101	V103	S121	F123	A126	P136	K141	E154	S155	Q161	V168	D174	S181	A182	G183	L188	A190	R191	H192
35	R165	Y166	V168	S186	V188	T191	P201	K206	E220	S221	R227	V234	D240	S247	A248	A249	L254	M277	K278	H279
36	R134	Y135	V137	S155	V157	T160	P170	K175	E191	S192	E198	V205	D211	S218	A219	G220	L225	I227	R228	H229
37	R95	Y96	V98	S116	V118	T121	P131	K136	E152	S153	C158	V165	D171	S178	G179	G180	L185	I187	R188	H189
38	R100	Y101	V103	S121	T123	A126	P136	H141	E158	S159	R165	V172	D178	A185	G186	A187	L192	I194	R195	H196
39	R98	Y99	A101	S119	F121	T124	P134	N139	E150	S151	Q157	V164	D170	C177	G178	G179	L184	M186	H187	L188
40	R95	Y96	V98	S116	V118	T121	P131	K136	E152	S153	C169	V176	D182	S189	G190	G191	L196	I198	R199	H200
41	R95	Y96	V98	S116	V118	T121	P131	K136	E152	S153	C169	V176	D182	S189	G190	G191	L196	I198	R199	H200
42	R96	Y97	V99	S117	V119	T122	P132	K137	E151	S152	Q158	V165	D171	S178	A179	A180	L185	M187	K188	H189
43	R97	Y98	V100	T118	L120	A123	P133	R138	E147	S148	E154	I161	D167	S174	G175	S176	I181	I183	R184	H185
44	R97	Y98	V100	T118	L120	A123	P133	R138	E147	S148	E154	I161	D167	S174	G175	S176	I181	I183	R184	H185
45	R128	Y129	A131	S149	I151	A154	P164	K169	E182	S183	E189	F196	D202	C209	G210	G211	L216	M218	H219	H220
46	R128	Y129	A131	S149	I151	A154	P164	K169	E182	S183	E189	F196	D202	C209	G210	-	L215	M217	H218	H219
47	-	-	-	S3	V5	T8	P18	K23	E39	S40	E46	V53	D59	S66	A67	G68	L73	I75	R76	H77
48	R30	Y31	V33	-	-	-	P47	K52	E68	S69	E75	V82	D88	S95	A96	G97	L102	I104	R105	H106
49	R89	Y90	V92	S110	I112	S115	P125	Q130	E140	S141	Q147	V154	D160	S167	G168	G169	L174	M176	R177	H178
50	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
51	R87	F88	V90	T108	L110	P113	P123	H126	A137	K138	-	V148	E154	F161	A162	G163	L168	V170	R171	Y172
52	R87	Y88	V90	T108	L110	T113	P123	G126	A136	R137	-	V147	A153	F160	A161	G162	L167	V169	Q170	H171

53	R87	Y88	V90	T108	L110	T113	P123	G126	A136	R137	-	V147	A153	F160	A161	G162	L167	V169	Q170	H171
54	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
55	R87	F88	V90	T108	L110	P113	P123	H126	A137	K138	-	V148	E154	F161	A162	G163	L168	V170	R171	Y172
56	R86	Y87	V89	T107	L109	W112	P122	P125	A135	D136	-	F146	N152	Y159	A160	G161	L166	A168	P169	A170
57	R103	Y104	V106	S124	L126	P129	L139	R142	A153	E154	-	F164	N170	Y177	A178	G179	L184	A186	R187	Q188
58	R91	Y92	I94	T112	L114	L117	P127	A130	A141	A142	-	F152	N158	Y165	A166	G167	L172	V174	Q175	H176
59	R88	Y89	L91	T109	L111	A114	P124	G127	A138	E139	-	F149	N155	Y162	A163	G164	L169	V171	K172	S173
60	R88	F89	A91	T109	L111	F114	P124	K127	A138	D139	-	V149	N155	Y162	G163	A164	L169	I171	K172	H173
61	R88	F89	V91	T109	L111	T114	P124	A127	A138	S139	-	V149	D155	F162	A163	G164	L169	L171	K172	H173
62	R98	Y99	V101	S119	F121	T124	P134	K139	E147	S148	Q154	V161	D167	S174	G175	G176	-	-	-	-
63	R88	Y89	L91	T109	L111	S114	P124	S127	A138	E139	-	F149	D155	F162	A163	G164	L169	V171	K172	S173
64	R97	F98	A100	S118	L120	M123	A133	K136	A145	E146	-	F156	D162	Y169	A170	G171	L176	V178	Q179	A180
65	Y98	Y99	M101	T119	L121	W124	P134	L139	S149	V150	Q155	V162	D168	Y175	S176	G177	L182	M184	K185	H186
66	R88	F89	I91	S109	I111	L114	P124	K127	A138	D139	-	P149	N155	Y162	A163	G164	L169	V171	E172	H173
67	R88	Y89	V91	S109	L111	W114	P124	G127	A136	D137	-	F147	N153	Y160	A161	G162	L167	V169	R170	F171
68	R88	Y89	V91	T109	L111	I114	P124	K127	A138	D139	-	L149	N155	Y162	A163	G164	L169	L171	R172	Y173
69	R90	Y91	L93	M111	H113	M116	P126	P129	A139	S140	-	V150	D156	Y163	S164	G165	M170	I172	K173	A174
70	R86	F87	V89	T107	L109	L112	L122	R125	G136	E137	-	L147	D153	Y160	A161	G162	L167	A169	R170	Y171
71	R87	F88	A90	S108	L110	P113	P123	S128	E145	S146	Q152	V159	D165	S172	A173	A174	L179	-	-	-
72	R105	F106	V108	T126	L128	L131	L141	R144	G155	E156	-	L166	D172	Y179	A180	G181	L186	A188	R189	Y190
73	R91	F92	L94	T112	L114	W117	P127	N130	A141	A142	-	A152	D158	Y165	A166	G167	L172	T174	A175	A176
74	R92	Y93	V95	T113	L115	W118	W128	P131	S142	H143	-	A153	D159	Y166	A167	S168	L173	V175	E176	A177
75	R92	Y93	V95	T113	L115	W118	W128	P131	S142	H143	-	A153	D159	Y166	A167	S168	L173	V175	E176	A177
76	R89	F90	I92	S110	F112	P115	P125	G128	A140	E141	-	V151	N157	Y164	A165	A166	L171	L173	K174	Y175
77	R92	Y93	L95	T113	L115	W118	P128	N131	A142	A143	-	A153	D159	Y166	A167	G168	L173	A175	A176	A177
78	R86	F87	Y89	S107	L109	W112	F122	P125	S136	E137	-	A147	D153	F160	A161	G162	L167	L169	K170	A171
79	R90	F91	F93	S111	V113	F116	Y126	P129	S140	S141	-	A151	D157	F164	A165	G166	L171	V173	K174	A175
80	R93	Y94	Y96	S114	L116	A119	A129	P134	T151	Q152	-	V162	Q168	Y175	A176	G177	L182	V184	R185	S186

81	R92	Y93	V95	T113	L115	W118	W128	P131	S142	H143	-	A153	D159	Y166	A167	S168	L173	V175	E176	A177
82	R87	Y88	V90	T108	L110	L113	P123	K126	A139	S140	-	F150	D156	Y163	A164	G165	L170	L172	E173	H174
83	R89	F90	I92	S110	F112	P115	P125	G128	A140	E141	-	V151	N157	Y164	A165	A166	L171	L173	K174	Y175
84	R101	Y102	Y104	S122	L124	V127	L137	P142	R152	Q153	-	V163	E169	Y176	A177	G178	L183	A185	V186	A187
85	R86	Y87	L89	N107	F109	W112	L122	A126	D136	A137	-	I147	N153	Y160	A161	G162	L167	I169	H170	K171
86	R85	Y86	L88	N106	L108	N111	R121	A126	S134	D135	-	Q145	A151	Y158	G159	G160	L165	V167	N168	K169
87	R92	F93	L95	T113	I115	L118	P128	P131	A147	D148	-	F158	D164	Y171	A172	S173	L178	M180	A181	D182
88	C89	R90	I92	T111	L113	L116	P126	R129	G139	A140	-	F150	D156	Y163	A164	G165	L170	T172	R173	L174
89	R84	Y85	F87	N105	F107	W110	L120	T125	A133	D134	-	I144	N150	Y157	A158	G159	L164	M166	E167	K168
90	R93	F94	Y96	S114	L116	W119	P129	S132	A143	S144	-	A154	S160	F167	A168	G169	M174	L176	R177	S178
91	R93	Y94	Y96	S114	L116	V119	L129	A134	R144	Q145	-	V155	E161	Y168	A169	G170	L175	A177	L178	A179
92	R85	F86	Y88	S106	L108	L111	A121	P126	A143	Q144	-	V154	A160	Y167	A168	G169	L174	A176	R177	S178
93	A99	L100	L102	T128	L130	P133	Y143	P146	A162	Q163	-	A173	Q179	Y186	T187	S188	L193	L195	R196	A197
94	R93	F94	Y96	S114	L116	W119	P129	A134	A145	A146	-	A156	A162	F169	A170	G171	M176	L178	V179	S180
95	R87	Y88	L90	G107	L109	W112	P122	S125	A137	D138	-	A148	D154	F161	A162	G163	L168	V170	Q171	A172
96	C88	R89	I91	T110	L112	L115	P125	K128	G138	S139	-	F149	D155	Y162	A163	G164	L169	T171	R172	L173
97	R86	F87	Y89	S107	L109	W112	L122	P125	A135	E136	-	A146	D152	F159	A160	G161	M166	L168	K169	A170
98	R143	F144	L146	F164	L166	I169	A179	P184	E191	S192	R198	V205	E211	Y218	A219	G220	L225	M227	K228	A229
99	R112	Y113	V115	S133	V135	T138	P148	K153	E167	S168	Q174	V181	D187	S194	A195	A196	L201	M203	K204	H205
10																				
0	R146	F147	L149	F167	L169	I172	A182	P187	E194	S195	R201	V208	E214	Y221	A222	G223	L228	M230	K231	A232
10																				
1	R98	Y99	V101	S119	I121	A124	P134	K139	E152	S153	Q159	V166	D172	S179	A180	G181	L186	M188	C189	H190
10																				
2	R142	F143	L145	F163	L165	L168	A178	P183	E190	S191	R197	V204	E210	Y217	A218	G219	L224	M226	K227	A228
10																				
3	R102	Y103	V105	S123	L125	T128	P138	K143	E151	S152	Q158	V165	N171	S178	G179	G180	L185	M187	R188	Y189
10	R172	F173	L175	F193	L195	F198	A208	P213	E220	S221	R227	V234	E240	Y247	A248	G249	L254	M256	K257	A258

[illegible]

	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos
ID	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40					
1	N227	S234	S246	K259	P260	R261	L295	Q301	G308	S324	R335	G346	F349	L351	D352	T358	L384	L397	F417	T418					
2	N227	S234	S246	K259	P260	R261	L295	Q301	G308	S324	R335	G346	F349	L351	D352	T358	L384	L397	F417	T418					
3	N226	S233	S245	K258	P259	R260	L294	Q300	G307	S323	R334	G345	F348	L350	D351	T357	L383	L396	F416	T417					
4	N226	S233	S245	K258	P259	R260	L294	Q300	G307	S323	R334	G345	F348	L350	D351	T357	L383	L396	F416	T417					
5	N227	S234	S246	K260	P261	R262	L296	Q302	G309	S325	R336	G347	F350	L352	D353	T359	L385	L398	F418	T419					
6	N197	S204	S216	K230	P231	R232	L266	Q272	G279	S295	R306	G317	F320	L322	D323	S329	L355	L368	F388	T389					
7	N226	S233	S245	K259	P260	R261	L295	H301	E308	P324	N335	E346	F349	L351	D352	S358	L384	L397	Y417	T418					
8	N199	S206	A218	K232	K234	R235	L269	H275	E282	S300	C311	G322	F325	L327	D328	S334	L360	L373	Y393	T394					
9	N198	S205	T217	K231	K233	Q234	F268	P274	E281	S299	C310	R321	F324	L326	N327	S333	L359	L372	Y392	T393					
10	D197	S204	A216	K229	K231	P232	L266	H272	E279	S297	C308	G319	F322	L324	N325	S331	L357	L370	Y390	T391					
11	N197	S204	A216	K230	K232	H233	L267	H273	Q280	D294	Y305	G316	F319	L321	N322	S328	L354	L367	Y387	T388					
12	N192	S199	A211	K225	K227	R228	L262	Q268	E275	S293	C304	G315	F318	L320	D321	V327	L353	L366	Y386	T387					
13	N197	S204	G216	K230	K232	H233	L267	H273	Q280	D294	G305	G316	F319	L321	N322	T328	L354	L367	Y387	T388					
14	N194	S201	S213	K227	K229	R230	L264	H270	E277	S295	C306	G317	F320	L322	D323	N329	L355	L368	Y388	T389					
15	N197	S204	A216	K230	H232	R233	L267	H273	E280	S297	C308	G319	F322	L324	D325	I331	L357	L370	Y390	T391					
16	N197	S204	A216	K230	H232	R233	L267	H273	E280	S297	C308	G319	F322	L324	D325	I331	L357	L370	Y390	T391					
17	N197	S204	G216	K230	K232	H233	L267	H273	E280	D294	G305	G316	F319	L321	N322	T328	L354	L367	Y387	T388					
18	N197	S204	T216	K230	K232	P233	L267	-	Q279	I295	C306	G317	F320	L322	N323	A329	L355	L368	Y388	T389					
19	N192	S199	T211	K225	K227	P228	L262	-	Q274	I290	C301	G312	F315	L317	N318	A324	L350	L363	Y383	T384					
20	N195	S202	P214	N228	K230	R231	L265	C271	D278	S296	C307	G318	F321	L323	N324	D330	L356	L369	Y389	T390					
21	N192	S199	P211	N225	K227	R228	L262	C268	D275	S293	C304	G315	F318	L320	N321	D327	L353	L366	Y386	T387					
22	N199	S206	A218	T232	K234	G235	L269	-	E280	H298	C309	G320	F323	L325	N326	N332	L358	L371	Y391	T392					
23	N203	S210	A222	T236	R238	G239	L273	-	E284	H302	C313	G324	F327	L329	N330	N336	L362	L375	Y395	T396					
24	N199	S203	A215	T229	K231	G232	L266	-	E277	H295	C302	G313	F316	L318	N319	N325	L351	L364	Y384	T385					
25	N245	S249	A261	T275	K277	G278	L312	-	E323	H341	C348	G359	F362	L364	N365	N371	L397	L410	Y430	T431					

26	D168	S175	S187	N197	K199	R200	L234	C240	G246	S263	N274	G285	F288	L290	N291	S297	L323	L336	Y356	T357
27	N230	S237	A249	K263	R265	N266	L300	F306	G313	T334	S345	G356	F359	L361	D362	N368	L394	L408	Y428	T429
28	N232	S239	A251	K265	R267	N268	L302	L308	G315	T336	S347	G358	F361	L363	D364	D370	L396	L410	Y430	T431
29	N169	S176	A188	T202	K204	G205	L239	-	E250	H268	C279	G290	F293	L295	N296	N302	L328	L341	Y361	T362
30	N232	S239	A251	K265	R267	N268	L302	F308	G315	T336	S347	G358	V361	L363	D364	D370	L396	L410	Y430	T431
31	N232	S239	A251	K265	R267	N268	L302	F308	G315	T336	S347	G358	V361	L363	D364	D370	L396	L410	Y430	T431
32	N205	S212	D224	K238	R240	-	L274	H280	D287	F308	G319	G330	F333	L335	D336	T342	L368	L381	Y401	T402
33	K243	S250	R262	P275	P277	K278	G312	N318	Y325	N335	Y346	-	N357	A359	A360	Y367	L399	L409	L429	L430
34	N199	S206	A218	K232	K234	R235	L269	Y275	E282	S300	C311	R322	F325	L327	D328	S334	L360	L373	Y393	T394
35	N286	S293	A305	-	-	-	L331	-	E342	H360	C371	G382	F385	L387	N388	K394	L420	L433	Y453	T454
36	D236	S243	A255	K269	R271	N272	L306	C312	D319	L340	S351	G362	F365	L367	D368	D374	L400	L414	F434	T435
37	N196	S203	T215	K229	R231	N232	L266	C272	G279	S300	S311	G322	F325	L327	D328	D334	L360	L374	Y394	T395
38	D203	S210	R222	Q236	K237	R238	L272	L278	N285	S306	-	-	-	-	-	T315	L341	L354	F374	T375
39	N195	S202	P214	N228	K230	R231	L265	C271	D278	S296	C307	G318	F321	L323	N324	D330	L356	L369	Y389	T390
40	N207	S214	T226	K240	R242	N243	L277	C283	G290	S311	S322	G333	F336	L338	D339	D345	L371	L385	Y405	T406
41	N207	S214	T226	K240	R242	D243	L277	C283	G290	S311	S322	G333	F336	L338	D339	D345	L371	L385	Y405	T406
42	N196	S203	A215	T229	K231	G232	L266	-	E277	H295	C306	G317	F320	L322	N323	K329	L355	L368	Y388	T389
43	S192	S199	K211	T233	P235	R236	T270	Q276	Q283	T303	D314	G325	Y328	L330	D331	I337	L363	L377	F397	T398
44	S192	S199	K211	T233	P235	R236	T270	Q276	Q283	T303	D314	G325	Y328	L330	D331	I337	L363	L377	F397	T398
45	N227	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
46	N226	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
47	N84	S91	A103	K117	R119	N120	L154	F160	G167	T188	S199	G210	V213	L215	D216	D222	L248	L262	Y282	T283
48	N113	S120	A132	K146	R148	S149	L183	C189	D196	S217	S228	G239	F242	L244	D245	D251	L277	L291	F311	T312
49	N185	S192	A204	N218	R220	R221	L255	N261	D268	G287	S298	-	-	-	-	-	-	-	-	-
50	-	-	S3	K17	K19	H20	L54	D60	S67	S88	R99	G110	Y113	L115	D116	M122	L148	L161	Y181	T182
51	E179	S186	-	-	A203	P204	L238	-	P247	F262	H273	P282	D285	-	R286	E293	L319	L330	L350	T351
52	A178	S185	-	-	D204	T205	H238	-	W247	S262	H273	T282	D285	-	L286	T293	L319	L330	L350	T351

53	A178	S185	-	-	-	D204	T205	H238	-	W247	S262	H273	T282	D285	-	L286	T293	L319	L330	L350	T351
54	-	-	-	-	-	-	-	-	-	-	-	S6	G17	V20	L22	D23	D29	L55	L69	Y89	T90
55	E179	S186	-	-	-	A203	P204	L238	-	P247	F262	H273	P282	D285	-	R286	E293	L319	L330	L350	T351
56	N177	S184	R196	-	-	K204	D205	R238	-	-	F261	Y272	S280	K283	R285	A286	L293	L319	L329	F349	T350
57	E195	S202	R214	-	-	E219	P220	D254	-	K261	S276	P287	T296	E299	P301	L302	E309	L335	L345	L365	T366
58	A183	S190	R202	-	-	K210	D211	E244	-	-	S263	H274	D283	D286	D288	M289	I296	L322	L332	L352	S353
59	A180	G187	R199	-	-	K207	Q208	I241	-	-	V264	Y275	K283	K286	F288	K289	Y296	L322	L332	F352	T353
60	N180	S187	-	G203	F205	F206	F206	I239	S243	-	-	P273	M283	A286	L288	A289	Q295	L321	L331	L351	T352
61	E180	S187	G199	-	A207	T208	T241	T241	-	T250	-	H272	P281	D284	-	T285	P292	L318	L329	L349	T350
62	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
63	R180	G187	R199	-	K207	Q208	Q208	L241	-	Q250	T265	Y276	E284	Q287	L289	A290	Y297	L323	L333	F353	T354
64	A187	S194	A206	-	-	-	A217	D250	I256	G263	H275	H286	-	G297	L299	A300	E307	L333	L343	L363	S364
65	R193	S200	T212	T222	K224	E225	E225	T259	T265	G272	-	H292	A303	K306	F308	K309	K316	L342	L352	L373	T374
66	Q180	S187	Q199	H207	L209	Q210	Q210	G244	R250	-	S270	H281	E290	L293	S295	L296	D303	L329	L339	I359	N360
67	A178	G185	R197	-	K205	I206	I206	L239	-	-	R262	Y273	R281	P284	A286	A287	V294	L320	L330	L350	T351
68	A180	G187	-	G204	K206	A207	A207	E240	Q244	-	-	H270	-	E278	P280	I281	D287	L313	L323	L343	T344
69	E181	S188	K200	G212	K214	M215	M215	T249	-	G257	E272	Y283	-	P294	A296	A297	R304	L330	L340	T360	I361
70	E178	S185	R197	P209	P211	P212	P212	V246	V252	A257	R283	E294	A303	E306	P308	L309	E316	L342	L352	L372	T373
71	-	-	-	-	-	-	-	T184	C190	L197	-	S213	-	-	-	-	-	-	L230	-	-
72	E197	S204	R216	P228	P230	P231	P231	V265	V271	A276	R299	E310	A319	E322	P324	L325	E332	L358	L368	L388	T389
73	E183	S190	K202	-	K209	M210	M210	V244	-	W252	I267	F278	-	Q289	A291	A292	P299	L325	L335	T355	T356
74	R184	G191	R203	G209	S211	P212	P212	V243	-	G252	T267	P278	-	D289	P291	S292	P299	L325	L335	L355	T356
75	R184	G191	R203	G209	S211	P212	P212	V243	-	G252	T267	P278	-	D289	P291	S292	P299	L325	L335	L355	T356
76	D182	S189	-	E203	I205	S206	S206	K239	K244	-	V264	H275	I285	S288	L290	L291	Y298	L324	L334	L354	T355
77	E184	S191	K203	-	K210	M211	M211	V245	-	Y253	T268	Y279	-	P290	A292	A293	P300	L326	L336	T356	I357
78	Y178	G185	A197	P206	G208	P209	P209	I241	-	G250	T265	Y276	-	L287	L289	S290	E297	L323	L333	I353	R354
79	H182	G189	K201	T205	G207	P208	P208	V240	-	K249	S264	Y275	-	E286	L288	A289	E296	L322	L332	I352	R353

80	A193	G200	K212	P224	T226	R227	R261	H267	F274	E284	H295	-	S306	I308	A309	P316	L342	L352	L372	S373
81	R184	G191	R203	G209	A211	P212	V243	-	G252	T267	P278	-	E289	P291	S292	P299	L325	L335	L355	T356
82	G181	S188	-	G204	A206	Y207	V240	R244	-	F263	H274	E283	A286	P288	L289	E296	L322	L332	L352	T353
83	D182	S189	-	E203	I205	S206	K239	K244	-	V264	H275	I285	S288	L290	L291	Y298	L324	L334	L354	T355
84	G194	S201	-	P223	P225	K226	Q260	G265	F272	A282	Y293	-	P304	A306	S307	L314	L340	L350	F370	L371
85	A178	S185	A197	-	-	G198	L232	G238	S245	S253	F264	-	P275	A277	A278	H285	L311	A321	F341	T342
86	E176	S183	G195	-	-	V196	F229	G235	A242	E251	H262	-	P273	M275	S276	N283	L309	S319	I339	T340
87	Q189	S196	Q207	P213	F215	A216	V247	-	G256	R271	A282	-	P293	I295	P296	P303	L329	L339	L359	T360
88	N181	S188	P200	-	R207	A208	L242	G248	K250	I261	Y272	-	K283	Q285	L286	Y293	L318	L328	Y348	A349
89	E175	S182	T194	-	-	Q195	E227	G233	-	K245	Y256	-	P267	S269	A270	N277	L303	A313	I333	T334
90	E185	S192	K204	A217	G219	P220	V253	-	-	D274	H285	-	A296	M298	A299	P306	L332	L342	L362	R363
91	G186	S193	R205	P226	P228	K229	H263	E268	F275	A294	Y305	-	P316	A318	S319	P326	L352	L362	L382	I383
92	Q185	G192	R204	P216	V218	R219	E253	N259	F266	E276	Y287	-	P298	A300	S301	P308	L334	L344	L364	T365
93	D204	S211	T223	T229	A231	R232	V266	-	G275	H290	P301	-	P312	L314	S315	E322	V348	F358	L378	R379
94	E187	G194	K206	A219	G221	P222	V255	-	-	D276	Y287	-	G298	M300	S301	P308	L334	L344	L364	R365
95	A179	S186	A194	-	-	-	E236	-	S244	Q255	G266	-	A277	L279	A280	P287	L313	L323	L343	T344
96	D180	S187	P199	-	R206	A207	L241	G247	K249	I260	Y271	-	K282	Q284	L285	Y292	L317	L327	Y347	A348
97	R177	G184	A196	P206	G208	P209	V241	-	K250	E265	Y276	-	R287	L289	S290	E297	L323	L333	I353	R354
98	K236	S243	A254	K269	P270	K271	S304	-	G312	-	-	L348	S351	A353	E354	Y360	L386	L402	L422	L423
99	N212	S219	A231	K246	K247	G248	L282	T288	E293	H311	C322	G333	F336	L338	N339	K345	L371	L384	Y404	T405
100	K239	S246	E257	K272	P273	K274	S307	-	G315	-	-	L351	A354	A356	D357	Y363	L389	L405	L425	L426
101	D197	S204	A216	R230	K231	A232	L266	H272	E279	S297	C308	G319	F322	L324	N325	S331	L357	L370	Y390	T391
102	K235	S242	A253	T268	P269	K270	V303	-	R311	-	-	L347	E350	A352	D353	Y359	L385	L401	L421	L422
103	D196	S203	S215	S226	K227	R228	L262	C268	G274	P292	G303	G314	F317	L319	N320	S326	L352	L365	Y385	T386
104	V265	N272	E283	K298	P299	K300	A333	-	G341	-	-	F377	A380	A382	D383	H389	L415	L431	I451	L452
105	R231	S238	D249	T264	P265	K266	T299	-	Q307	-	-	L343	D346	A348	D349	Y355	L381	L397	L417	L418
106	N199	S206	A218	G233	R234	N235	L269	C275	N282	P303	S314	G325	F328	L330	D331	D337	L363	L377	F397	T398

107	K239	S246	R258	K272	P273	K274	S307	G313	T320	S334	S345	A356	L359	Q361	F362	A368	L395	L405	L425	L426
108	K260	S267	R279	K293	P294	K295	S328	L334	T341	S355	S366	A377	L380	K382	F383	A389	L416	L426	I446	L447
109	R230	S237	K249	A263	P264	K265	T298	D304	G311	S325	S336	A347	L350	K352	F353	A359	L386	L396	L416	L417
110	N244	S251	A263	G278	R279	N280	L314	C320	D327	S348	S359	G370	F373	L375	D376	D382	L408	L422	F442	T443
111	R231	S238	K250	A264	P265	K266	T299	D305	G312	S326	S337	A348	L351	K353	F354	A360	L387	L397	L417	L418
112	N192	S199	P211	K226	K227	R228	L262	C268	D275	S293	C304	G315	F318	L320	N321	D327	L353	L366	Y386	T387
113	R246	S253	K265	A279	P280	K281	T314	D320	G327	S341	S352	A363	L366	K368	F369	A375	L402	L412	L432	L433
114	K239	S246	R258	K272	P273	K274	S307	G313	T320	S334	S345	A356	L359	Q361	F362	A368	L395	L405	L425	L426
115	D197	S204	A216	R230	K231	A232	L266	H272	E279	S297	C308	G319	F322	L324	N325	S331	L357	L370	Y390	T391
116	K260	S267	R279	K293	P294	K295	S328	L334	T341	S355	S366	A377	L380	K382	F383	A389	L416	L426	I446	L447
117	N199	S206	A218	K233	K234	G235	L269	A275	E280	H298	C309	G320	F323	L325	N326	K332	L358	L371	Y391	T392

	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos
ID	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56				
1	T419	F420	A432	T434	K438	L449	T451	F462	Y470	S476	V477	D482	Y493	K498	E515	K528				
2	T419	F420	A432	T434	K438	L449	T451	F462	Y470	S476	V477	D482	Y493	K498	E515	K528				
3	T418	F419	A431	T433	K437	L448	T450	F461	Y469	C475	V476	D481	Y492	K497	E514	K527				
4	T418	F419	A431	T433	K437	L448	T450	F461	Y469	S475	V476	D481	Y492	K497	E514	K527				
5	T420	F421	A433	T435	K439	L450	T452	F463	Y471	S477	V478	D483	Y494	K499	E516	K529				
6	T390	F391	A403	T405	K409	L420	T422	F433	Y441	S447	V448	D453	Y464	K469	E486	K499				
7	T419	F420	A432	T434	K438	L449	T451	Y462	Y470	S476	V477	E482	Y493	K498	E515	K525				
8	T395	F396	A408	T410	K414	L425	A427	Y438	F446	S452	V453	D458	Y469	K474	D491	K504				
9	T394	F395	A407	T409	K413	L424	A426	Y437	Y445	A451	V452	D457	Y468	K473	D490	K503				
10	T392	F393	A405	T407	K411	L422	V424	Y435	Y443	S449	V450	E455	Y466	K471	D488	K500				
11	T389	F390	A402	T404	R408	L419	A421	Y432	Y440	S446	V447	D452	F463	K468	D485	T498				
12	T388	F389	A401	T403	K407	L418	A420	Y431	Y439	S445	V446	E451	Y462	R467	E484	K497				

[illegible]

40	S407	F408	A420	T422	K426	L437	V439	H450	Y458	L464	V465	A470	Y481	-	K493	-
41	S407	F408	A420	T422	K426	L437	V439	H450	Y458	L464	V465	A470	Y481	-	K493	-
42	T390	F391	A403	T405	-	-	-	-	-	-	-	-	-	-	-	-
43	T399	F400	R412	K414	L418	I429	V431	Y442	Y450	N456	V457	Q462	Y473	R478	E495	K508
44	T399	F400	R412	K414	L418	I429	V431	Y442	Y450	N456	V457	Q462	Y473	R478	E495	K508
45	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
46	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
47	T284	F285	A297	T299	K303	L314	V316	Y327	Y335	S341	V342	E347	Y358	K363	D380	N393
48	T313	F314	A326	T328	K332	L343	V345	H356	Y364	S370	A371	G376	-	K383	D400	V413
49	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
50	T183	F184	A196	L198	R202	L213	V215	Y226	Y234	M240	V241	E246	Y257	S262	-	-
51	T352	F353	L365	E367	E371	L382	I384	R395	Y403	A409	V410	H415	L426	M431	R448	G461
52	T352	F353	S365	A367	Q371	L382	V384	H395	Y403	T409	V410	D415	F426	R431	-	A458
53	T352	F353	S365	A367	Q371	L382	V384	H395	Y403	T409	V410	D415	F426	R431	-	T458
54	T91	F92	A104	T106	K110	L121	V123	Y134	Y142	S148	V149	E154	Y165	K170	D187	N200
55	T352	F353	L365	E367	E371	L382	I384	R395	Y403	A409	V410	H415	L426	M431	R448	G461
56	T351	F352	K364	D366	K370	V381	L383	R394	Y402	K408	I409	D414	F425	R430	E447	-
57	V367	M368	L380	A382	L386	L397	V399	F410	Y418	H424	F425	A430	M441	R446	E463	-
58	T354	Y355	L367	D369	D373	L384	V386	V397	Y405	K411	I412	N417	F428	R433	Q450	-
59	L354	F355	E367	R369	L373	M384	I386	F397	Y405	E411	H412	D417	I428	R433	N450	-
60	N353	Y354	L366	R368	R372	L383	V385	V396	Y404	E410	Y411	D416	L427	R432	A449	-
61	T351	F352	A364	D366	R370	L381	V383	A394	Y402	A408	A409	E414	F425	R430	R447	V460
62	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
63	L355	F356	M368	K370	I374	M385	I387	L398	Y406	E412	H413	E418	L429	R434	K451	-
64	A365	F366	G378	D380	L384	L395	I397	R408	Y416	E422	L423	S428	L439	R444	E461	-
65	V375	Y376	R388	A390	V394	L405	V407	T418	Y426	E432	S433	A438	F449	R454	E471	-
66	V361	M362	L374	E376	R380	L391	V393	H404	L412	I418	V419	I424	L435	R440	E457	-

67	T352	F353	R365	N367	I371	L382	L384	R395	Y403	E409	I410	D415	F426	R431	E448	-
68	V345	F346	P358	T360	L364	L375	I377	H388	Y396	K402	V403	T408	L419	R424	N441	-
69	N362	L363	Q375	D377	I381	I392	A394	R405	Y413	E419	A420	E425	F436	R441	E458	A471
70	V374	L375	M387	L389	M393	L404	V406	V417	Y425	R431	F432	E437	V448	R453	R470	-
71	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
72	V390	L391	M403	L405	M409	L420	V422	V433	Y441	R447	F448	E453	V464	R469	R486	-
73	T357	L358	R370	D372	I376	L387	I389	R400	Y408	E414	R415	V420	F431	R436	E453	A466
74	V357	F358	A370	D372	E376	L387	V389	R400	L408	E414	T415	R420	L429	L434	E451	-
75	V357	F358	A370	D372	E376	L387	V389	R400	L408	E414	T415	R420	L429	L434	E451	-
76	T356	Y357	L369	Q371	L375	L386	I388	L399	P407	D413	R414	S419	I430	I435	-	-
77	T358	L359	Q371	E373	I377	L388	I390	R401	Y409	E415	R416	E421	L432	R437	E454	A467
78	V355	M356	L368	D370	V374	M385	I387	K398	Y406	E412	R413	F418	L429	Y434	R451	-
79	A354	M355	A367	E369	A373	M384	I386	K397	Y405	E411	K412	F417	L428	Y433	E450	-
80	N374	Y375	M387	D389	V393	L404	A406	L418	Y426	N432	R433	D438	L449	I454	S471	N484
81	V357	F358	T370	D372	E376	L387	V389	R400	F408	E414	T415	R420	L429	L434	E451	-
82	V354	M355	L367	Q369	L373	L384	L386	S397	Y405	P411	W412	K417	F428	V433	E450	-
83	T356	F357	L369	Q371	L375	L386	I388	L399	P407	D413	R414	S419	I430	I435	-	-
84	S372	F373	L394	P396	A400	L411	T413	L425	Y433	Q439	R440	Q445	V457	L462	Q479	-
85	T343	F344	Q356	E358	K362	-	D374	L387	Y395	-	R398	H403	S416	R421	D438	-
86	S341	Y342	L354	E356	L360	-	Q372	L385	F393	-	Y396	H401	I414	Y419	A436	-
87	V361	F362	A374	D376	L380	L391	V393	R404	S412	E418	R419	E424	L433	L438	E455	-
88	F350	F351	K363	D365	R369	L380	Y382	R395	Y403	S409	R410	D415	I426	K431	E448	-
89	S335	F336	L348	D350	K354	-	K366	R378	Y386	-	D389	H394	V407	E412	E429	-
90	S364	M365	L377	D379	M383	M394	I396	R407	Y415	K421	R422	Q427	L438	Y443	D460	-
91	S384	F385	L406	P408	A412	L423	T425	L437	Y445	Q451	R452	Q457	V469	L474	Q491	-
92	N366	F367	L379	N381	V385	L396	K398	L410	Y418	L424	R425	N430	L441	T446	P463	-
93	T380	F381	H393	D395	N399	L410	V412	R423	Y431	Q437	L438	E443	L454	Y459	E476	-

94	S366	M367	L379	D381	V385	M396	I398	R409	Y417	R423	R424	E429	L440	Y445	D462	-
95	A345	F346	R357	D359	L363	L374	I376	T387	Y395	D401	R402	D407	F418	R423	Q440	-
96	C349	F350	K362	D364	I368	L379	Y381	R394	Y402	A408	R409	D414	I425	K430	E447	-
97	V355	M356	K368	E370	T374	M385	I387	R398	Y406	E412	K413	F418	F429	Y434	E451	-
98	N424	Y425	K437	E439	V443	L454	S458	V469	F477	D483	L484	K489	L502	V507	T524	-
99	T406	F407	A419	T421	K425	L436	I438	Y449	Y457	S463	V464	D469	Y480	R485	D502	N515
100	N427	Y428	K440	E442	V446	L457	N461	V472	F480	D486	L487	K492	L505	V510	A527	-
101	T392	F393	A405	T407	K411	L422	V424	Y435	Y443	S449	V450	E455	Y466	K471	D488	K500
102	N423	Y424	K436	E438	V442	L453	K457	V468	F476	D482	I483	K488	L501	V506	A523	-
103	T387	F388	A400	R402	K406	L417	A419	Y430	Y438	L444	V445	E450	Y461	K466	E483	K496
104	S453	F454	K466	Q468	A472	L483	S487	V498	F506	D512	L513	K518	L531	V536	A553	-
105	N419	Y420	K432	E434	V438	L449	T453	V464	F472	D478	R479	K484	L497	V502	S519	-
106	T399	F400	A412	T414	K418	L429	V431	H442	Y450	S456	A457	G462	Y473	K478	D495	D508
107	N427	Y428	K440	E442	V446	L457	N461	V472	F480	D486	L487	K492	L505	V510	A527	-
108	S448	Y449	K461	K463	A467	L478	D482	V493	F501	D507	L508	K513	L526	V531	A548	-
109	N418	Y419	K431	E433	V437	L448	R452	V463	F471	D477	R478	K483	L496	V501	S518	-
110	T444	F445	A457	T459	K463	L474	V476	H487	Y495	L501	A502	G507	Y518	K523	D540	G549
111	N419	Y420	K432	E434	V438	L449	R453	V464	F472	D478	R479	K484	L497	V502	S519	-
112	T388	F389	A401	R403	K407	L418	A420	C431	Y439	S445	V446	D451	Y462	K467	D484	S494
113	N434	Y435	K447	E449	V453	L464	R468	V479	F487	D493	R494	K499	L512	V517	S534	-
114	N427	Y428	K440	E442	V446	L457	N461	V472	F480	D486	L487	K492	L505	V510	A527	-
115	T392	F393	A405	T407	K411	L422	V424	Y435	Y443	S449	V450	E455	Y466	K471	D488	S497
116	S448	Y449	K461	K463	A467	L478	D482	V493	F501	D507	L508	K513	L526	V531	A548	-
117	T393	F394	A406	T408	K412	L423	V425	Y436	Y444	S450	V451	D456	Y467	R472	D489	K502

Assays to test for the functionality of such mutants are readily available in the art, and respectively, described in the Example section of the present invention.

In a preferred embodiment, the mutated PPO refers to a polypeptide of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, or 117, in which the amino acid sequence differs at Mutated site 1 (which corresponds to Arg128 of SEQ ID NO: 1) according to Table 2a, and/or at Mutated site 5 (which corresponds to Phe420 of SEQ ID NO: 1) according to Table 2a.

Examples of differences at these amino acid positions include, but are not limited to, one or more of the following:

the amino acid at Mutated site 1 is other than Arginine (or Tryosine, or Cysteine; as the case may be according to Table 2a);

the amino acid at Mutated site 5 is other than Phenylalanine (or Methionine, or Tyrosine, or Leucine, as the case may be according to Table 2a),

In particularly preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 (which corresponds to Arg128 of SEQ ID NO: 1) is Leu, Ala, Val, Ile, Met, Tyr, Gly, Asn, Cys, Phe, Ser, Thr, Gln, or His, and the amino acid at Mutated site 5 (which corresponds to Phe420 of SEQ ID NO: 1) is Ala, Leu, Val, Ile, or Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 1 is Leu, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

5 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
10 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 1 is Leu, and the amino acid at Mutated site 5 is Leu.

15 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
20 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 1 is Leu, and the amino acid at Mutated site 5 is Val.

25 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
30 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

35 the amino acid at Mutated site 1 is Leu, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
40 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is Leu, and the amino acid at Mutated site 5 is Met.

5

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

10

15 the amino acid at Mutated site 1 is Ala, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20

25

the amino acid at Mutated site 1 is Ala, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30

35

the amino acid at Mutated site 1 is Ala, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,

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76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 5 homologue thereof, in which :
 the amino acid at Mutated site 1 is Ala, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 10 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 15 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 1 is Ala, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 20 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 25 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 1 is Val, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 30 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 35 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 1 is Val, and the amino acid at Mutated site 5 is Leu.

40 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,

52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 5 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 1 is Val, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
10 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 15 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 1 is Val, and the amino acid at Mutated site 5 is Ile.

20 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 25 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 1 is Val, and the amino acid at Mutated site 5 is Met.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 35 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
40 the amino acid at Mutated site 1 is Ile, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 5 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is Ile, and the amino acid at Mutated site 5 is Leu.

10

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 15 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20 the amino acid at Mutated site 1 is Ile, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 25 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 30 homologue thereof, in which :

the amino acid at Mutated site 1 is Ile, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 35 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 40 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is Ile, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is Met, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is Met, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is Met, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 1 is Met, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

5 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
10 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 1 is Met, and the amino acid at Mutated site 5 is Met.

15 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
20 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 1 is Tyr, and the amino acid at Mutated site 5 is Ala.

25

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
30 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

35 the amino acid at Mutated site 1 is Tyr, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
40 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is Tyr, and the amino acid at Mutated site 5 is Val.

5

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

10

15 the amino acid at Mutated site 1 is Tyr, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20

25

the amino acid at Mutated site 1 is Tyr, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30

35

the amino acid at Mutated site 1 is Gly, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,

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76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 5 homologue thereof, in which :
 the amino acid at Mutated site 1 is Gly, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 10 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 15 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 1 is Gly, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 20 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 25 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 1 is Gly, and the amino acid at Mutated site 5 is Ile.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 35 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 1 is Gly, and the amino acid at Mutated site 5 is Met.

40 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,

52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 5 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 1 is Asn, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
10 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 15 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 1 is Asn, and the amino acid at Mutated site 5 is Leu.

20 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 25 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 1 is Asn, and the amino acid at Mutated site 5 is Val.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 35 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
40 the amino acid at Mutated site 1 is Asn, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 5 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is Asn, and the amino acid at Mutated site 5 is Met.

10

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 15 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20 the amino acid at Mutated site 1 is Cys, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 25 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 30 homologue thereof, in which :

the amino acid at Mutated site 1 is Cys, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 35 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 40 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is Cys, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is Cys, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is Cys, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is Phe, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 1 is Phe, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

5 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
10 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 1 is Phe, and the amino acid at Mutated site 5 is Val.

15 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
20 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 1 is Phe, and the amino acid at Mutated site 5 is Ile.

25

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
30 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

35 the amino acid at Mutated site 1 is Phe, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
40 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is Ser, and the amino acid at Mutated site 5 is Ala.

5

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

10

15 the amino acid at Mutated site 1 is Ser, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20

25

the amino acid at Mutated site 1 is Ser, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30

35

the amino acid at Mutated site 1 is Ser, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,

40

76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 5 homologue thereof, in which :
 the amino acid at Mutated site 1 is Ser, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 10 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 15 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 1 is Thr, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 20 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 25 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 1 is Thr, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 30 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 35 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 1 is Thr, and the amino acid at Mutated site 5 is Val.

40

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,

28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 5 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is Thr, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 10 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 15 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is Thr, and the amino acid at Mutated site 5 is Met.

20 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 25 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is Gln, and the amino acid at Mutated site 5 is Ala.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 35 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

40 the amino acid at Mutated site 1 is Gln, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 5 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is Gln, and the amino acid at Mutated site 5 is Val.

10

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 15 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20 the amino acid at Mutated site 1 is Gln, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 25 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 30 homologue thereof, in which :

the amino acid at Mutated site 1 is Gln, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 35 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 40 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is His, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is His, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is His, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 1 is His, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 1 is His, and the amino acid at Mutated site 5 is Met.

5 In another preferred embodiment, the mutated PPO refers to a polypeptide of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, or 117, in which the amino acid sequence differs at Mutated site 4 (which corresponds to Leu397 of SEQ ID NO: 1) according to Table 2a, and/or at Mutated site 5 (which corresponds to Phe420 of SEQ ID NO: 1) according to Table 2a.

15 Examples of differences at these amino acid positions include, but are not limited to, one or more of the following:
the amino acid at Mutated site 4 is other than Leucine (or Alanine, or Serine, or Phenylalanine, as the case may be according to Table 2a);
the amino acid at Mutated site 5 is other than Phenylalanine (or Methionine, or Tyrosine, or Leucine, as the case may be according to Table 2a),

In particularly preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 (which corresponds to Leu397 of SEQ ID NO: 1) is Ala, Arg, Val, Ile, Met, His, Lys, Asp, Glu, Ser, Thr, Asn, Gln, Cys, Gly, Pro, Phe, Tyr, or Trp, and the amino acid at Mutated site 5 (which corresponds to Phe420 of SEQ ID NO: 1) is Ala, Leu, Val, Ile, Met, His, Lys, Asp, Glu, Ser, Thr, Asn, Gln, Cys, Gly, Pro, Arg, Tyr, or Trp.

35 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,

613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Ala, and the amino acid at Mutated site 5 is Ala.

5 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007, 1008, 1009, 1010, 1011, 1012, 1013, 1014, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052, 1053, 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, 1064, 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092, 1093, 1094, 1095, 1096, 1097, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, 1109, 1110, 1111, 1112, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168, 1169, 1170, 1171, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181, 1182, 1183, 1184, 1185, 1186, 1187, 1188, 1189, 1190, 1191, 1192, 1193, 1194, 1195, 1196, 1197, 1198, 1199, 1200, 1201, 1202, 1203, 1204, 1205, 1206, 1207, 1208, 1209, 1210, 1211, 1212, 1213, 1214, 1215, 1216, 1217, 1218, 1219, 1220, 1221, 1222, 1223, 1224, 1225, 1226, 1227, 1228, 1229, 1230, 1231, 1232, 1233, 1234, 1235, 1236, 1237, 1238, 1239, 1240, 1241, 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251, 1252, 1253, 1254, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1265, 1266, 1267, 1268, 1269, 1270, 1271, 1272, 1273, 1274, 1275, 1276, 1277, 1278, 1279, 1280, 1281, 1282, 1283, 1284, 1285, 1286, 1287, 1288, 1289, 1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1301, 1302, 1303, 1304, 1305, 1306, 1307, 1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1345, 1346, 1347, 1348, 1349, 1350, 1351, 1352, 1353, 1354, 1355, 1356, 1357, 1358, 1359, 1360, 1361, 1362, 1363, 1364, 1365, 1366, 1367, 1368, 1369, 1370, 1371, 1372, 1373, 1374, 1375, 1376, 1377, 1378, 1379, 1380, 1381, 1382, 1383, 1384, 1385, 1386, 1387, 1388, 1389, 1390, 1391, 1392, 1393, 1394, 1395, 1396, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425, 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434, 1435, 1436, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 1448, 1449, 1450, 1451, 1452, 1453, 1454, 1455, 1456, 1457, 1458, 1459, 1460, 1461, 1462, 1463, 1464, 1465, 1466, 1467, 1468, 1469, 1470, 1471, 1472, 1473, 1474, 1475, 1476, 1477, 1478, 1479, 1480, 1481, 1482, 1483, 1484, 1485, 1486, 1487, 1488, 1489, 1490, 1491, 1492, 1493, 1494, 1495, 1496, 1497, 1498, 1499, 1500, 1501, 1502, 1503, 1504, 1505, 1506, 1507, 1508, 1509, 1510, 1511, 1512, 1513, 1514, 1515, 1516, 1517, 1518, 1519, 1520, 1521, 1522, 1523, 1524, 1525, 1526, 1527, 1528, 1529, 1530, 1531, 1532, 1533, 1534, 1535, 1536, 1537, 1538, 1539, 1540, 1541, 1542, 1543, 1544, 1545, 1546, 1547, 1548, 1549, 1550, 1551, 1552, 1553, 1554, 1555, 1556, 1557, 1558, 1559, 1560, 1561, 1562, 1563, 1564, 1565, 1566, 1567, 1568, 1569, 1570, 1571, 1572, 1573, 1574, 1575, 1576, 1577, 1578, 1579, 1580, 1581, 1582, 1583, 1584, 1585, 1586, 1587, 1588, 1589, 1590, 1591, 1592, 1593, 1594, 1595, 1596, 1597, 1598, 1599, 1600, 1601, 1602, 1603, 1604, 1605, 1606, 1607, 1608, 1609, 1610, 1611, 1612, 1613, 1614, 1615, 1616, 1617, 1618, 1619, 1620, 1621, 1622, 1623, 1624, 1625, 1626, 1627, 1628, 1629, 1630, 1631, 1632, 1633, 1634, 1635, 1636, 1637, 1638, 1639, 1640, 1641, 1642, 1643, 1644, 1645, 1646, 1647, 1648, 1649, 1650, 1651, 1652, 1653, 1654, 1655, 1656, 1657, 1658, 1659, 1660, 1661, 1662, 1663, 1664, 1665, 1666, 1667, 1668, 1669, 1670, 1671, 1672, 1673, 1674, 1675, 1676, 1677, 1678, 1679, 1680, 1681, 1682, 1683, 1684, 1685, 1686, 1687, 1688, 1689, 1690, 1691, 1692, 1693, 1694, 1695, 1696, 1697, 1698, 1699, 1700, 1701, 1702, 1703, 1704, 1705, 1706, 1707, 1708, 1709, 1710, 1711, 1712, 1713, 1714, 1715, 1716, 1717, 1718, 1719, 1720, 1721, 1722, 1723, 1724, 1725, 1726, 1727, 1728, 1729, 1730, 1731, 1732, 1733, 1734, 1735, 1736, 1737, 1738, 1739, 1740, 1741, 1742, 1743, 1744, 1745, 1746, 1747, 1748, 1749, 1750, 1751, 1752, 1753, 1754, 1755, 1756, 1757, 1758, 1759, 1760, 1761, 1762, 1763, 1764, 1765, 1766, 1767, 1768, 1769, 1770, 1771, 1772, 1773, 1774, 1775, 1776, 1777, 1778, 1779, 1780, 1781, 1782, 1783, 1784, 1785, 1786, 1787, 1788, 1789, 1790, 1791, 1792, 1793, 1794, 1795, 1796, 1797, 1798, 1799, 1800, 1801, 1802, 1803, 1804, 1805, 1806, 1807, 1808, 1809, 1810, 1811, 1812, 1813, 1814, 1815, 1816, 1817, 1818, 1819, 1820, 1821, 1822, 1823, 1824, 1825, 1826, 1827, 1828, 1829, 1830, 1831, 1832, 1833, 1834, 1835, 1836, 1837, 1838, 1839, 1840, 1841, 1842, 1843, 1844, 1845, 1846, 1847, 1848, 1849, 1850, 1851, 1852, 1853, 1854, 1855, 1856, 1857, 1858, 1859, 1860, 1861, 1862, 1863, 1864, 1865, 1866, 1867, 1868, 1869, 1870, 1871, 1872, 1873, 1874, 1875, 1876, 1877, 1878, 1879, 1880, 1881, 1882, 1883, 1884, 1885, 1886, 1887, 1888, 1889, 1890, 1891, 1892, 1893, 1894, 1895, 1896, 1897, 1898, 1899, 1900, 1901, 1902, 1903, 1904, 1905, 1906, 1907, 1908, 1909, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 1927, 1928, 1929, 1930, 1931, 1932, 1933, 1934, 1935, 1936, 1937, 1938, 1939, 1940, 1941, 1942, 1943, 1944, 1945, 1946, 1947, 1948, 1949, 1950, 1951, 1952, 1953, 1954, 1955, 1956, 1957, 1958, 1959, 1960, 1961, 1962, 1963, 1964, 1965, 1966, 1967, 1968, 1969, 1970, 1971, 1972, 1973, 1974, 1975, 1976, 1977, 1978, 1979, 1980, 1981, 1982, 1983, 1984, 1985, 1986, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2

100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

5 the amino acid at Mutated site 4 is Ala, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 10 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 15 homologue thereof, in which :

the amino acid at Mutated site 4 is Ala, and the amino acid at Mutated site 5 is His.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 20 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 25 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Ala, and the amino acid at Mutated site 5 is Lys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 30 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 35 homologue thereof, in which :

the amino acid at Mutated site 4 is Ala, and the amino acid at Mutated site 5 is Asp.

40 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,

52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 5 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Ala, and the amino acid at Mutated site 5 is Glu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
10 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 15 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Ala, and the amino acid at Mutated site 5 is Ser.

20 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 25 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Ala, and the amino acid at Mutated site 5 is Thr.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 35 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
40 the amino acid at Mutated site 4 is Ala, and the amino acid at Mutated site 5 is Asn.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 5 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Ala, and the amino acid at Mutated site 5 is Gln.

10

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 15 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20 the amino acid at Mutated site 4 is Ala, and the amino acid at Mutated site 5 is Cys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 25 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 30 homologue thereof, in which :

the amino acid at Mutated site 4 is Ala, and the amino acid at Mutated site 5 is Gly.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 35 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 40 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Ala, and the amino acid at Mutated site 5 is Pro.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Ala, and the amino acid at Mutated site 5 is Arg.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Ala, and the amino acid at Mutated site 5 is Tyr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Ala, and the amino acid at Mutated site 5 is Trp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

5 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
10 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is Leu.

15 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
20 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is Val.

25 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
30 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

35 the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
40 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is Met.

5 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
10 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is His.

15

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

25 the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is Lys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof. in which :

the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is Asp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99.

100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

5 the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is Glu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 10 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 15 homologue thereof, in which :

the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is Ser.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 20 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 25 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is Thr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 30 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 35 homologue thereof, in which :

the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is Asn.

40 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,

52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 5 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is Gln.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
10 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 15 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is Cys.

20 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 25 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is Gly.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 35 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
40 the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is Pro.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 5 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is Arg.

10

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 15 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20 the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is Tyr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 25 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 30 homologue thereof, in which :

the amino acid at Mutated site 4 is Arg, and the amino acid at Mutated site 5 is Trp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 35 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 40 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

5 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
10 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is His.

15 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
20 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is Lys.

25 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
30 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

35 the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is Asp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
40 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is Glu.

5

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

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15 the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is Ser.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20

25 the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is Thr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30

35

the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is Asn.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,

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100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

5 the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is Gln.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 10 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 15 homologue thereof, in which :

the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is Cys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 20 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 25 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is Gly.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 30 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 35 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is Pro.

40 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,

52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 5 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is Arg.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
10 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 15 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is Tyr.

20 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 25 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Val, and the amino acid at Mutated site 5 is Trp.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 35 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
40 the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 5 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is Leu.

10

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 15 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20 the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 25 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 30 homologue thereof, in which :

the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 35 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 40 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is His.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is Lys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is Asp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is Glu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

5 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
10 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is Ser.

15 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
20 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is Thr.

25 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
30 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

35 the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is Asn.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
40 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is Gln.

5

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

10

15 the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is Cys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20

25

the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is Gly.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30

35

the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is Pro.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,

40

100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

5 the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is Arg.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 10 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 15 homologue thereof, in which :

the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is Tyr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 20 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 25 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Ile, and the amino acid at Mutated site 5 is Trp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 30 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 35 homologue thereof, in which :

the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is Ala.

40 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,

52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 5 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
10 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 15 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is Val.

20 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 25 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is Ile.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 35 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
40 the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 5 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is His.

10

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 15 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20 the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is Lys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 25 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 30 homologue thereof, in which :

the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is Asp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 35 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 40 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is Glu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is Ser.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is Thr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is Asn.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is Gln.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

5 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
10 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is Cys.

15 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
20 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is Gly.

25 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
30 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

35 the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is Pro.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
40 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is Arg.

5

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

10

15 the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is Tyr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20

25

the amino acid at Mutated site 4 is Met, and the amino acid at Mutated site 5 is Trp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30

35

the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,

40

76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 5 homologue thereof, in which :
 the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 10 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 15 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 20 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 25 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 30 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 35 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is Met.

40

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,

28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 5 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is His.

10 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 15 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is Lys.

20

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 25 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30 the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is Asp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 35 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 40 homologue thereof, in which :

the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is Glu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 5 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

10 the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is Ser.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 15 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 20 homologue thereof, in which :

the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is Thr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 25 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 30 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is Asn.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 35 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 40 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is Gln.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 5 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 10 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :

the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is Cys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

15 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 20 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :

the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is Gly.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

25 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 30 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :

the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is Pro.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

35 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 40 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,

613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is Arg.

5 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
10 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is Tyr.

15

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

25 the amino acid at Mutated site 4 is His, and the amino acid at Mutated site 5 is Trp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99.

100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

5 the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 10 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 15 homologue thereof, in which :

the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 20 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 25 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 30 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 35 homologue thereof, in which :

the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is Met.

40 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,

52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 5 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is His.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
10 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 15 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is Lys.

20 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 25 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is Asp.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 35 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
40 the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is Glu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 5 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is Ser.

10

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 15 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20 the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is Thr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 25 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 30 homologue thereof, in which :

the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is Asn.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 35 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 40 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is Gln.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is Cys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is Gly.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is Pro.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is Arg.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

5 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
10 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is Tyr.

15 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
20 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Lys, and the amino acid at Mutated site 5 is Trp.

25 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
30 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

35 the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
40 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is Leu.

5

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

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15 the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20

25

the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30

35

the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,

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76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

5 homologue thereof, in which :

the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is His.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 10 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

15 homologue thereof, in which :

the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is Lys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 20 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 25 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is Asp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 35 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is Glu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,

52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 5 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is Ser.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
10 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 15 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is Thr.

20 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 25 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is Asn.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 35 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
40 the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is Gln.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 5 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is Cys.

10

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 15 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20 the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is Gly.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 25 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 30 homologue thereof, in which :

the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is Pro.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 35 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 40 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is Arg.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is Tyr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Asp, and the amino acid at Mutated site 5 is Trp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

5 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
10 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is Val.

15 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
20 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is Ile.

25

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
30 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

35 the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
40 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is His.

5

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

10

15 the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is Lys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20

25

the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is Asp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30

35

the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is Glu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,

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76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 5 homologue thereof, in which :
 the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is Ser.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 10 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 15 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is Thr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 20 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 25 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is Asn.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 30 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 35 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is Gln.

40 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,

52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 5 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is Cys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
10 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 15 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is Gly.

20 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 25 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is Pro.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 35 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
40 the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is Arg.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 5 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is Tyr.

10

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 15 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20 the amino acid at Mutated site 4 is Glu, and the amino acid at Mutated site 5 is Trp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 25 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 30 homologue thereof, in which :

the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 35 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 40 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is His.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

5 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
10 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is Lys.

15 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
20 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is Asp.

25

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
30 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

35 the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is Glu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
40 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is Ser.

5

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

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15 the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is Thr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20

25

the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is Asn.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30

35

the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is Gln.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,

40

76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 5 homologue thereof, in which :
 the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is Cys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 10 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 15 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is Gly.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 20 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 25 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is Pro.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 30 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 35 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is Arg.

40 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,

52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 5 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is Tyr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
10 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 15 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Ser, and the amino acid at Mutated site 5 is Trp.

20 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 25 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is Ala.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 35 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
40 the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 5 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is Val.

10

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 15 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20 the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 25 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 30 homologue thereof, in which :

the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 35 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 40 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is His.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is Lys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is Asp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is Glu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is Ser.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

5 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
10 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is Thr.

15 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
20 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is Asn.

25 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
30 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

35 the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is Gln.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
40 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is Cys.

5

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

10

15 the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is Gly.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20

25

the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is Pro.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30

35

the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is Arg.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,

40

76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 5 homologue thereof, in which :
 the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is Tyr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 10 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 15 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is Thr, and the amino acid at Mutated site 5 is Trp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 20 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 25 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is Ala.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 35 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is Leu.

40 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,

52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 5 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
10 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 15 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is Ile.

20 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 25 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is Met.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 35 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
40 the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is His.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 5 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is Lys.

10

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 15 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20 the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is Asp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 25 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 30 homologue thereof, in which :

the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is Glu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 35 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 40 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is Ser.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is Thr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is Asn.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is Gln.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is Cys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

5 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
10 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is Gly.

15 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
20 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is Pro.

25 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
30 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

35 the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is Arg.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
40 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is Tyr.

5

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

10

15 the amino acid at Mutated site 4 is Asn, and the amino acid at Mutated site 5 is Trp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20

25

the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30

35

the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,

40

76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

5 homologue thereof, in which :

the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
10 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
15 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
20 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
25 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is Met.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
35 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is His.

40

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,

28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 5 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is Lys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

10 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 15 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is Asp.

20 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 25 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is Glu.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 35 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

40 the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is Ser.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 5 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is Thr.

10

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 15 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20 the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is Asn.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 25 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 30 homologue thereof, in which :

the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is Gln.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 35 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 40 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is Cys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is Gly.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is Pro.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is Arg.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is Tyr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

5 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
10 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Gln, and the amino acid at Mutated site 5 is Trp.

15 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
20 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is Ala.

25

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
30 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

35 the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
40 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is Val.

5

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

10

15 the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20

25

the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30

35

the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is His.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,

40

76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

5 homologue thereof, in which :

the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is Lys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
10 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,

15 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is Asp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
20 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

25 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is Glu.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
35 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is Ser.

40

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,

28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 5 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is Thr.

10 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 15 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is Asn.

20 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 25 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is Gln.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 35 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

40 the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is Cys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

210

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 5 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is Gly.

10

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 15 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20 the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is Pro.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 25 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 30 homologue thereof, in which :

the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is Arg.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 35 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 40 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is Tyr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Cys, and the amino acid at Mutated site 5 is Trp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

5 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
10 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is Ile.

15 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
20 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is Met.

25 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
30 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

35 the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is His.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
40 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is Lys.

5

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

10

15 the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is Asp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20

25

the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is Glu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30

35

the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is Ser.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,

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76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 5 homologue thereof, in which :
 the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is Thr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 10 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 15 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is Asn.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 20 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 25 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is Gln.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 30 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 35 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is Cys.

40

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,

28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 5 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is Gly.

10 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 15 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is Pro.

20

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 25 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30 the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is Arg.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 35 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

40 the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is Tyr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 5 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Gly, and the amino acid at Mutated site 5 is Trp.

10

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 15 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20 the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 25 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 30 homologue thereof, in which :

the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 35 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 40 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is His.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is Lys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

5 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
10 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is Asp.

15 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
20 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is Glu.

25 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
30 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

35 the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is Ser.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
40 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is Thr.

5

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

10

15 the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is Asn.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20

25

the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is Gln.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30

35

the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is Cys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,

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76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 5 homologue thereof, in which :
 the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is Gly.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 10 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 15 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is Pro.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 20 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 25 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is Arg.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 30 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 35 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is Tyr.

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In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,

28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 5 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Pro, and the amino acid at Mutated site 5 is Trp.

10 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 15 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is Ala.

20

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 25 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30 the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 35 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 40 homologue thereof, in which :

the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 5 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is Ile.

10

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 15 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20 the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 25 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 30 homologue thereof, in which :

the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is His.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 35 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 40 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is Lys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is Asp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is Glu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is Ser.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is Thr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

5 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
10 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is Asn.

15 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
20 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is Gln.

25

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
30 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

35 the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is Cys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
40 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is Gly.

5

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

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15 the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is Pro.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20

25

the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is Arg.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30

35

the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is Tyr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,

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76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

5 homologue thereof, in which :

the amino acid at Mutated site 4 is Phe, and the amino acid at Mutated site 5 is Trp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
10 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,

15 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
20 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

25 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is Leu.

30 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,

35 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is Val.

40

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,

28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 5 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is Ile.

10 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 15 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is Met.

20

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 25 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30 the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is His.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 35 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 40 homologue thereof, in which :

the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is Lys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 5 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

10 the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is Asp.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 15 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20 the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is Glu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 25 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 30 homologue thereof, in which :

the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is Ser.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 35 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 40 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is Thr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is Asn.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is Gln.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is Cys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is Gly.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

5 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
10 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is Pro.

15 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
20 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is Arg.

25

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
30 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
homologue thereof, in which :

35 the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is Tyr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
40 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,

577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Tyr, and the amino acid at Mutated site 5 is Trp.

5

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

10

15 the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20

25

the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30

35

the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,

40

76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 5 homologue thereof, in which :
 the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 10 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 15 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 20 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 25 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is His.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 30 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51,
 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99,
 35 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,
 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611,
 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or
 homologue thereof, in which :
 the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is Lys.

40

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO:
 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,

28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 5 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is Asp.

10 In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 15 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is Glu.

20

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 25 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30 the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is Ser.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 35 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or 40 homologue thereof, in which :

the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is Thr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 5 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

10 the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is Asn.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 15 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

20 the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is Gln.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 25 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

30 the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is Cys.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 35 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :

40 the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is Gly.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is Pro.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is Arg.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or homologue thereof, in which :
the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is Tyr.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, a variant, derivative, orthologue, paralogue or

homologue thereof, in which :

the amino acid at Mutated site 4 is Trp, and the amino acid at Mutated site 5 is Trp.

It will be within the knowledge of the skilled artisan to identify conserved regions and motifs shared between the homologues, orthologues and paralogues of PPO polypeptides comprising SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, or 117. Having identified such conserved regions that may represent suitable binding motifs, amino acids corresponding to the amino acids listed in Table 2a and 2b can be chosen to be substituted by any other amino acid, preferably by the amino acids listed under mutated sites 1, 2, 3, 4, or 5.

Accordingly, preferred motifs shared between the homologues, orthologues and paralogues of PPO polypeptides described above are Motif 1: SQ[N/K/H]KRYI, wherein the Arg at position 5 within said motif is substituted by Leu, Ala, Val, Ile, Met, Tyr, Gly, Asn, Cys, Phe, Ser, Thr, Gln, or His; Motif 2: TLGTLFSS, wherein the Leu at position 2 within said motif is substituted by Ala, Arg, Val, Ile, Met, His, Lys, Asp, Glu, Ser, Thr, Asn, Gln, Cys, Gly, Pro, Phe, Tyr, or Trp; Motif 3: [F/Y]TTF[V/I]GG, wherein the Phe at position 4 within said motif is substituted by Ala, Leu, Val, Ile, Met, His, Lys, Asp, Glu, Ser, Thr, Asn, Gln, Cys, Gly, Pro, Arg, Tyr, or Trp.

Further examples of such homologues, orthologues and paralogues are PPO polypeptides comprising the amino acid sequence of SEQ ID NO: 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627.

In addition, the present invention refers to a method for identifying a phenylpyridine herbicide by using a herbicide tolerant PPO polypeptide as defined SUPRA.

Said method comprises the steps of:

- a) generating a transgenic cell or plant comprising a nucleic acid encoding a mutated PPO, wherein the mutated PPO is expressed;
- b) applying a phenylpyridine herbicide to the transgenic cell or plant of a) and to a control cell or plant of the same variety;
- c) determining the growth or the viability of the transgenic cell or plant and the control cell or plant after application of said phenylpyridine herbicide, and
- d) selecting "phenylpyridine herbicides" which confer reduced growth to the control cell or plant as compared to the growth of the transgenic cell or plant.

By "control cell" or "similar, wild-type, plant, plant tissue, plant cell or host cell" is intended a plant, plant tissue, plant cell, or host cell, respectively, that lacks the herbicide-resistance characteristics and/or particular polynucleotide of the invention that are disclosed herein.

The use of the term "wild-type" is not, therefore, intended to imply that a plant, plant tissue,
 5 plant cell, or other host cell lacks recombinant DNA in its genome, and/or does not possess herbicide-resistant characteristics that are different from those disclosed herein.

Another object refers to a method of identifying a nucleotide sequence encoding a mutated PPO which is resistant or tolerant to a phenylpyridine herbicide, the method comprising:

- 10 a) generating a library of mutated PPO-encoding nucleic acids,
- b) screening a population of the resulting mutated PPO-encoding nucleic acids by expressing each of said nucleic acids in a cell or plant and treating said cell or plant with a phenylpyridine herbicide,
- c) comparing the phenylpyridine herbicide-tolerance levels provided by said population of
 15 mutated PPO encoding nucleic acids with the phenylpyridine herbicide-tolerance level provided by a control PPO-encoding nucleic acid,
- d) selecting at least one mutated PPO-encoding nucleic acid that provides a significantly increased level of tolerance to a phenylpyridine herbicide as compared to that provided by the control PPO-encoding nucleic acid.

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In a preferred embodiment, the mutated PPO-encoding nucleic acid selected in step d) provides at least 2-fold as much resistance or tolerance of a cell or plant to a phenylpyridine herbicide as compared to that provided by the control PPO-encoding nucleic acid.

- 25 In a further preferred embodiment, the mutated PPO-encoding nucleic acid selected in step d) provides at least 2-fold, at least 5-fold, at least 10-fold, at least 20-fold, at least 50-fold, at least 100-fold, at least 500-fold, as much resistance or tolerance of a cell or plant to a phenylpyridine herbicide as compared to that provided by the control PPO-encoding nucleic acid.

30

The resistance or tolerance can be determined by generating a transgenic plant or host cell, preferably a plant cell, comprising a nucleic acid sequence of the library of step a) and comparing said transgenic plant with a control plant or host cell, preferably a plant cell.

- 35 Another object refers to a method of identifying a plant or algae containing a nucleic acid comprising a nucleotide sequence encoding a wild-type or mutated PPO which is resistant or tolerant to a phenylpyridine herbicide, the method comprising:

- a) identifying an effective amount of a phenylpyridine herbicide in a culture of plant cells or green algae that leads to death of said cells.
- 40 b) treating said plant cells or green algae with a mutagenizing agent,
- c) contacting said mutagenized cells population with an effective amount of phenylpyridine herbicide, identified in a),

- d) selecting at least one cell surviving these test conditions,
- e) PCR-amplification and sequencing of PPO genes from cells selected in d) and comparing such sequences to wild-type PPO gene sequences, respectively.

5 In a preferred embodiment, said mutagenizing agent is ethylmethanesulfonate (EMS). Many methods well known to the skilled artisan are available for obtaining suitable candidate nucleic acids for identifying a nucleotide sequence encoding a mutated PPO from a variety of different potential source organisms including microbes, plants, fungi, algae, mixed cultures etc. as well as environmental sources of DNA such as soil. These methods
10 include inter alia the preparation of cDNA or genomic DNA libraries, the use of suitably degenerate oligonucleotide primers, the use of probes based upon known sequences or complementation assays (for example, for growth upon tyrosine) as well as the use of mutagenesis and shuffling in order to provide recombined or shuffled mutated PPO-encoding sequences.

15 Nucleic acids comprising candidate and control PPO encoding sequences can be expressed in yeast, in a bacterial host strain, in an alga or in a higher plant such as tobacco or Arabidopsis and the relative levels of inherent tolerance of the PPO encoding sequences screened according to a visible indicator phenotype of the transformed strain or plant in the
20 presence of different concentrations of the selected phenylpyridine herbicide. Dose responses and relative shifts in dose responses associated with these indicator phenotypes (formation of brown color, growth inhibition, herbicidal effect etc) are conveniently expressed in terms, for example, of GR50 (concentration for 50% reduction of growth) or MIC (minimum inhibitory concentration) values where increases in values correspond to
25 increases in inherent tolerance of the expressed PPO. For example, in a relatively rapid assay system based upon transformation of a bacterium such as *E. coli*, each mutated PPO encoding sequence may be expressed, for example, as a DNA sequence under expression control of a controllable promoter such as the *lacZ* promoter and taking suitable account, for example by the use of synthetic DNA, of such issues as codon usage in order to obtain as
30 comparable a level of expression as possible of different PPO sequences. Such strains expressing nucleic acids comprising alternative candidate PPO sequences may be plated out on different concentrations of the selected phenylpyridine herbicide in, optionally, a tyrosine supplemented medium and the relative levels of inherent tolerance of the expressed PPO enzymes estimated on the basis of the extent and MIC for inhibition of the
35 formation of the brown, ochronotic pigment.

In another embodiment, candidate nucleic acids are transformed into plant material to generate a transgenic plant, regenerated into morphologically normal fertile plants which are then measured for differential tolerance to selected phenylpyridine herbicides as
40 described in the Example section hereinafter. Many suitable methods for transformation using suitable selection markers such as kanamycin, binary vectors such as from *Agrobacterium* and plant regeneration as, for example, from tobacco leaf discs are well

known in the art. Optionally, a control population of plants is likewise transformed with a nucleic acid expressing the control PPO. Alternatively, an untransformed dicot plant such as Arabidopsis or Tobacco can be used as a control since this, in any case, expresses its own endogenous PPO. The average, and distribution, of herbicide tolerance levels of a range of primary plant transformation events or their progeny to phenylpyridine herbicides described supra are evaluated in the normal manner based upon plant damage, meristematic bleaching symptoms etc. at a range of different concentrations of herbicides. These data can be expressed in terms of, for example, GR50 values derived from dose/response curves having "dose" plotted on the x-axis and "percentage kill", "herbicidal effect", "numbers of emerging green plants" etc. plotted on the y-axis where increased GR50 values correspond to increased levels of inherent tolerance of the expressed PPO. Herbicides can suitably be applied pre-emergence or post-emergence.

In another embodiment, the invention refers to a plant cell transformed by a nucleic acid encoding a herbicide tolerant PPO polypeptide disclosed herein or to a plant cell which has been mutated to obtain a plant expressing a nucleic acid encoding a mutated PPO polypeptide according to the present invention, wherein expression of the nucleic acid in the plant cell results in increased resistance or tolerance to a phenylpyridine herbicide as compared to a wild type variety of the plant cell.

The term "expression/expressing" or "gene expression" means the transcription of a specific gene or specific genes or specific genetic construct. The term "expression" or "gene expression" in particular means the transcription of a gene or genes or genetic construct into structural RNA (rRNA, tRNA) or mRNA with or without subsequent translation of the latter into a protein. The process includes transcription of DNA and processing of the resulting mRNA product.

To obtain the desired effect, i.e. plants that are tolerant or resistant to the phenylpyridine herbicide derivative herbicide of the present invention, it will be understood that the at least one nucleic acid is "over-expressed" by methods and means known to the person skilled in the art.

The term "increased expression" or "overexpression" as used herein means any form of expression that is additional to the original wild-type expression level. Methods for increasing expression of genes or gene products are well documented in the art and include, for example, overexpression driven by appropriate promoters, the use of transcription enhancers or translation enhancers. Isolated nucleic acids which serve as promoter or enhancer elements may be introduced in an appropriate position (typically upstream) of a non-heterologous form of a polynucleotide so as to upregulate expression of a nucleic acid encoding the polypeptide of interest. For example, endogenous promoters may be altered in vivo by mutation, deletion, and/or substitution (see, Kmiec, US 5,565,350; Zarling et al., WO9322443), or isolated promoters may be introduced into a plant cell in the

proper orientation and distance from a gene of the present invention so as to control the expression of the gene.

If polypeptide expression is desired, it is generally desirable to include a polyadenylation region at the 3'-end of a polynucleotide coding region. The polyadenylation region can be derived from the natural gene, from a variety of other plant genes, or from T-DNA. The 3' end sequence to be added may be derived from, for example, the nopaline synthase or octopine synthase genes, or alternatively from another plant gene, or less preferably from any other eukaryotic gene.

An intron sequence may also be added to the 5' untranslated region (UTR) or the coding sequence of the partial coding sequence to increase the amount of the mature message that accumulates in the cytosol. Inclusion of a spliceable intron in the transcription unit in both plant and animal expression constructs has been shown to increase gene expression at both the mRNA and protein levels up to 1000-fold (Buchman and Berg (1988) *Mol. Cell Biol.* 8: 4395-4405; Callis et al. (1987) *Genes Dev* 1:1183-1200). Such intron enhancement of gene expression is typically greatest when placed near the 5' end of the transcription unit. Use of the maize introns Adh1-S intron 1, 2, and 6, the Bronze-1 intron are known in the art. For general information see: *The Maize Handbook*, Chapter 116, Freeling and Walbot, Eds., Springer, N.Y. (1994)

The term "introduction" or "transformation" as referred to herein encompasses the transfer of an exogenous polynucleotide into a host cell, irrespective of the method used for transfer. Plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a genetic construct of the present invention and a whole plant regenerated there from. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen, embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristem, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and hypocotyl meristem). The polynucleotide may be transiently or stably introduced into a host cell and may be maintained non-integrated, for example, as a plasmid. Alternatively, it may be integrated into the host genome. The resulting transformed plant cell may then be used to regenerate a transformed plant in a manner known to persons skilled in the art.

The transfer of foreign genes into the genome of a plant is called transformation. Transformation of plant species is now a fairly routine technique. Advantageously, any of several transformation methods may be used to introduce the gene of interest into a suitable ancestor cell. The methods described for the transformation and regeneration of plants from plant tissues or plant cells may be utilized for transient or for stable transformation. Transformation methods include the use of liposomes, electroporation,

chemicals that increase free DNA uptake, injection of the DNA directly into the plant, particle gun bombardment, transformation using viruses or pollen and microprojection. Methods may be selected from the calcium/polyethylene glycol method for protoplasts (Krens, F.A. et al., (1982) Nature 296, 72-74; Negrutiu I et al. (1987) Plant Mol Biol 8: 363-373); electroporation of protoplasts (Shillito R.D. et al. (1985) Bio/Technol 3, 1099-1102); microinjection into plant material (Crossway A et al., (1986) Mol. Gen Genet 202: 179-185); DNA or RNA-coated particle bombardment (Klein TM et al., (1987) Nature 327: 70) infection with (non-integrative) viruses and the like. Transgenic plants, including transgenic crop plants, are preferably produced via Agrobacterium-mediated transformation. An advantageous transformation method is the transformation in planta. To this end, it is possible, for example, to allow the agrobacteria to act on plant seeds or to inoculate the plant meristem with agrobacteria. It has proved particularly expedient in accordance with the invention to allow a suspension of transformed agrobacteria to act on the intact plant or at least on the flower primordia. The plant is subsequently grown on until the seeds of the treated plant are obtained (Clough and Bent, Plant J. (1998) 16, 735-743). Methods for Agrobacterium-mediated transformation of rice include well known methods for rice transformation, such as those described in any of the following: European patent application EP 1198985 A1, Aldemita and Hodges (Planta 199: 612-617, 1996); Chan et al. (Plant Mol Biol 22 (3): 491-506, 1993), Hiei et al. (Plant J 6 (2): 271-282, 1994), which disclosures are incorporated by reference herein as if fully set forth. In the case of corn transformation, the preferred method is as described in either Ishida et al. (Nat. Biotechnol 14(6): 745-50, 1996) or Frame et al. (Plant Physiol 129(1): 13-22, 2002), which disclosures are incorporated by reference herein as if fully set forth. Said methods are further described by way of example in B. Jenes et al., Techniques for Gene Transfer, in: Transgenic Plants, Vol. 1, Engineering and Utilization, eds. S.D. Kung and R. Wu, Academic Press (1993) 128-143 and in Potrykus Annu. Rev. Plant Physiol. Plant Molec. Biol. 42 (1991) 205-225). The nucleic acids or the construct to be expressed is preferably cloned into a vector, which is suitable for transforming Agrobacterium tumefaciens, for example pBin19 (Bevan et al., Nucl. Acids Res. 12 (1984) 8711). Agrobacteria transformed by such a vector can then be used in known manner for the transformation of plants, such as plants used as a model, like Arabidopsis (Arabidopsis thaliana is within the scope of the present invention not considered as a crop plant), or crop plants such as, by way of example, tobacco plants, for example by immersing bruised leaves or chopped leaves in an agrobacterial solution and then culturing them in suitable media. The transformation of plants by means of Agrobacterium tumefaciens is described, for example, by Höfgen and Willmitzer in Nucl. Acid Res. (1988) 16, 9877 or is known inter alia from F.F. White, Vectors for Gene Transfer in Higher Plants; in Transgenic Plants, Vol. 1, Engineering and Utilization, eds. S.D. Kung and R. Wu, Academic Press, 1993, pp. 15-38.

In addition to the transformation of somatic cells, which then have to be regenerated into intact plants, it is also possible to transform the cells of plant meristems and in particular those cells which develop into gametes. In this case, the transformed gametes follow the

natural plant development, giving rise to transgenic plants. Thus, for example, seeds of *Arabidopsis* are treated with agrobacteria and seeds are obtained from the developing plants of which a certain proportion is transformed and thus transgenic [Feldman, KA and Marks MD (1987). *Mol Gen Genet* 208:274-289; Feldmann K (1992). In: C Koncz, N-H Chua and J Shell, eds, *Methods in Arabidopsis Research*. Word Scientific, Singapore, pp. 274-289]. Alternative methods are based on the repeated removal of the inflorescences and incubation of the excision site in the center of the rosette with transformed agrobacteria, whereby transformed seeds can likewise be obtained at a later point in time (Chang (1994). *Plant J.* 5: 551-558; Katavic (1994). *Mol Gen Genet*, 245: 363-370). However, an especially effective method is the vacuum infiltration method with its modifications such as the "floral dip" method. In the case of vacuum infiltration of *Arabidopsis*, intact plants under reduced pressure are treated with an agrobacterial suspension [Bechthold, N (1993). *C R Acad Sci Paris Life Sci*, 316: 1194-1199], while in the case of the "floral dip" method the developing floral tissue is incubated briefly with a surfactant-treated agrobacterial suspension [Clough, SJ and Bent AF (1998) *The Plant J.* 16, 735-743]. A certain proportion of transgenic seeds are harvested in both cases, and these seeds can be distinguished from non-transgenic seeds by growing under the above-described selective conditions. In addition the stable transformation of plastids is of advantages because plastids are inherited maternally is most crops reducing or eliminating the risk of transgene flow through pollen. The transformation of the chloroplast genome is generally achieved by a process which has been schematically displayed in Klaus et al., 2004 [*Nature Biotechnology* 22 (2), 225-229]. Briefly the sequences to be transformed are cloned together with a selectable marker gene between flanking sequences homologous to the chloroplast genome. These homologous flanking sequences direct site specific integration into the plastome. Plastidal transformation has been described for many different plant species and an overview is given in Bock (2001) *Transgenic plastids in basic research and plant biotechnology. J Mol Biol.* 2001 Sep 21; 312 (3):425-38 or Maliga, P (2003) *Progress towards commercialization of plastid transformation technology. Trends Biotechnol.* 21, 20-28. Further biotechnological progress has recently been reported in form of marker free plastid transformants, which can be produced by a transient co-integrated marker gene (Klaus et al., 2004, *Nature Biotechnology* 22(2), 225-229). The genetically modified plant cells can be regenerated via all methods with which the skilled worker is familiar. Suitable methods can be found in the abovementioned publications by S.D. Kung and R. Wu, Potrykus or Höfgen and Willmitzer.

Generally after transformation, plant cells or cell groupings are selected for the presence of one or more markers which are encoded by plant-expressible genes co-transferred with the gene of interest, following which the transformed material is regenerated into a whole plant. To select transformed plants, the plant material obtained in the transformation is, as a rule, subjected to selective conditions so that transformed plants can be distinguished from untransformed plants. For example, the seeds obtained in the above-described manner can be planted and, after an initial growing period, subjected to a suitable selection by spraying. A further possibility consists in growing the seeds, if appropriate after sterilization, on agar

plates using a suitable selection agent so that only the transformed seeds can grow into plants. Alternatively, the transformed plants are screened for the presence of a selectable marker such as the ones described above.

- 5 Following DNA transfer and regeneration, putatively transformed plants may also be evaluated, for instance using Southern analysis, for the presence of the gene of interest, copy number and/or genomic organisation. Alternatively or additionally, expression levels of the newly introduced DNA may be monitored using Northern and/or Western analysis, both techniques being well known to persons having ordinary skill in the art.

10

The generated transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, a first generation (or T1) transformed plant may be selfed and homozygous second-generation (or T2) transformants selected, and the T2 plants may then further be propagated through classical breeding techniques. The generated transformed organisms may take a variety of forms. For example, they may be chimeras of transformed cells and non-transformed cells; clonal transformants (e.g., all cells transformed to contain the expression cassette); grafts of transformed and untransformed tissues (e.g., in plants, a transformed rootstock grafted to an untransformed scion).

20

Preferably, the wild-type or mutated PPO nucleic acid comprises a polynucleotide sequence selected from the group consisting of : a) a polynucleotide encoding a polypeptide as shown in SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 25 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, or a variant or derivative thereof; b) 30 a polynucleotide comprising at least 60 consecutive nucleotides of any of a); and c) a polynucleotide complementary to the polynucleotide of any of a) through b).

Preferably, the expression of the nucleic acid in the plant results in the plant's increased resistance to phenylpyridine herbicide as compared to a wild type variety of the plant.

35

In another embodiment, the invention refers to a plant, preferably a transgenic plant, comprising a plant cell according to the present invention, wherein expression of the nucleic acid in the plant results in the plant's increased resistance to phenylpyridine herbicide as compared to a wild type variety of the plant.

40

The plants described herein can be either transgenic crop plants or non-transgenic plants.

For the purposes of the invention, "transgenic", "transgene" or "recombinant" means with regard to, for example, a nucleic acid sequence, an expression cassette, gene construct or a vector comprising the nucleic acid sequence or an organism transformed with the nucleic acid sequences, expression cassettes or vectors according to the invention, all those

5 constructions brought about by recombinant methods in which either

(a) the nucleic acid sequences encoding proteins useful in the methods of the invention, or

(b) genetic control sequence(s) which is operably linked with the nucleic acid sequence according to the invention, for example a promoter, or

10 (c) a) and b)

are not located in their natural genetic environment or have been modified by recombinant methods, it being possible for the modification to take the form of, for example, a

substitution, addition, deletion, inversion or insertion of one or more nucleotide residues in order to allow for the expression of the mutated PPO of the present invention. The natural

15 genetic environment is understood as meaning the natural genomic or chromosomal locus in the original plant or the presence in a genomic library. In the case of a genomic library,

the natural genetic environment of the nucleic acid sequence is preferably retained, at least in part. The environment flanks the nucleic acid sequence at least on one side and has a

sequence length of at least 50 bp, preferably at least 500 bp, especially preferably at least

20 1000 bp, most preferably at least 5000 bp. A naturally occurring expression cassette – for example the naturally occurring combination of the natural promoter of the nucleic acid

sequences with the corresponding nucleic acid sequence encoding a polypeptide useful in the methods of the present invention, as defined above – becomes a transgenic expression cassette when this expression cassette is modified by non-natural, synthetic ("artificial")

25 methods such as, for example, mutagenic treatment. Suitable methods are described, for example, in US 5,565,350 or WO 00/15815.

A transgenic plant for the purposes of the invention is thus understood as meaning, as

above, that the nucleic acids of the invention are not at their natural locus in the genome of

30 said plant, it being possible for the nucleic acids to be expressed homologously or

heterologously. However, as mentioned, transgenic also means that, while the nucleic acids according to the invention or used in the inventive method are at their natural position in the genome of a plant, the sequence has been modified with regard to the natural sequence, and/or that the regulatory sequences of the natural sequences have been modified.

35 Transgenic is preferably understood as meaning the expression of the nucleic acids

according to the invention at an unnatural locus in the genome, i.e. homologous or,

preferably, heterologous expression of the nucleic acids takes place. Preferred transgenic plants are mentioned herein. Furthermore, the term "transgenic" refers to any plant, plant cell, callus, plant tissue, or plant part, that contains all or part of at least one recombinant

40 polynucleotide. In many cases, all or part of the recombinant polynucleotide is stably

integrated into a chromosome or stable extra-chromosomal element, so that it is passed on to successive generations. For the purposes of the invention, the term "recombinant

polynucleotide” refers to a polynucleotide that has been altered, rearranged, or modified by genetic engineering. Examples include any cloned polynucleotide, or polynucleotides, that are linked or joined to heterologous sequences. The term “recombinant” does not refer to alterations of polynucleotides that result from naturally occurring events, such as
5 spontaneous mutations, or from non-spontaneous mutagenesis followed by selective breeding.

Plants containing mutations arising due to non-spontaneous mutagenesis and selective breeding are referred to herein as non-transgenic plants and are included in the present
10 invention. In embodiments wherein the plant is transgenic and comprises multiple mutated PPO nucleic acids, the nucleic acids can be derived from different genomes or from the same genome. Alternatively, in embodiments wherein the plant is non-transgenic and comprises multiple mutated PPO nucleic acids, the nucleic acids are located on different genomes or on the same genome. As used herein, “mutagenized” refers to an organism or
15 DNA thereof having alteration(s) in the biomolecular sequence of its native genetic material as compared to the sequence of the genetic material of a corresponding wild-type organism or DNA, wherein the alteration(s) in genetic material were induce and/or selected by human action. Methods of inducing mutations can induce mutations in random positions in the genetic material or can induce mutations in specific locations in the genetic material (i.e.,
20 can be directed mutagenesis techniques), such as by use of a genoplasty technique.

In certain embodiments, the present invention involves herbicide-resistant plants that are produced by mutation breeding. Such plants comprise a polynucleotide encoding a mutated PPO and are tolerant to one or more phenylpyridine herbicides. Such methods can involve,
25 for example, exposing the plants or seeds to a mutagen, particularly a chemical mutagen such as, for example, ethyl methanesulfonate (EMS) and selecting for plants that have enhanced tolerance to at least one or more phenylpyridine herbicide.

However, the present invention is not limited to herbicide-tolerant plants that are produced
30 by a mutagenesis method involving the chemical mutagen EMS. Any mutagenesis method known in the art may be used to produce the herbicide-resistant plants of the present invention. Such mutagenesis methods can involve, for example, the use of any one or more of the following mutagens: radiation, such as X-rays, Gamma rays (e.g., cobalt 60 or cesium 137), neutrons, (e.g., product of nuclear fission by uranium 235 in an atomic
35 reactor), Beta radiation (e.g., emitted from radioisotopes such as phosphorus 32 or carbon 14), and ultraviolet radiation (preferably from 2500 to 2900 nm), and chemical mutagens such as base analogues (e.g., 5-bromo-uracil), related compounds (e.g., 8-ethoxy caffeine), antibiotics (e.g., streptonigrin), alkylating agents (e.g., sulfur mustards, nitrogen mustards, epoxides, ethylenamines, sulfates, sulfonates, sulfones, lactones), azide, hydroxylamine,
40 nitrous acid, or acridines. Herbicide-resistant plants can also be produced by using tissue culture methods to select for plant cells comprising herbicide-resistance mutations and then regenerating herbicide-resistant plants therefrom. See, for example, U.S. Patent Nos.

5,773,702 and 5,859,348, both of which are herein incorporated in their entirety by reference. Further details of mutation breeding can be found in "Principals of Cultivar Development" Fehr, 1993 Macmillan Publishing Company the disclosure of which is incorporated herein by reference

5

In addition to the definition above, the term "plant" is intended to encompass crop plants at any stage of maturity or development, as well as any tissues or organs (plant parts) taken or derived from any such plant unless otherwise clearly indicated by context. Plant parts include, but are not limited to, stems, roots, flowers, ovules, stamens, leaves, embryos, meristematic regions, callus tissue, anther cultures, gametophytes, sporophytes, pollen, microspores, protoplasts, and the like.

The plant of the present invention comprises at least one mutated PPO nucleic acid or over-expressed wild-type PPO nucleic acid, and has increased tolerance to a phenylpyridine herbicide as compared to a wild-type variety of the plant. It is possible for the plants of the present invention to have multiple wild-type or mutated PPO nucleic acids from different genomes since these plants can contain more than one genome. For example, a plant contains two genomes, usually referred to as the A and B genomes. Because PPO is a required metabolic enzyme, it is assumed that each genome has at least one gene coding for the PPO enzyme (i.e. at least one PPO gene). As used herein, the term "PPO gene locus" refers to the position of an PPO gene on a genome, and the terms "PPO gene" and "PPO nucleic acid" refer to a nucleic acid encoding the PPO enzyme. The PPO nucleic acid on each genome differs in its nucleotide sequence from an PPO nucleic acid on another genome. One of skill in the art can determine the genome of origin of each PPO nucleic acid through genetic crossing and/or either sequencing methods or exonuclease digestion methods known to those of skill in the art.

The present invention includes plants comprising one, two, three, or more mutated PPO alleles, wherein the plant has increased tolerance to a phenylpyridine herbicide as compared to a wild-type variety of the plant. The mutated PPO alleles can comprise a nucleotide sequence selected from the group consisting of a polynucleotide encoding a polypeptide as defined in SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341,

342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, or a variant or derivative, homologue, orthologue, paralogue thereof, a polynucleotide comprising at least 60 consecutive nucleotides of any of the aforementioned polynucleotides; and a polynucleotide complementary to any of the aforementioned polynucleotides.

“Alleles” or “allelic variants” are alternative forms of a given gene, located at the same chromosomal position. Allelic variants encompass Single Nucleotide Polymorphisms (SNPs), as well as Small Insertion/Deletion Polymorphisms (INDELs). The size of INDELs is usually less than 100 bp. SNPs and INDELs form the largest set of sequence variants in naturally occurring polymorphic strains of most organisms

The term “variety” refers to a group of plants within a species defined by the sharing of a common set of characteristics or traits accepted by those skilled in the art as sufficient to distinguish one cultivar or variety from another cultivar or variety. There is no implication in either term that all plants of any given cultivar or variety will be genetically identical at either the whole gene or molecular level or that any given plant will be homozygous at all loci. A cultivar or variety is considered “true breeding” for a particular trait if, when the true-breeding cultivar or variety is self-pollinated, all of the progeny contain the trait. The terms “breeding line” or “line” refer to a group of plants within a cultivar defined by the sharing of a common set of characteristics or traits accepted by those skilled in the art as sufficient to distinguish one breeding line or line from another breeding line or line. There is no implication in either term that all plants of any given breeding line or line will be genetically identical at either the whole gene or molecular level or that any given plant will be homozygous at all loci. A breeding line or line is considered “true breeding” for a particular trait if, when the true-breeding line or breeding line is self-pollinated, all of the progeny contain the trait. In the present invention, the trait arises from a mutation in a PPO gene of the plant or seed.

In some embodiments, traditional plant breeding is employed whereby the phenylpyridine herbicides-tolerant trait is introduced in the progeny plant resulting therefrom. In one

embodiment, the present invention provides a method for producing a phenylpyridine herbicides-tolerant progeny plant, the method comprising: crossing a parent plant with a phenylpyridine herbicides-tolerant plant to introduce the phenylpyridine herbicides-tolerance characteristics of the phenylpyridine herbicides-tolerant plant into the germplasm of the progeny plant, wherein the progeny plant has increased tolerance to the phenylpyridine herbicides relative to the parent plant. In other embodiments, the method further comprises the step of introgressing the phenylpyridine herbicides-tolerance characteristics through traditional plant breeding techniques to obtain a descendent plant having the phenylpyridine herbicides-tolerance characteristics.

The herbicide-resistant plants of the invention that comprise polynucleotides encoding mutated PPO polypeptides also find use in methods for increasing the herbicide-resistance of a plant through conventional plant breeding involving sexual reproduction. The methods comprise crossing a first plant that is a herbicide-resistant plant of the invention to a second plant that may or may not be resistant to the same herbicide or herbicides as the first plant or may be resistant to different herbicide or herbicides than the first plant. The second plant can be any plant that is capable of producing viable progeny plants (i.e., seeds) when crossed with the first plant. Typically, but not necessarily, the first and second plants are of the same species. The methods can optionally involve selecting for progeny plants that comprise the mutated PPO polypeptides of the first plant and the herbicide resistance characteristics of the second plant. The progeny plants produced by this method of the present invention have increased resistance to a herbicide when compared to either the first or second plant or both. When the first and second plants are resistant to different herbicides, the progeny plants will have the combined herbicide tolerance characteristics of the first and second plants. The methods of the invention can further involve one or more generations of backcrossing the progeny plants of the first cross to a plant of the same line or genotype as either the first or second plant. Alternatively, the progeny of the first cross or any subsequent cross can be crossed to a third plant that is of a different line or genotype than either the first or second plant. The present invention also provides plants, plant organs, plant tissues, plant cells, seeds, and non-human host cells that are transformed with the at least one polynucleotide molecule, expression cassette, or transformation vector of the invention. Such transformed plants, plant organs, plant tissues, plant cells, seeds, and non-human host cells have enhanced tolerance or resistance to at least one herbicide, at levels of the herbicide that kill or inhibit the growth of an untransformed plant, plant tissue, plant cell, or non-human host cell, respectively. Preferably, the transformed plants, plant tissues, plant cells, and seeds of the invention are *Arabidopsis thaliana* and crop plants.

In other aspects, plants of the invention include those plants which, in addition to being tolerant to phenylpyridine herbicides, have been subjected to further genetic modifications by breeding, mutagenesis or genetic engineering, e.g. have been rendered tolerant to applications of specific other classes of herbicides, such as AHAS inhibitors; auxinic

herbicides; bleaching herbicides such as hydroxyphenylpyruvate dioxygenase (HPPD) inhibitors or phytoene desaturase (PDS) inhibitors; EPSPS inhibitors such as glyphosate; glutamine synthetase (GS) inhibitors such as glufosinate; lipid biosynthesis inhibitors such as acetyl CoA carboxylase (ACCase) inhibitors; or oxynil {i.e. bromoxynil or ioxynil}

5 herbicides as a result of conventional methods of breeding or genetic engineering, Thus, phenylpyridine herbicides-tolerant plants of the invention can be made resistant to multiple classes of herbicides through multiple genetic modifications, such as resistance to both glyphosate and glufosinate or to both glyphosate and a herbicide from another class such as HPPD inhibitors, AHAS inhibitors, or ACCase inhibitors. These herbicide resistance
10 technologies are, for example, described in Pest Management Science (at volume, year, page): 61, 2005, 246; 61, 2005, 258; 61, 2005, 277; 61, 2005, 269; 61, 2005, 286; 64, 2008, 326; 64, 2008, 332; Weed Science 57, 2009, 108; Australian Journal of Agricultural Research 58, 2007, 708; Science 316, 2007, 1185; and references quoted therein. For example, phenylpyridine herbicides-tolerant plants of the invention, in some embodiments,
15 may be tolerant to ACCase inhibitors, such as "dims" {e.g., cycloxydim, sethoxydim, clethodim, or tepraloxym), "fops" {e.g. , clodinafop, diclofop, fluazifop, haloxyfop, or quizalofop), and "dens" (such as pinoxaden); to auxinic herbicides, such as dicamba; to EPSPS inhibitors, such as glyphosate; to other PPO inhibitors; and to GS inhibitors, such as glufosinate.

20 In addition to these classes of inhibitors, phenylpyridine herbicides-tolerant plants of the invention may also be tolerant to herbicides having other modes of action, for example, chlorophyll/carotenoid pigment inhibitors, cell membrane disrupters, photosynthesis inhibitors, cell division inhibitors, root inhibitors, shoot inhibitors, and combinations thereof.

25 Such tolerance traits may be expressed, e.g. : as mutant or wildtype PPO proteins, as mutant AHASL proteins, mutant ACCase proteins, mutant EPSPS proteins, or mutant glutamine synthetase proteins; or as mutant native, inbred, or transgenic aryloxyalkanoate dioxygenase (AAD or DHT), haloarylnitrilase (BXN), 2,2-dichloropropionic acid
30 dehalogenase (DEH), glyphosate-N- acetyltransferase (GAT), glyphosate decarboxylase (GDC), glyphosate oxidoreductase (GOX), glutathione-S-transferase (GST), phosphinothricin acetyltransferase (PAT or bar), or CYP450s proteins having an herbicide-degrading activity.

35 phenylpyridine herbicides- tolerant plants hereof can also be stacked with other traits including, but not limited to, pesticidal traits such as Bt Cry and other proteins having pesticidal activity toward coleopteran, lepidopteran, nematode, or other pests; nutrition or nutraceutical traits such as modified oil content or oil profile traits, high protein or high amino acid concentration traits, and other trait types known in the art.

40 Furthermore, in other embodiments, phenylpyridine herbicides-tolerant plants are also covered which are, by the use of recombinant DNA techniques and/or by breeding and/or

otherwise selected for such characteristics, rendered able to synthesize one or more insecticidal proteins, especially those known from the bacterial genus *Bacillus*, particularly from *Bacillus thuringiensis*, such as [delta]-endotoxins, e.g. CryIA(b), CryIA(c), CryIF, CryIF(a2), CryIIA(b), CryIIIA, CryIIIB(bI) or Cry9c; vegetative insecticidal proteins (VIP), e.g. VIP1, VIP2, VIP3 or VIP3A; insecticidal proteins of bacteria colonizing nematodes, e.g. *Photorhabdus* spp. or *Xenorhabdus* spp.; toxins produced by animals, such as scorpion toxins, arachnid toxins, wasp toxins, or other insect-specific neurotoxins; toxins produced by fungi, such streptomycete toxins; plant lectins, such as pea or barley lectins; agglutinins; proteinase inhibitors, such as trypsin inhibitors, serine protease inhibitors, patatin, cystatin or papain inhibitors; ribosome-inactivating proteins (RIP), such as ricin, maize-RIP, abrin, luffin, saporin or bryodin; steroid metabolism enzymes, such as 3-hydroxy-steroid oxidase, ecdysteroid-IDP-glycosyl-transferase, cholesterol oxidases, ecdysone inhibitors or HMG-CoA-reductase; ion channel blockers, such as blockers of sodium or calcium channels; juvenile hormone esterase; diuretic hormone receptors (helicokinin receptors); stilben synthase, bibenzyl synthase, chitinases or glucanases. In the context of the present invention these insecticidal proteins or toxins are to be understood expressly also as pre-toxins, hybrid proteins, truncated or otherwise modified proteins. Hybrid proteins are characterized by a new combination of protein domains, (see, e.g. WO 02/015701). Further examples of such toxins or genetically modified plants capable of synthesizing such toxins are disclosed, e.g., in EP-A 374 753, WO 93/007278, WO 95/34656, EP-A 427 529, EP-A 451 878, WO 03/18810 und WO 03/52073. The methods for producing such genetically modified plants are generally known to the person skilled in the art and are described, e.g. in the publications mentioned above. These insecticidal proteins contained in the genetically modified plants impart to the plants producing these proteins tolerance to harmful pests from all taxonomic groups of arthropods, especially to beetles (Coleoptera), two-winged insects (Diptera), and moths (Lepidoptera) and to nematodes (Nematoda).

In some embodiments, expression of one or more protein toxins (e.g., insecticidal proteins) in the phenylpyridine herbicides-tolerant plants is effective for controlling organisms that include, for example, members of the classes and orders: Coleoptera such as the American bean weevil *Acanthoscelides obtectus*; the leaf beetle *Agelastica alni*; click beetles (*Agriotes lineatus*, *Agriotes obscurus*, *Agriotes bicolor*); the grain beetle *Ahasverus advena*; the summer schaffer *Amphimallon solstitialis*; the furniture beetle *Anobium punctatum*; *Anthonomus* spp. (weevils); the Pygmy mangold beetle *Atomaria linearis*; carpet beetles (*Anthrenus* spp., *Attagenus* spp.); the cowpea weevil *Callosobruchus maculatus*; the fried fruit beetle *Carpophilus hemipterus*; the cabbage seedpod weevil *Ceutorhynchus assimilis*; the rape winter stem weevil *Ceutorhynchus picipitarsis*; the wireworms *Conoderus vespertinus* and *Conoderus falli*; the banana weevil *Cosmopolites sordidus*; the New Zealand grass grub *Costelytra zealandica*; the June beetle *Cotinis nitida*; the sunflower stem weevil *Cylindrocopturus adspersus*; the larder beetle *Dermestes lardarius*; the corn rootworms *Diabrotica virgifera*, *Diabrotica virgifera virgifera*, and *Diabrotica barberi*; the Mexican bean beetle *Epilachna varivestis*; the old house borer *Hylotropes bajulus*; the

lucerne weevil *Hypera postica*; the shiny spider beetle *Gibbium psylloides*; the cigarette beetle *Lasioderma serricorne*; the Colorado potato beetle *Leptinotarsa decemlineata*; *Lyctus* beetles {*Lyctus* spp. , the pollen beetle *Meligethes aeneus*; the common cockshafer *Melolontha melolontha*; the American spider beetle *Mezium americanum*; the golden spider beetle *Niptus hololeucus*; the grain beetles *Oryzaephilus surinamensis* and *Oryzaephilus Mercator*; the black vine weevil *Otiorhynchus sulcatus*; the mustard beetle *Phaedon cochleariae*, the crucifer flea beetle *Phyllotreta cruciferae*; the striped flea beetle *Phyllotreta striolata*; the cabbage steam flea beetle *Psylliodes chrysocephala*; *Ptinus* spp. (spider beetles); the lesser grain borer *Rhizopertha dominica*; the pea and bean weevil *Sitona lineatus*; the rice and granary beetles *Sitophilus oryzae* and *Sitophilus granaries*; the red sunflower seed weevil *Smicronyx fulvus*; the drugstore beetle *Stegobium paniceum*; the yellow mealworm beetle *Tenebrio molitor*, the flour beetles *Tribolium castaneum* and *Tribolium confusum*; warehouse and cabinet beetles {*Trogoderma* spp.}; the sunflower beetle *Zygogramma exclamationis*; Dermaptera (earwigs) such as the European earwig *Forficula auricularia* and the striped earwig *Labidura riparia*; Dictyoptera such as the oriental cockroach *Blatta orientalis*; the greenhouse millipede *Oxidus gracilis*; the beet fly *Pegomya betae*; the frit fly *Oscinella frit*; fruitflies (*Dacus* spp., *Drosophila* spp.); Isoptera (termites) including species from the families Hodotermitidae, Kalotermitidae, Mastotermitidae, Rhinotermitidae, Serritermitidae, Termitidae, Termopsidae; the tarnished plant bug *Lygus lineolaris*; the black bean aphid *Aphis fabae*; the cotton or melon aphid *Aphis gossypii*; the green apple aphid *Aphis pomi*; the citrus spiny whitefly *Aleurocanthus spiniferus*; the sweet potato whitefly *Bemisia tabaci*; the cabbage aphid *Brevicoryne brassicae*; the pear psylla *Cacopsylla pyricola*; the currant aphid *Cryptomyzus ribis*; the grape phylloxera *Daktulosphaira vitifoliae*; the citrus psylla *Diaphorina citri*; the potato leafhopper *Empoasca fabae*; the bean leafhopper *Empoasca Solana*; the vine leafhopper *Empoasca vitis*; the woolly aphid *Eriosoma lanigerum*; the European fruit scale *Eulecanium corni*; the mealy plum aphid *Hyalopterus arundinis*; the small brown planthopper *Laodelphax striatellus*; the potato aphid *Macrosiphum euphorbiae*; the green peach aphid *Myzus persicae*; the green rice leafhopper *Nephotettix cincticeps*; the brown planthopper *Nilaparvata lugens*; the hop aphid *Phorodon humuli*; the bird-cherry aphid *Rhopalosiphum padi*; the grain aphid *Sitobion avenae*; Lepidoptera such as *Adoxophyes orana* (summer fruit tortrix moth); *Archips podana* (fruit tree tortrix moth); *Bucculatrix pyrivorella* (pear leafminer); *Bucculatrix thurberiella* (cotton leaf perforator); *Bupalus piniarius* (pine looper); *Carpocapsa pomonella* (codling moth); *Chilo suppressalis* (striped rice borer); *Choristoneura fumiferana* (eastern spruce budworm); *Cochylis hospes* (banded sunflower moth); *Diatraea grandiosella* (southwestern corn borer); *Eupoecilia ambiguella* (European grape berry moth); *Helicoverpa armigera* (cotton bollworm); *Helicoverpa zea* (cotton bollworm); *Heliothis virescens* (tobacco budworm), *Homeosoma electellum* (sunflower moth); *Homona magnanima* (oriental tea tree tortrix moth); *Lithocolletis blancardella* (spotted tentiform leafminer); *Lymantria dispar* (gypsy moth); *Malacosoma neustria* (tent caterpillar); *Mamestra brassicae* (cabbage armyworm); *Mamestra configurata* (Bertha armyworm); *Operophtera brumata* (winter moth); *Ostrinia nubilalis* (European corn borer), *Panolis flammea* (pine beauty

moth), *Phyllocnistis citrella* (citrus leafminer); *Pieris brassicae* (cabbage white butterfly); *Rachiplusia ni* (soybean looper); *Spodoptera exigua* (beet armyworm); *Spodoptera littoralis* (cotton leafworm); *Sylepta derogata* (cotton leaf roller); *Trichoplusia ni* (cabbage looper); Orthoptera such as the common cricket *Acheta domesticus*, tree locusts (*Anacridium* spp.),
 5 the migratory locust *Locusta migratoria*, the two-striped grasshopper *Melanoplus bivittatus*, the differential grasshopper *Melanoplus differentialis*, the red-legged grasshopper *Melanoplus femurrubrum*, the migratory grasshopper *Melanoplus sanguinipes*, the northern mole cricket *Neocurtilla hexadactyla*, the red locust *Nomadacris septemfasciata*, the short-winged mole cricket *Scapteriscus abbreviatus*, the southern mole cricket *Scapteriscus*
 10 *borellii*, the tawny mole cricket *Scapteriscus vicinus*, and the desert locust *Schistocerca gregaria*; Symphyla such as the garden symphylan *Scutigera immaculata*; Thysanoptera such as the tobacco thrips *Frankliniella fusca*, the flower thrips *Frankliniella intonsa*, the western flower thrips *Frankliniella occidentalis*, the cotton bud thrips *Frankliniella schultzei*, the banded greenhouse thrips *Hercinothrips femoralis*, the soybean thrips *Neohydatothrips*
 15 *variabilis*, Kelly's citrus thrips *Pezothrips kellyanus*, the avocado thrips *Scirtothrips perseae*, the melon thrips *Thrips palmi*, and the onion thrips *Thrips tabaci*; and the like, and combinations comprising one or more of the foregoing organisms.

In some embodiments, expression of one or more protein toxins (e.g., insecticidal proteins)
 20 in the phenylpyridine herbicides-tolerant plants is effective for controlling flea beetles, i.e. members of the flea beetle tribe of family Chrysomelidae, preferably against *Phyllotreta* spp., such as *Phyllotreta cruciferae* and/or *Phyllotreta triolita*. In other embodiments, expression of one or more protein toxins (e.g., insecticidal proteins) in the phenylpyridine herbicides-tolerant plants is effective for controlling cabbage seedpod weevil, the Bertha
 25 armyworm, *Lygus* bugs, or the diamondback moth.

Furthermore, in one embodiment, phenylpyridine herbicides-tolerant plants are also covered which are, e.g. by the use of recombinant DNA techniques and/or by breeding and/or otherwise selected for such traits, rendered able to synthesize one or more proteins to increase the resistance or tolerance of those plants to bacterial, viral or fungal
 30 pathogens. The methods for producing such genetically modified plants are generally known to the person skilled in the art.

Furthermore, in another embodiment, phenylpyridine herbicides-tolerant plants are also covered which are, e.g. by the use of recombinant DNA techniques and/or by breeding
 35 and/or otherwise selected for such traits, rendered able to synthesize one or more proteins to increase the productivity (e.g. oil content), tolerance to drought, salinity or other growth-limiting environmental factors or tolerance to pests and fungal, bacterial or viral pathogens of those plants.

Furthermore, in other embodiments, phenylpyridine herbicides-tolerant plants are also
 40 covered which are, e.g. by the use of recombinant DNA techniques and/or by breeding and/or otherwise selected for such traits, altered to contain a modified amount of one or more substances or new substances, for example, to improve human or animal nutrition,

e.g. oil crops that produce health-promoting long-chain omega-3 fatty acids or unsaturated omega-9 fatty acids (e.g. Nexera(R) rape, Dow Agro Sciences, Canada).

Furthermore, in some embodiments, phenylpyridine herbicides-tolerant plants are also covered which are, e.g. by the use of recombinant DNA techniques and/or by breeding and/or otherwise selected for such traits, altered to contain increased amounts of vitamins and/or minerals, and/or improved profiles of nutraceutical compounds.

In one embodiment, phenylpyridine herbicides-tolerant plants of the present invention, relative to a wild-type plant, comprise an increased amount of, or an improved profile of, a compound selected from the group consisting of: glucosinolates (e.g., glucoraphanin (4-methylsulfinylbutyl-glucosinolate), sulforaphane, 3-indolylmethyl-glucosinolate(glucobrassicin), 1-methoxy-3-indolylmethyl-glucosinolate (neoglucobrassicin)); phenolics (e.g., flavonoids (e.g., quercetin, kaempferol), hydroxycinnamoyl derivatives (e.g., 1,2,2'- trisinpoylgentiobiose, 1,2-diferuloylgentiobiose, 1,2'-disinpoyl-2-feruloylgentiobiose, 3-O-caffeoyl-quinic (neochlorogenic acid)); and vitamins and minerals (e.g., vitamin C, vitamin E, carotene, folic acid, niacin, riboflavin, thiamine, calcium, iron, magnesium, potassium, selenium, and zinc).

In another embodiment, phenylpyridine herbicides-tolerant plants of the present invention, relative to a wild-type plant, comprise an increased amount of, or an improved profile of, a compound selected from the group consisting of: progoitrin; isothiocyanates; indoles (products of glucosinolate hydrolysis); glutathione; carotenoids such as beta-carotene, lycopene, and the xanthophyll carotenoids such as lutein and zeaxanthin; phenolics comprising the flavonoids such as the flavonols (e.g. quercetin, rutin), the flavans/tannins (such as the procyanidins comprising coumarin, proanthocyanidins, catechins, and anthocyanins); flavones; phytoestrogens such as coumestans, lignans, resveratrol, isoflavones e.g. genistein, daidzein, and glycitein; resorcylic acid lactones; organosulphur compounds; phytosterols; terpenoids such as carnosol, rosmarinic acid, glycyrrhizin and saponins; chlorophyll; chlorophyllin, sugars, anthocyanins, and vanilla. In other embodiments, phenylpyridine herbicides-tolerant plants of the present invention, relative to a wild-type plant, comprise an increased amount of, or an improved profile of, a compound selected from the group consisting of: vincristine, vinblastine, taxanes (e.g., taxol (paclitaxel), baccatin III, 10-desacetylbaccatin III, 10-desacetyl taxol, xylosyl taxol, 7-epitaxol, 7-epibaccatin III, 10-desacetylcephalomannine, 7-epicephalomannine, taxotere, cephalomannine, xylosyl cephalomannine, taxagifine, 8-benzoyloxy taxagifine, 9-acetyloxy taxusin, 9-hydroxy taxusin, taiwanxam, taxane Ia, taxane Ib, taxane Ic, taxane Id, GMP paclitaxel, 9-dihydro 13-acetylbaccatin III, 10-desacetyl-7-epitaxol, tetrahydrocannabinol (THC), cannabidiol (CBD), genistein, diadzein, codeine, morphine, quinine, shikonin, ajmalacine, serpentine, and the like.

It is to be understood that the plant of the present invention can comprise a wild type PPO nucleic acid in addition to a mutated PPO nucleic acid. It is contemplated that the

phenylpyridine herbicide tolerant lines may contain a mutation in only one of multiple PPO isoenzymes. Therefore, the present invention includes a plant comprising one or more mutated PPO nucleic acids in addition to one or more wild type PPO nucleic acids.

- 5 In another embodiment, the invention refers to a seed produced by a transgenic plant comprising a plant cell of the present invention, wherein the seed is true breeding for an increased resistance to a phenylpyridine herbicide as compared to a wild type variety of the seed.
- 10 In another embodiment, the invention refers to a method of producing a transgenic plant cell with an increased resistance to a phenylpyridine herbicide as compared to a wild type variety of the plant cell comprising, transforming the plant cell with an expression cassette comprising a mutated PPO nucleic acid.
- 15 In another embodiment, the invention refers to a method of producing a transgenic plant comprising, (a) transforming a plant cell with an expression cassette comprising a mutated PPO nucleic acid, and (b) generating a plant with an increased resistance to phenylpyridine herbicide from the plant cell.
- 20 Consequently, mutated PPO nucleic acids of the invention are provided in expression cassettes for expression in the plant of interest. The cassette will include regulatory sequences operably linked to a mutated PPO nucleic acid sequence of the invention. The term "regulatory element" as used herein refers to a polynucleotide that is capable of regulating the transcription of an operably linked polynucleotide. It includes, but not limited to, promoters, enhancers, introns, 5' UTRs, and 3' UTRs. By "operably linked" is intended a functional linkage between a promoter and a second sequence, wherein the promoter sequence initiates and mediates transcription of the DNA sequence corresponding to the second sequence. Generally, operably linked means that the nucleic acid sequences being linked are contiguous and, where necessary to join two protein coding regions, contiguous and in the same reading frame. The cassette may additionally contain at least one additional gene to be cotransformed into the organism. Alternatively, the additional gene(s) can be provided on multiple expression cassettes.
- 25
- 30

In a preferred embodiment, the expression cassette comprises the sequence of SEQ ID NO: 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, or 262.

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Such an expression cassette is provided with a plurality of restriction sites for insertion of the mutated PPO nucleic acid sequence to be under the transcriptional regulation of the regulatory regions. The expression cassette may additionally contain selectable marker genes.

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The expression cassette of the present invention will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region (i.e., a promoter), a mutated PPO encoding nucleic acid sequence of the invention, and a transcriptional and translational termination region (i.e., termination region) functional in plants. The promoter may be native or analogous, or foreign or heterologous, to the plant host and/or to the mutated PPO nucleic acid sequence of the invention. Additionally, the promoter may be the natural sequence or alternatively a synthetic sequence. Where the promoter is "foreign" or "heterologous" to the plant host, it is intended that the promoter is not found in the native plant into which the promoter is introduced. Where the promoter is "foreign" or "heterologous" to the mutated PPO nucleic acid sequence of the invention, it is intended that the promoter is not the native or naturally occurring promoter for the operably linked mutated PPO nucleic acid sequence of the invention. As used herein, a chimeric gene comprises a coding sequence operably linked to a transcription initiation region that is heterologous to the coding sequence.

While it may be preferable to express the mutated PPO nucleic acids of the invention using heterologous promoters, the native promoter sequences may be used. Such constructs would change expression levels of the mutated PPO protein in the plant or plant cell. Thus, the phenotype of the plant or plant cell is altered.

The termination region may be native with the transcriptional initiation region, may be native with the operably linked mutated PPO sequence of interest, may be native with the plant host, or may be derived from another source (i.e., foreign or heterologous to the promoter, the mutated PPO nucleic acid sequence of interest, the plant host, or any combination thereof). Convenient termination regions are available from the Ti-plasmid of *Agrobacterium tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also Guerineau et al. (1991) *Mol. Gen. Genet.* 262: 141-144; Proudfoot (1991) *Cell* 64:671-674; Sanfacon et al. (1991) *Genes Dev.* 5: 141-149; Mogen et al. (1990) *Plant Cell* 2: 1261-1272; Munroe et al. (1990) *Gene* 91: 151-158; Ballas et al. (1989) *Nucleic Acids Res.* 17:7891-7903; and Joshi et al. (1987) *Nucleic Acid Res.* 15:9627-9639. Where appropriate, the gene(s) may be optimized for increased expression in the transformed plant. That is, the genes can be synthesized using plant-preferred codons for improved expression. See, for example, Campbell and Gowri (1990) *Plant Physiol.* 92: 1-11 for a discussion of host-preferred codon usage. Methods are available in the art for synthesizing plant-preferred genes. See, for example, U.S. Patent Nos. 5,380,831, and 5,436,391, and Murray et al. (1989) *Nucleic Acids Res.* 17:477-498, herein incorporated by reference.

Additional sequence modifications are known to enhance gene expression in a cellular host. These include elimination of sequences encoding spurious polyadenylation signals, exon-intron splice site signals, transposon-like repeats, and other such well-characterized sequences that may be deleterious to gene expression. The G-C content of the sequence may be adjusted to levels average for a given cellular host, as calculated by reference to

known genes expressed in the host cell. When possible, the sequence is modified to avoid predicted hairpin secondary mRNA structures. Nucleotide sequences for enhancing gene expression can also be used in the plant expression vectors. These include the introns of the maize Adhl, intron1 gene (Callis et al. *Genes and Development* 1: 1183-1200, 1987), and leader sequences, (W- sequence) from the Tobacco Mosaic virus (TMV), Maize Chlorotic Mottle Virus and Alfalfa Mosaic Virus (Gallie et al. *Nucleic Acid Res.* 15:8693-8711, 1987 and Skuzeski et al. *Plant Mol. Biol.* 15:65-79, 1990). The first intron from the shrunken- 1 locus of maize, has been shown to increase expression of genes in chimeric gene constructs. U.S. Pat. Nos. 5,424,412 and 5,593,874 disclose the use of specific introns in gene expression constructs, and Gallie et al. (*Plant Physiol.* 106:929-939, 1994) also have shown that introns are useful for regulating gene expression on a tissue specific basis. To further enhance or to optimize mutated PPO gene expression, the plant expression vectors of the invention may also contain DNA sequences containing matrix attachment regions (MARs). Plant cells transformed with such modified expression systems, then, may exhibit overexpression or constitutive expression of a nucleotide sequence of the invention.

The expression cassettes of the present invention may additionally contain 5' leader sequences in the expression cassette construct. Such leader sequences can act to enhance translation. Translation leaders are known in the art and include: picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5' noncoding region) (Elroy-Stein et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:6126-6130); potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Gallie et al. (1995) *Gene* 165(2):233-238), MDMV leader (Maize Dwarf Mosaic Virus) (*Virology* 154:9-20), and human immunoglobulin heavy-chain binding protein (BiP) (Macejak et al. (1991) *Nature* 353:90-94); untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4) (Jobling et al. (1987) *Nature* 325:622-625); tobacco mosaic virus leader (TMV) (Gallie et al. (1989) in *Molecular Biology of RNA*, ed. Cech (Liss, New York), pp. 237-256); and maize chlorotic mottle virus leader (MCMV) (Lommel et al. (1991) *Virology* 81:382-385). See also, Della-Cioppa et al. (1987) *Plant Physiol.* 84:965-968. Other methods known to enhance translation can also be utilized, for example, introns, and the like.

In preparing the expression cassette, the various DNA fragments may be manipulated, so as to provide for the DNA sequences in the proper orientation and, as appropriate, in the proper reading frame. Toward this end, adapters or linkers may be employed to join the DNA fragments or other manipulations may be involved to provide for convenient restriction sites, removal of superfluous DNA, removal of restriction sites, or the like. For this purpose, in vitro mutagenesis, primer repair, restriction, annealing, resubstitutions, e.g., transitions and trans versions, may be involved.

A number of promoters can be used in the practice of the invention. The promoters can be selected based on the desired outcome. The nucleic acids can be combined with

constitutive, tissue -preferred, or other promoters for expression in plants. Such constitutive promoters include, for example, the core promoter of the Rsyn7 promoter and other constitutive promoters disclosed in WO 99/43838 and U.S. Patent No. 6,072,050; the core CaMV 35S promoter (Odell et al. (1985) Nature 313:810-812); rice actin (McElroy et al. (1990) Plant Cell 2: 163-171); ubiquitin (Christensen et al. (1989) Plant Mol. Biol. 12:619-632 and Christensen et al. (1992) Plant Mol. Biol. 18:675-689); pEMU (Last et al. (1991) Theor. Appl. Genet. 81:581- 588); MAS (Velten et al. (1984) EMBO J. 3:2723-2730); ALS promoter (U.S. Patent No. 5,659,026), and the like. Other constitutive promoters include, for example, U.S. Patent Nos. 5,608,149; 5,608,144; 5,604,121; 5,569,597; 5,466,785; 5,399,680; 5,268,463; 5,608,142; and 6,177,611.

Tissue-preferred promoters can be utilized to target enhanced mutated PPO expression within a particular plant tissue. Such tissue-preferred promoters include, but are not limited to, leaf -preferred promoters, root-preferred promoters, seed- preferred promoters, and stem-preferred promoters. Tissue-preferred promoters include Yamamoto et al. (1997) Plant J. 12(2):255-265; Kawamata et al. (1997) Plant Cell Physiol. 38(7):792-803; Hansen et al. (1997) Mol. Gen Genet. 254(3):337-343; Russell et al. (1997) Transgenic Res. 6(2): 157-168; Rinehart et al. (1996) Plant Physiol. 112(3): 1331-1341; Van Camp et al. (1996) Plant Physiol. 112(2):525-535; Canevascini et al. (1996) Plant Physiol. 112(2):513-524; Yamamoto et al. (1994) Plant Cell Physiol. 35(5):773-778; Lam (1994) Results Probl. Cell Differ. 20: 181- 196; Orozco et al. (1993) Plant Mol Biol. 23(6): 1129-1138; Matsuoka et al. (1993) Proc Natl. Acad. Sci. USA 90(20):9586-9590; and Guevara-Garcia et al. (1993) Plant J. 4(3):495-505. Such promoters can be modified, if necessary, for weak expression. In one embodiment, the nucleic acids of interest are targeted to the chloroplast for expression. In this manner, where the nucleic acid of interest is not directly inserted into the chloroplast, the expression cassette will additionally contain a chloroplast-targeting sequence comprising a nucleotide sequence that encodes a chloroplast transit peptide to direct the gene product of interest to the chloroplasts. Such transit peptides are known in the art. With respect to chloroplast-targeting sequences, "operably linked" means that the nucleic acid sequence encoding a transit peptide (i.e., the chloroplast-targeting sequence) is linked to the mutated PPO nucleic acid of the invention such that the two sequences are contiguous and in the same reading frame. See, for example, Von Heijne et al. (1991) Plant Mol. Biol. Rep. 9: 104-126; Clark et al. (1989) J. Biol. Chem. 264:17544-17550; Della-Cioppa et al. (1987) Plant Physiol. 84:965-968; Romer et al. (1993) Biochem. Biophys. Res. Commun. 196:1414-1421; and Shah et al. (1986) Science 233:478-481. While the mutated PPO proteins of the invention include a native chloroplast transit peptide, any chloroplast transit peptide known in the art can be fused to the amino acid sequence of a mature mutated PPO protein of the invention by operably linking a chloroplast-targeting sequence to the 5'-end of a nucleotide sequence encoding a mature mutated PPO protein of the invention. Chloroplast targeting sequences are known in the art and include the chloroplast small subunit of ribulose-1,5-bisphosphate carboxylase (Rubisco) (de Castro Silva Filho et al. (1996) Plant Mol. Biol. 30:769-780; Schnell et al. (1991) J. Biol. Chem. 266(5):3335-

3342); 5 -(enolpyruvyl)shikimate-3 -phosphate synthase (EPSPS) (Archer et al. (1990) J. Bioenerg. Biomemb. 22(6):789-810); tryptophan synthase (Zhao et al. (1995) J. Biol. Chem. 270(11):6081-6087); plastocyanin(Lawrence et al. (1997) J. Biol. Chem. 272(33):20357-20363); chorismate synthase (Schmidt et al. (1993) J. Biol. Chem. 268(36):27447-27457);
 5 and the light harvesting chlorophyll a/b binding protein (LHBP) (Lamppa et al. (1988) J. Biol. Chem. 263: 14996-14999). See also Von Heijne et al. (1991) Plant Mol. Biol. Rep. 9: 104-126; Clark et al. (1989) J. Biol. Chem. 264:17544-17550; Della-Cioppa et al. (1987) Plant Physiol. 84:965-968; Romer et al. (1993) Biochem. Biophys. Res. Commun. 196: 1414-1421; and Shah et al. (1986) Science 233:478-481.

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In a preferred embodiment, the transit peptide comprises the amino acid sequence of SEQ ID NO: 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180,
 15 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226.

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Preferred expression cassettes comprise a transit peptide from Amaranthus PPO-2 fused to PPO or PPO like polypeptides, such as chimeric expression cassettes having the SEQ ID NO: 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, or 262

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Methods for transformation of chloroplasts are known in the art. See, for example, Svab et al. (1990) Proc. Natl. Acad. Sci. USA 87:8526-8530; Svab and Maliga (1993) Proc. Natl. Acad. Sci. USA 90:913-917; Svab and Maliga (1993) EMBO J. 12:601-606. The method relies on particle gun delivery of DNA containing a selectable marker and targeting of the DNA to the plastid genome through homologous recombination. Additionally, plastid transformation can be accomplished by transactivation of a silent plastid-borne transgene
 30 by tissue-preferred expression of a nuclear-encoded and plastid-directed RNA polymerase. Such a system has been reported in McBride et al. (1994) Proc. Natl. Acad. Sci. USA 91:7301-7305. The nucleic acids of interest to be targeted to the chloroplast may be optimized for expression in the chloroplast to account for differences in codon usage between the plant nucleus and this organelle. In this manner, the nucleic acids of interest
 35 may be synthesized using chloroplast-preferred codons. See, for example, U.S. Patent No. 5,380,831 , herein incorporated by reference.

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In a preferred embodiment, the mutated PPO nucleic acid comprises a polynucleotide sequence selected from the group consisting of: a) a polynucleotide encoding a polypeptide as shown in SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68,

69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, or a variant or
 5 derivative thereof; b) a polynucleotide comprising at least 60 consecutive nucleotides of any of a); and c) a polynucleotide complementary to the polynucleotide of any of a) through b)

Preferably, the expression cassette of the present invention further comprises a transcription initiation regulatory region and a translation initiation regulatory region that are
 10 functional in the plant.

While the polynucleotides of the invention find use as selectable marker genes for plant transformation, the expression cassettes of the invention can include another selectable marker gene for the selection of transformed cells. Selectable marker genes, including
 15 those of the present invention, are utilized for the selection of transformed cells or tissues. Marker genes include, but are not limited to, genes encoding antibiotic resistance, such as those encoding neomycin phosphotransferase II (NEO) and hygromycin phosphotransferase (HPT), as well as genes conferring resistance to herbicidal compounds, such as glufosinate ammonium, bromoxynil, imidazolinones, and 2,4-
 20 dichlorophenoxyacetate (2,4-D). See generally, Yarranton (1992) Curr. Opin. Biotech. 3 :506-511 ; Christophers on et al (1992) Proc. Natl. Acad. Sci USA 89:6314-6318; Yao et al. (1992) Cell 71:63-72; Reznikoff (1992) Mol Microbiol 6:2419-2422; Barkley et al (1980) in The Operon, pp. 177-220; Hu et al (1987) Cell 48:555-566; Brown et al (1987) Cell 49:603-612; Figge et al (1988) Cell 52:713-722; Deuschle et al (1989) Proc. Natl Acad. Sci USA
 25 86:5400-5404; Fuerst et al (1989) Proc. Natl Acad. Sci USA 86:2549-2553; Deuschle et al (1990) Science 248:480-483; Gossen (1993) Ph.D. Thesis, University of Heidelberg; Reines et al (1993) Proc. Natl Acad. Sci USA 90: 1917-1921; Labow et al (1990) Mol Cell Biol 10:3343-3356; Zambretti et al (1992) Proc. Natl Acad. Sci USA 89:3952-3956; Bairn et al (1991) Proc. Natl Acad. Sci USA 88:5072-5076; Wyborski et al (1991) Nucleic Acids Res.
 30 19:4647-4653; Hillenand-Wissman (1989) Topics Mol Struc. Biol 10: 143- 162; Degenkolb et al (1991) Antimicrob. Agents Chemother. 35: 1591-1595; Kleinschmidt et al (1988) Biochemistry 27: 1094-1104; Bonin (1993) Ph.D. Thesis, University of Heidelberg; Gossen et al (1992) Proc. Natl Acad. Sci USA 89:5547- 5551; Oliva et al (1992) Antimicrob. Agents Chemother. 36:913-919; Hlavka et al (1985) Handbook of Experimental Pharmacology, Vol.
 35 78 (Springer-Verlag, Berlin); Gill et al (1988) Nature 334:721-724. Such disclosures are herein incorporated by reference. The above list of selectable marker genes is not meant to be limiting. Any selectable marker gene can be used in the present invention.

The invention further provides an isolated recombinant expression vector comprising the
 40 expression cassette containing a mutated PPO nucleic acid as described above, wherein expression of the vector in a host cell results in increased tolerance to a phenylpyridine herbicide as compared to a wild type variety of the host cell. As used herein, the term

“vector” refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a “plasmid,” which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as “expression vectors.” In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, “plasmid” and “vector” can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses, and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cells and those that direct expression of the nucleotide sequence only in certain host cells or under certain conditions. It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of polypeptide desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce polypeptides or peptides, including fusion polypeptides or peptides, encoded by nucleic acids as described herein (e.g., mutated PPO polypeptides, fusion polypeptides, etc.).

In a preferred embodiment of the present invention, the mutated PPO polypeptides are expressed in plants and plants cells such as unicellular plant cells (such as algae) (See Falciatore et al., 1999, *Marine Biotechnology* 1(3):239-251 and references therein) and plant cells from higher plants (e.g., the spermatophytes, such as crop plants). A mutated PPO polynucleotide may be “introduced” into a plant cell by any means, including transfection, transformation or transduction, electroporation, particle bombardment, agroinfection, biolistics, and the like.

Suitable methods for transforming or transfecting host cells including plant cells can be found in Sambrook et al. (*Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989)

and other laboratory manuals such as Methods in Molecular Biology, 1995, Vol. 44, Agrobacterium protocols, ed: Gartland and Davey, Humana Press, Totowa, New Jersey. As increased tolerance to phenylpyridine herbicides is a general trait wished to be inherited into a wide variety of plants like maize, wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed and canola, manihot, pepper, sunflower and tagetes, solanaceous plants like potato, tobacco, eggplant, and tomato, Vicia species, pea, alfalfa, bushy plants (coffee, cacao, tea), Salix species, trees (oil palm, coconut), perennial grasses, and forage crops, these crop plants are also preferred target plants for a genetic engineering as one further embodiment of the present invention. In a preferred embodiment, the plant is a crop plant. Forage crops include, but are not limited to, Wheatgrass, Canarygrass, Bromegrass, Wildrye Grass, Bluegrass, Orchardgrass, Alfalfa, Salfoin, Birdsfoot Trefoil, Alsike Clover, Red Clover, and Sweet Clover.

In one embodiment of the present invention, transfection of a mutated PPO polynucleotide into a plant is achieved by Agrobacterium mediated gene transfer. One transformation method known to those of skill in the art is the dipping of a flowering plant into an Agrobacteria solution, wherein the Agrobacteria contains the mutated PPO nucleic acid, followed by breeding of the transformed gametes. Agrobacterium mediated plant transformation can be performed using for example the GV3101(pMP90) (Koncz and Schell, 1986, Mol. Gen. Genet. 204:383-396) or LBA4404 (Clontech) Agrobacterium tumefaciens strain. Transformation can be performed by standard transformation and regeneration techniques (Deblaere et al., 1994, Nucl. Acids. Res. 13:4777-4788; Gelvin, Stanton B. and Schilperoort, Robert A, Plant Molecular Biology Manual, 2nd Ed. - Dordrecht : Kluwer Academic Publ., 1995. - in Sect., Ringbuc Zentrale Signatur: BT11-P ISBN 0-7923-2731-4; Glick, Bernard R. and Thompson, John E., Methods in Plant Molecular Biology and Biotechnology, Boca Raton : CRC Press, 1993 360 S., ISBN 0-8493-5164-2). For example, rapeseed can be transformed via cotyledon or hypocotyl transformation (Moloney et al., 1989, Plant Cell Report 8:238-242; De Block et al., 1989, Plant Physiol. 91:694-701). Use of antibiotics for Agrobacterium and plant selection depends on the binary vector and the Agrobacterium strain used for transformation. Rapeseed selection is normally performed using kanamycin as selectable plant marker. Agrobacterium mediated gene transfer to flax can be performed using, for example, a technique described by Mlynarova et al., 1994, Plant Cell Report 13:282-285. Additionally, transformation of soybean can be performed using for example a technique described in European Patent No. 0424 047, U.S. Patent No. 5,322,783, European Patent No. 0397 687, U.S. Patent No. 5,376,543, or U.S. Patent No. 5,169,770. Transformation of maize can be achieved by particle bombardment, polyethylene glycol mediated DNA uptake, or via the silicon carbide fiber technique. (See, for example, Freeling and Walbot "The maize handbook" Springer Verlag: New York (1993) ISBN 3-540-97826-7). A specific example of maize transformation is found in U.S. Patent No. 5,990,387, and a specific example of wheat transformation can be found in PCT Application No. WO 93/07256.

According to the present invention, the introduced mutated PPO polynucleotide may be maintained in the plant cell stably if it is incorporated into a non-chromosomal autonomous replicon or integrated into the plant chromosomes. Alternatively, the introduced mutated PPO polynucleotide may be present on an extra-chromosomal non-replicating vector and
5 be transiently expressed or transiently active. In one embodiment, a homologous recombinant microorganism can be created wherein the mutated PPO polynucleotide is integrated into a chromosome, a vector is prepared which contains at least a portion of an PPO gene into which a deletion, addition, or substitution has been introduced to thereby alter, e.g., functionally disrupt, the endogenous PPO gene and to create a mutated PPO
10 gene. To create a point mutation via homologous recombination, DNA-RNA hybrids can be used in a technique known as chimeraplasty (Cole-Strauss et al., 1999, Nucleic Acids Research 27(5):1323-1330 and Kmiec, 1999, Gene therapy American Scientist 87(3):240-247). Other homologous recombination procedures in Triticum species are also well known in the art and are contemplated for use herein.

15 In the homologous recombination vector, the mutated PPO gene can be flanked at its 5' and 3' ends by an additional nucleic acid molecule of the PPO gene to allow for homologous recombination to occur between the exogenous mutated PPO gene carried by the vector and an endogenous PPO gene, in a microorganism or plant. The additional
20 flanking PPO nucleic acid molecule is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several hundreds of base pairs up to kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see e.g., Thomas, K. R., and Capecchi, M. R., 1987, Cell 51:503 for a description of homologous recombination vectors or Strepp et al., 1998, PNAS, 95(8):4368-4373 for cDNA based
25 recombination in *Physcomitrella patens*). However, since the mutated PPO gene normally differs from the PPO gene at very few amino acids, a flanking sequence is not always necessary. The homologous recombination vector is introduced into a microorganism or plant cell (e.g., via polyethylene glycol mediated DNA), and cells in which the introduced mutated PPO gene has homologously recombined with the endogenous PPO gene are
30 selected using art-known techniques.

In another embodiment, recombinant microorganisms can be produced that contain selected systems that allow for regulated expression of the introduced gene. For example, inclusion of a mutated PPO gene on a vector placing it under control of the lac operon
35 permits expression of the mutated PPO gene only in the presence of IPTG. Such regulatory systems are well known in the art.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host
40 cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but they also apply to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation

or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein. A host cell can be any prokaryotic or eukaryotic cell. For example, a mutated PPO polynucleotide can be expressed in bacterial cells such as *C. glutamicum*, insect cells, fungal cells, or mammalian
5 cells (such as Chinese hamster ovary cells (CHO) or COS cells), algae, ciliates, plant cells, fungi or other microorganisms like *C. glutamicum*. Other suitable host cells are known to those skilled in the art.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be
10 used to produce (i.e., express) a mutated PPO polynucleotide. Accordingly, the invention further provides methods for producing mutated PPO polypeptides using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a mutated PPO polypeptide has been introduced, or into which genome has been introduced a gene encoding a wild-type or
15 mutated PPO polypeptide) in a suitable medium until mutated PPO polypeptide is produced. In another embodiment, the method further comprises isolating mutated PPO polypeptides from the medium or the host cell. Another aspect of the invention pertains to isolated mutated PPO polypeptides, and biologically active portions thereof. An "isolated" or "purified" polypeptide or biologically active portion thereof is free of some of the cellular
20 material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of mutated PPO polypeptide in which the polypeptide is separated from some of the cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular
25 material" includes preparations of a mutated PPO polypeptide having less than about 30% (by dry weight) of non-mutated PPO material (also referred to herein as a "contaminating polypeptide"), more preferably less than about 20% of non-mutated PPO material, still more preferably less than about 10% of non-mutated PPO material, and most preferably less than about 5% non-mutated PPO material.

30 When the mutated PPO polypeptide, or biologically active portion thereof, is recombinantly produced, it is also preferably substantially free of culture medium, i.e., culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the polypeptide preparation. The language
35 "substantially free of chemical precursors or other chemicals" includes preparations of mutated PPO polypeptide in which the polypeptide is separated from chemical precursors or other chemicals that are involved in the synthesis of the polypeptide. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of a mutated PPO polypeptide having less than about 30% (by dry weight) of
40 chemical precursors or non-mutated PPO chemicals, more preferably less than about 20% chemical precursors or non-mutated PPO chemicals, still more preferably less than about 10% chemical precursors or non-mutated PPO chemicals, and most preferably less than

about 5% chemical precursors or non-mutated PPO chemicals. In preferred embodiments, isolated polypeptides, or biologically active portions thereof, lack contaminating polypeptides from the same organism from which the mutated PPO polypeptide is derived. Typically, such polypeptides are produced by recombinant expression of, for example, a
5 mutated PPO polypeptide in plants other than, or in microorganisms such as *C. glutamicum*, ciliates, algae, or fungi.

In other aspects, a method for treating a plant of the present invention is provided.

10 In some embodiments, the method comprises contacting the plant with an agronomically acceptable composition.

In another aspect, the present invention provides a method for preparing a descendent seed. The method comprises planting a seed of or capable of producing a plant of the
15 present invention. In one embodiment, the method further comprises growing a descendent plant from the seed; and harvesting a descendant seed from the descendent plant. In other embodiments, the method further comprises applying a phenylpyridine herbicides herbicidal composition to the descendent plant.

20 In another embodiment, the invention refers to harvestable parts of the transgenic plant according to the present invention. Preferably, the harvestable parts comprise the PPO nucleic acid or PPO protein of the present invention. The harvestable parts may be seeds, roots, leaves and/or flowers comprising the PPO nucleic acid or PPO protein or parts thereof. Preferred parts of soy plants are soy beans comprising the PPO nucleic acid or
25 PPO protein.

In another embodiment, the invention refers to products derived from a plant according to the present invention, parts thereof or harvestable parts thereof. A preferred plant product is fodder, seed meal, oil, or seed-treatment-coated seeds. Preferably, the meal and/or oil
30 comprises the mutated PPO nucleic acids or PPO proteins of the present invention.

In another embodiment, the invention refers to a method for the production of a product, which method comprises

- 35 a) growing the plants of the invention or obtainable by the methods of invention and
b) producing said product from or by the plants of the invention and/or parts, e.g. seeds, of these plants.

In a further embodiment the method comprises the steps

- 40 a) growing the plants of the invention,
b) removing the harvestable parts as defined above from the plants and
c) producing said product from or by the harvestable parts of the invention.

DEMANDE OU BREVET VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

CECI EST LE TOME 1 DE 2
CONTENANT LES PAGES 1 À 264

NOTE : Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE THAN ONE VOLUME

THIS IS VOLUME 1 OF 2
CONTAINING PAGES 1 TO 264

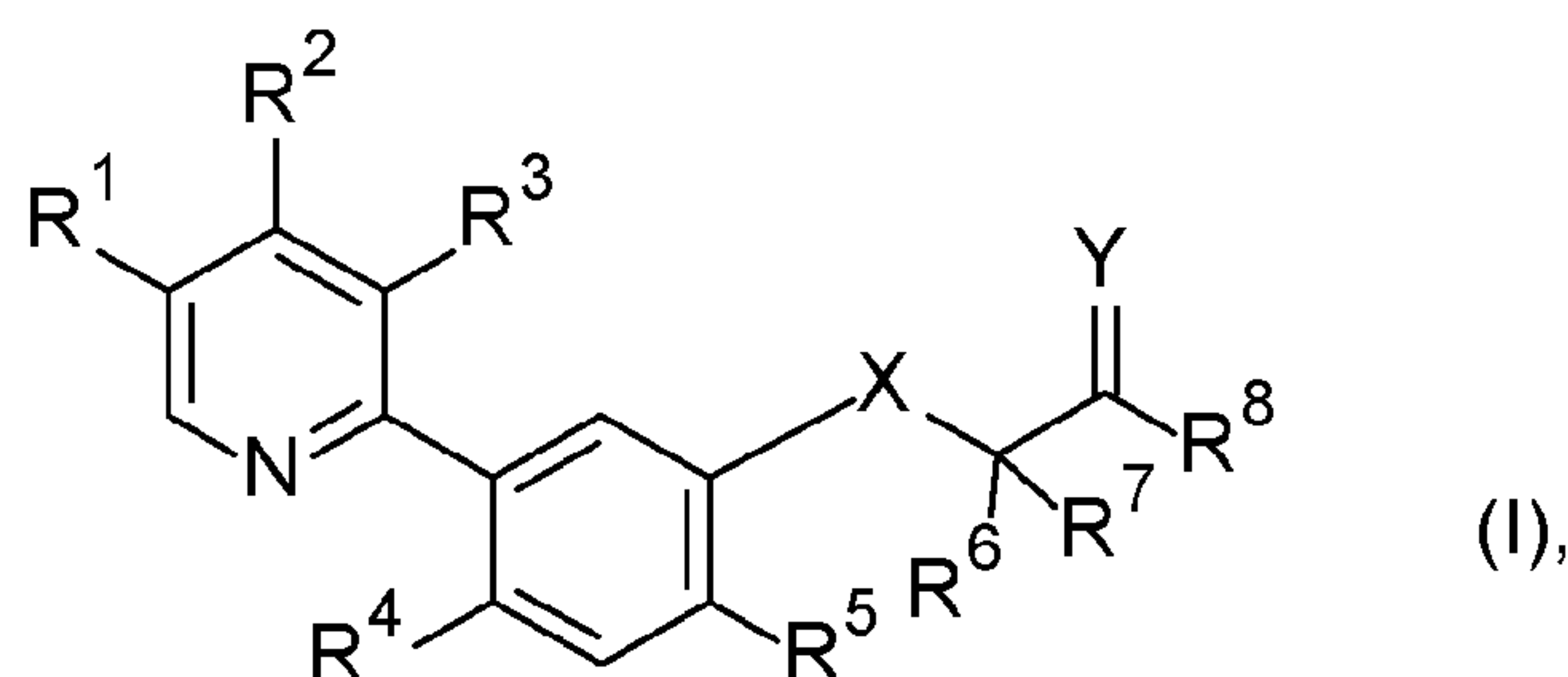
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Claims:

1. A method for controlling undesired vegetation at a plant cultivation site, the method comprising the steps of:
- 5 a) providing, at said site, a plant that comprises at least one nucleic acid comprising a nucleotide sequence encoding a protoporphyrinogen oxidase (PPO) polypeptide which is resistant or tolerant to a "PPO inhibiting herbicide";
- b) applying to said site an effective amount of said herbicide,
- wherein the PPO inhibiting herbicide is a phenylpyridine of formula (I)



wherein the variables have the following meanings:

- 15 R¹ halogen, C₁-C₄-haloalkyl or SO₂CH₃;
 R² H, CH₃ or NH₂;
 R³ halogen;
 R⁴ H or halogen;
 R⁵ halogen or CN;
 20 R⁶ H or CH₃;
 R⁷ C₁-C₆-alkoxy, C₁-C₆-haloalkoxy, C₃-C₆-alkenyloxy, C₃-C₆-alkynyloxy;
 R⁸ OR⁹, SR⁹, NR¹⁰R¹¹, NR⁹S(O)R¹⁰, NR⁹S(O)₂R¹⁰, NR⁹S(O)NR¹⁰R¹¹, or
 NR⁹S(O)₂NR¹⁰R¹¹,
 wherein
 25 R⁹ is hydrogen, C₁-C₆-alkyl, C₃-C₆-alkenyl, C₃-C₆-alkynyl, C₁-C₆-haloalkyl, C₃-C₆-haloalkenyl, C₃-C₆-haloalkynyl, C₁-C₆-cyanoalkyl, C₁-C₆-alkoxy-C₁-C₆-alkyl, C₁-C₆-alkoxy-C₁-C₆-alkoxy-C₁-C₆-alkyl, di(C₁-C₆-alkoxy)C₁-C₆-alkyl, C₁-C₆-haloalkoxy-C₁-C₆-alkyl, C₃-C₆-alkenyloxy-C₁-C₆-alkyl, C₃-C₆-haloalkenyloxy-C₁-C₆-alkyl, C₃-C₆-alkenyloxy-C₁-C₆-alkoxy-C₁-C₆-alkyl, C₁-C₆-alkylthio-C₁-C₆-alkyl, C₁-C₆-alkylsulfinyl-C₁-C₆-alkyl, C₁-C₆-alkylsulfonyl-C₁-C₆-alkyl, C₁-C₆-alkylcarbonyl-C₁-C₆-alkyl, C₁-C₆-alkoxycarbonyl-C₁-C₆-alkyl, C₁-C₆-haloalkoxycarbonyl-C₁-C₆-alkyl, C₃-C₆-alkenyloxycarbonyl-C₁-C₆-alkyl, amino, (C₁-C₆-alkyl)amino, di(C₁-C₆-alkyl)amino, (C₁-C₆-alkylcarbonyl)amino, amino-C₁-C₆-alkyl, (C₁-C₆-alkyl)amino-C₁-C₆-alkyl, di(C₁-C₆-alkyl)amino-C₁-C₆-alkyl, aminocarbonyl-C₁-C₆-alkyl, (C₁-C₆-alkyl)aminocarbonyl-C₁-C₆-alkyl, di(C₁-C₆-alkyl)aminocarbonyl-C₁-C₆-alkyl,

-N=CR¹²R¹³, wherein R¹² and R¹³ independently of one another are H, C₁-C₄-alkyl or phenyl;

C₃-C₆-cycloalkyl, C₃-C₆-cycloalkyl-C₁-C₆-alkyl, C₃-C₆-heterocyclyl, C₃-C₆-heterocyclyl-C₁-C₆-alkyl, phenyl, phenyl-C₁-C₄-alkyl or a 5- or 6 membered heteroaryl,

wherein each phenyl or heteroaryl ring can be substituted by one to four substituents selected from R¹⁴ or a 3- to 7-membered carbocyclus,

which carbocyclus optionally has in addition to carbon atoms one or two ring members selected from the group consisting of -N(R¹²)-, -N=N-, -C(=O)-, -O- and -S-, and

which carbocyclus is optionally substituted with one to four substituents selected from R¹⁴;

wherein R¹⁴ is halogen, NO₂, CN, C₁-C₄-alkyl, C₁-C₄-haloalkyl, C₁-C₄-alkoxy or C₁-C₄-alkoxycarbonyl;

R¹⁰, R¹¹ independently of one another are R⁹, or together form a 3- to 7-membered carbocyclus,

which carbocyclus optionally has in addition to carbon atoms one or two ring members selected from the group consisting of -N(R¹²)-, -N=N-, -C(=O)-, -O- and -S-, and

which carbocyclus is optionally substituted with one to four substituents selected from R¹⁴;

X O or S; and

Y O or S;

including their agriculturally acceptable salts, and wherein the effective amount of said herbicide does not kill or inhibit the growth of the herbicide-tolerant plant of a).

2. The method according to claim 1, wherein the herbicide resistant or tolerant PPO polypeptide comprises one or more of the following motifs 1, 2, and/or 3:

a. Motif 1: SQ[N/K/H]KRYI, wherein the Arg at position 5 within said motif is substituted by any other amino acid;

b. Motif 2: TLGTLFSS, wherein the Leu at position 2 within said motif is substituted by any other amino acid;

c. Motif 3: [F/Y]TTF[V/I]GG, wherein the Phe at position 4 within said motif is substituted by any other amino acid.

3. The method according to claim 1, wherein the herbicide resistant or tolerant PPO polypeptide comprises a variant of the amino acid sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 577, 579, 581,

583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, or 627, which variant comprises one or more of the following substitutions:

- a. the amino acid corresponding to Arg128 of SEQ ID NO: 1 is substituted by any other amino acid.
- b. the amino acid corresponding to Leu397 of SEQ ID NO: 1 is substituted by any other amino acid.
- c. the amino acid corresponding to Phe420 of SEQ ID NO: 1 is substituted by any other amino acid.

4. The method according to claim 1, wherein the herbicide resistant or tolerant PPO polypeptide comprises the amino acid sequence of SEQ ID NO: 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, or a variant thereof.

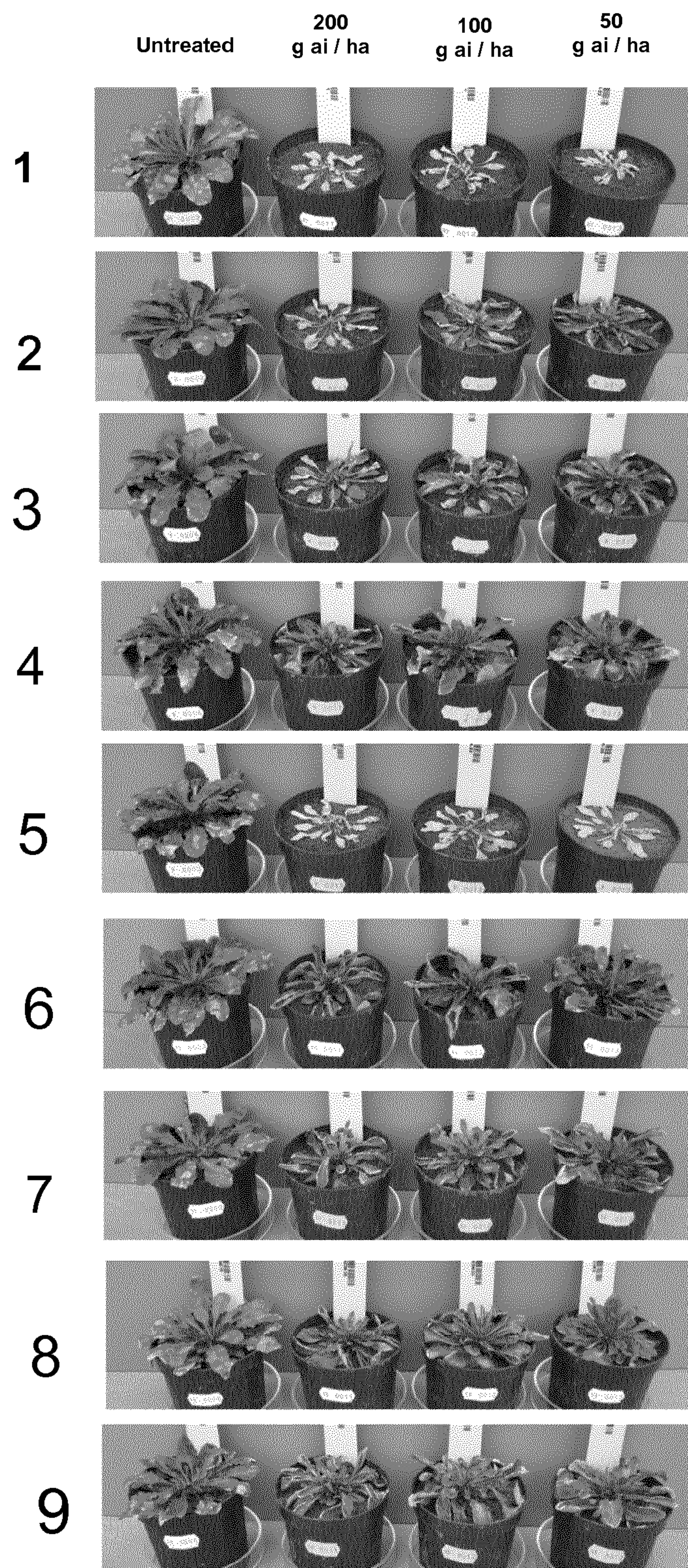
5. The method according to claim 1, wherein the herbicide resistant or tolerant PPO polypeptide comprises the amino acid sequence of SEQ ID NO: 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, or 262.

6. The method according to claims any of claims 1 to 5, wherein the plant comprises at least one additional heterologous nucleic acid comprising a nucleotide sequence encoding a herbicide tolerance enzyme.

7. The method according to any of claims 1 to 6 wherein the phenylpyridine of formula (I) is applied in conjunction with one or more additional herbicides.

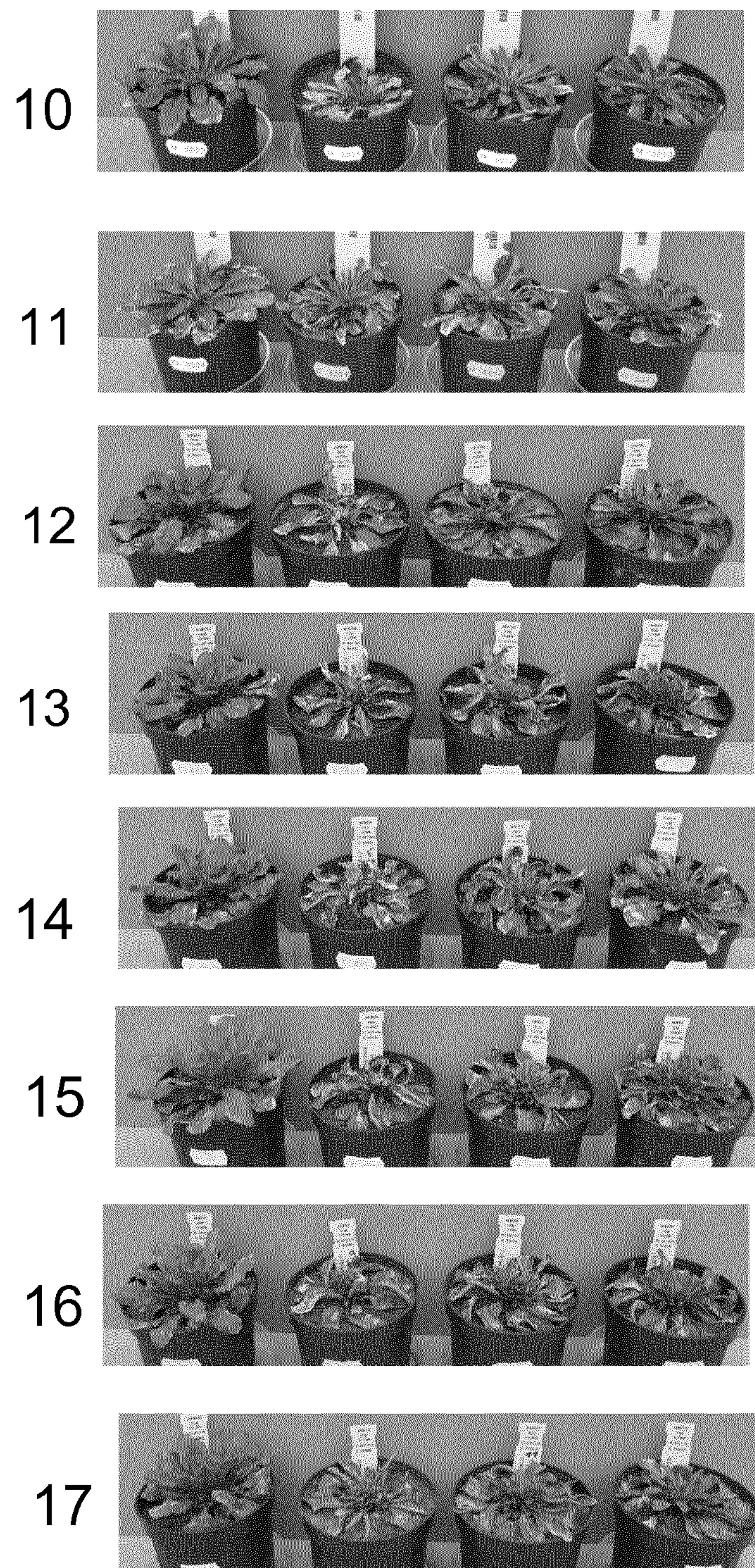
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Figure 1A



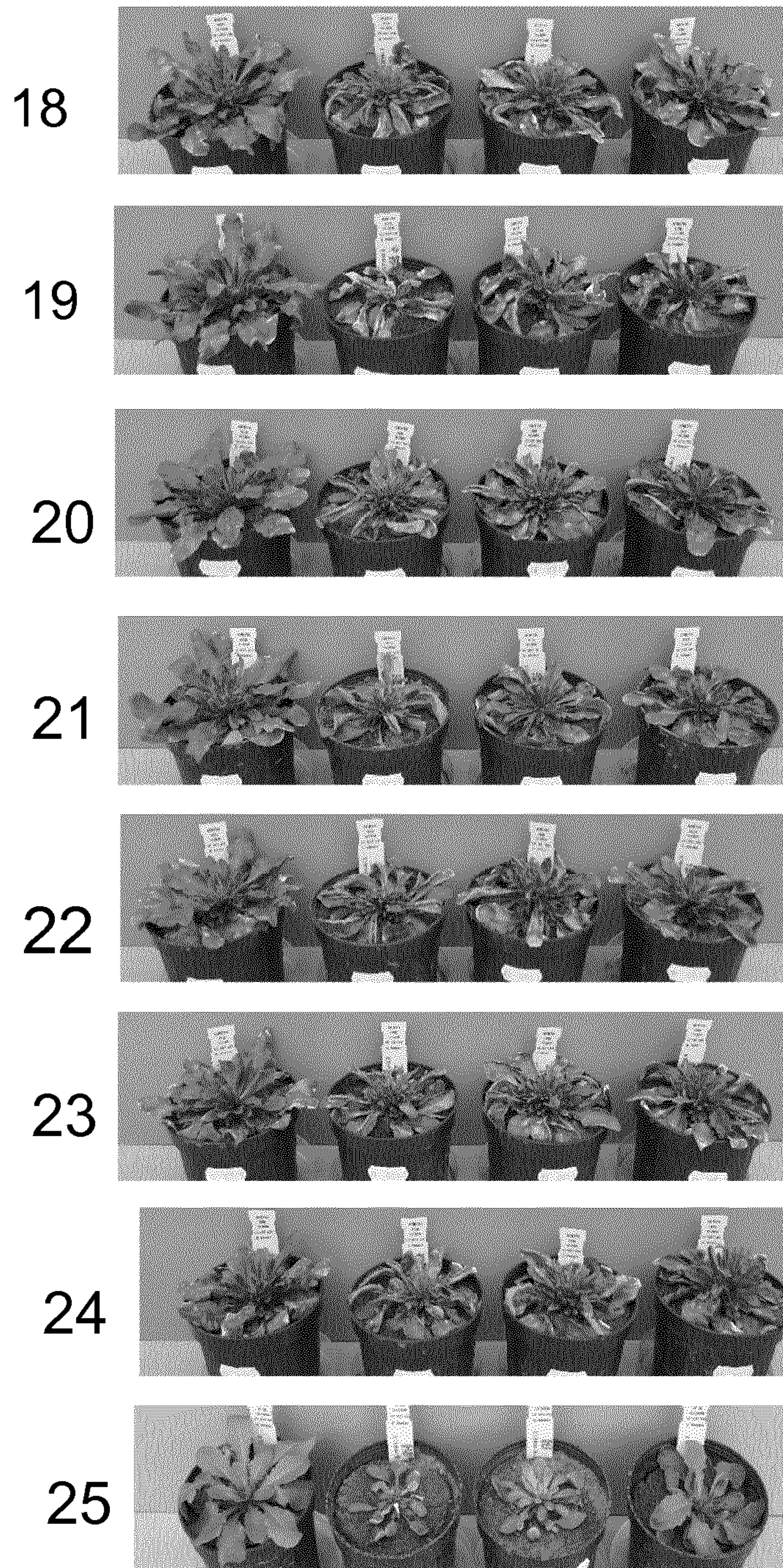
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Figure 1B



3/8

Figure 1 C



4/8

Figure 1 D

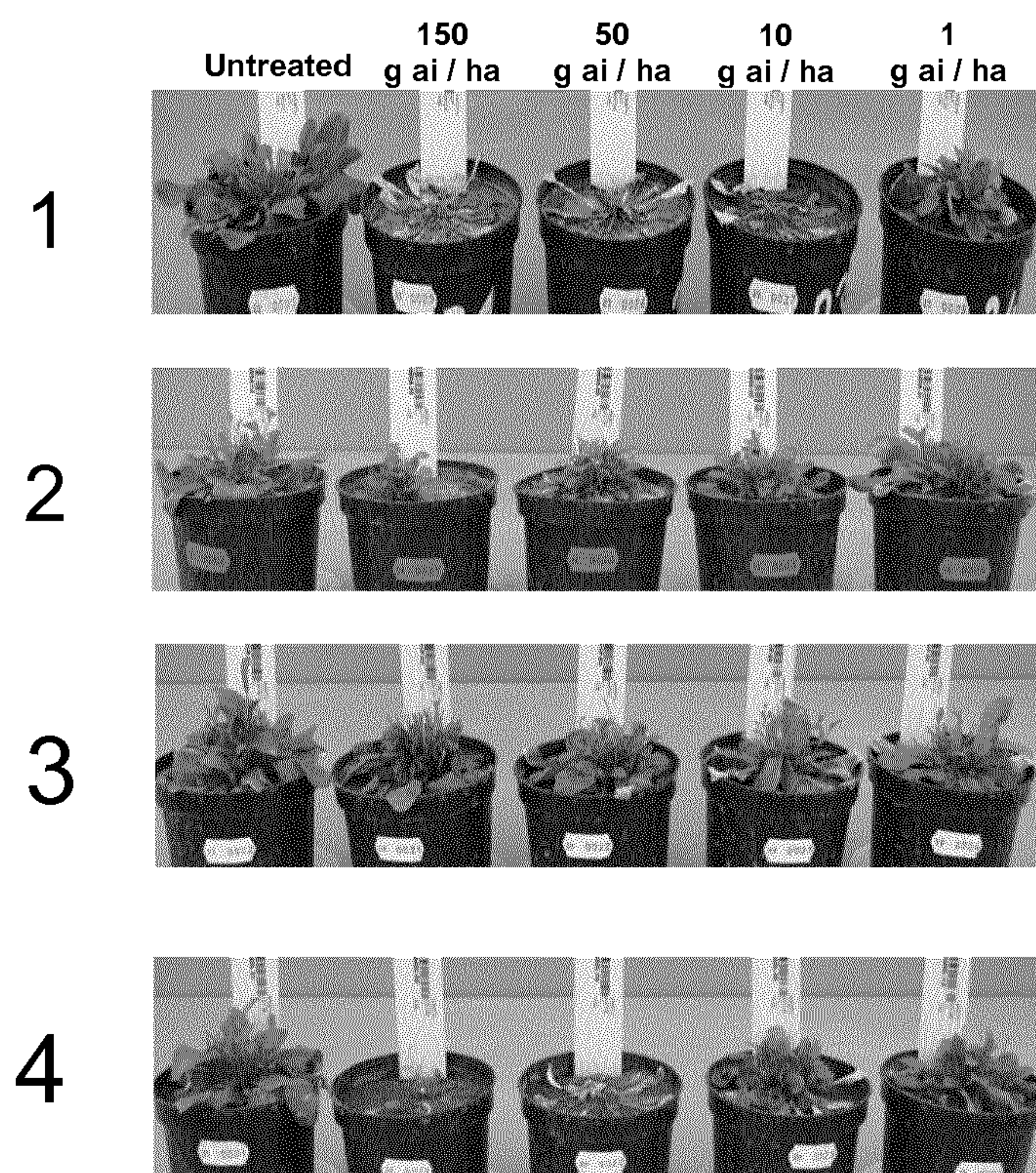


Figure 2A

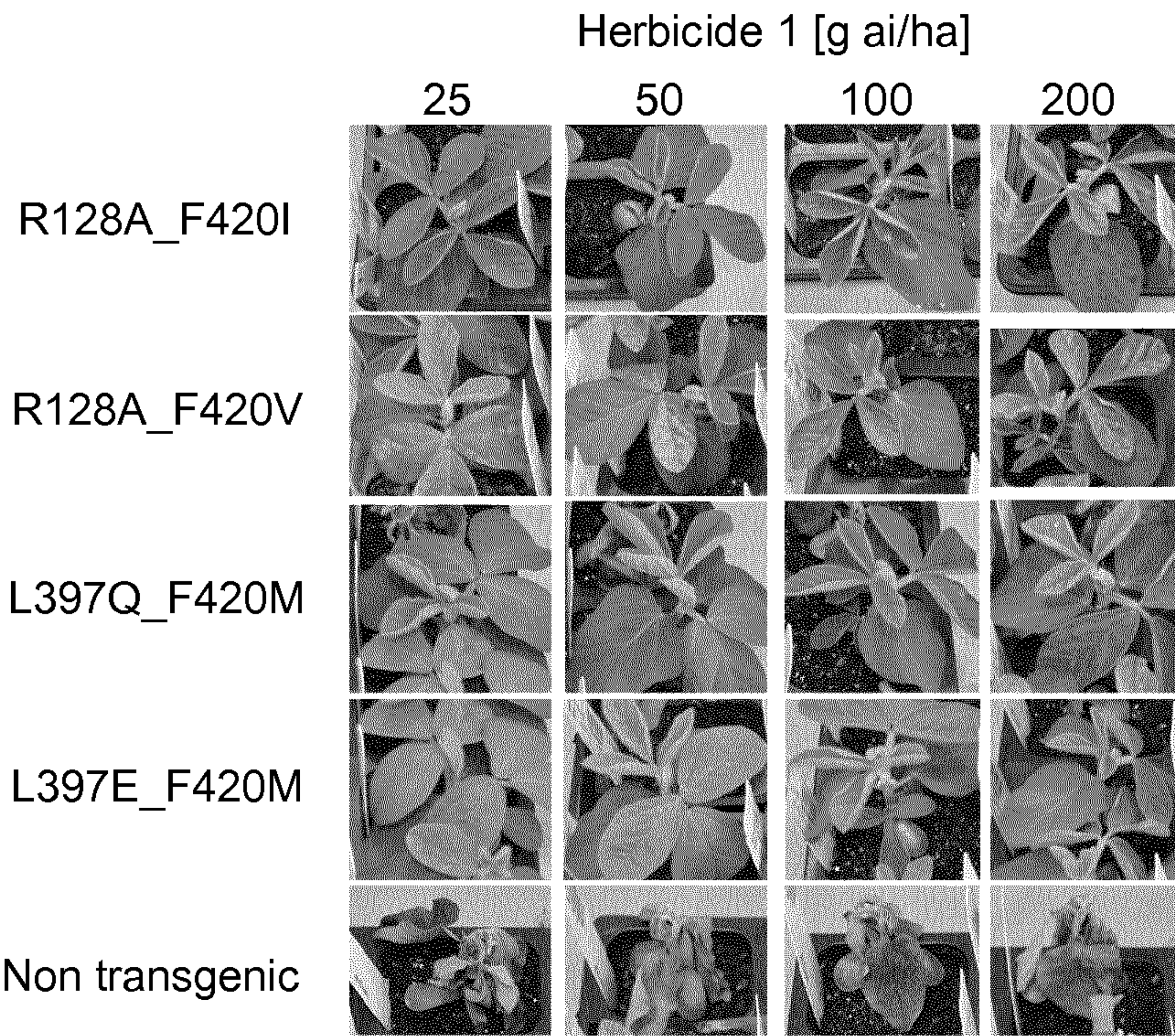


Figure 2 B

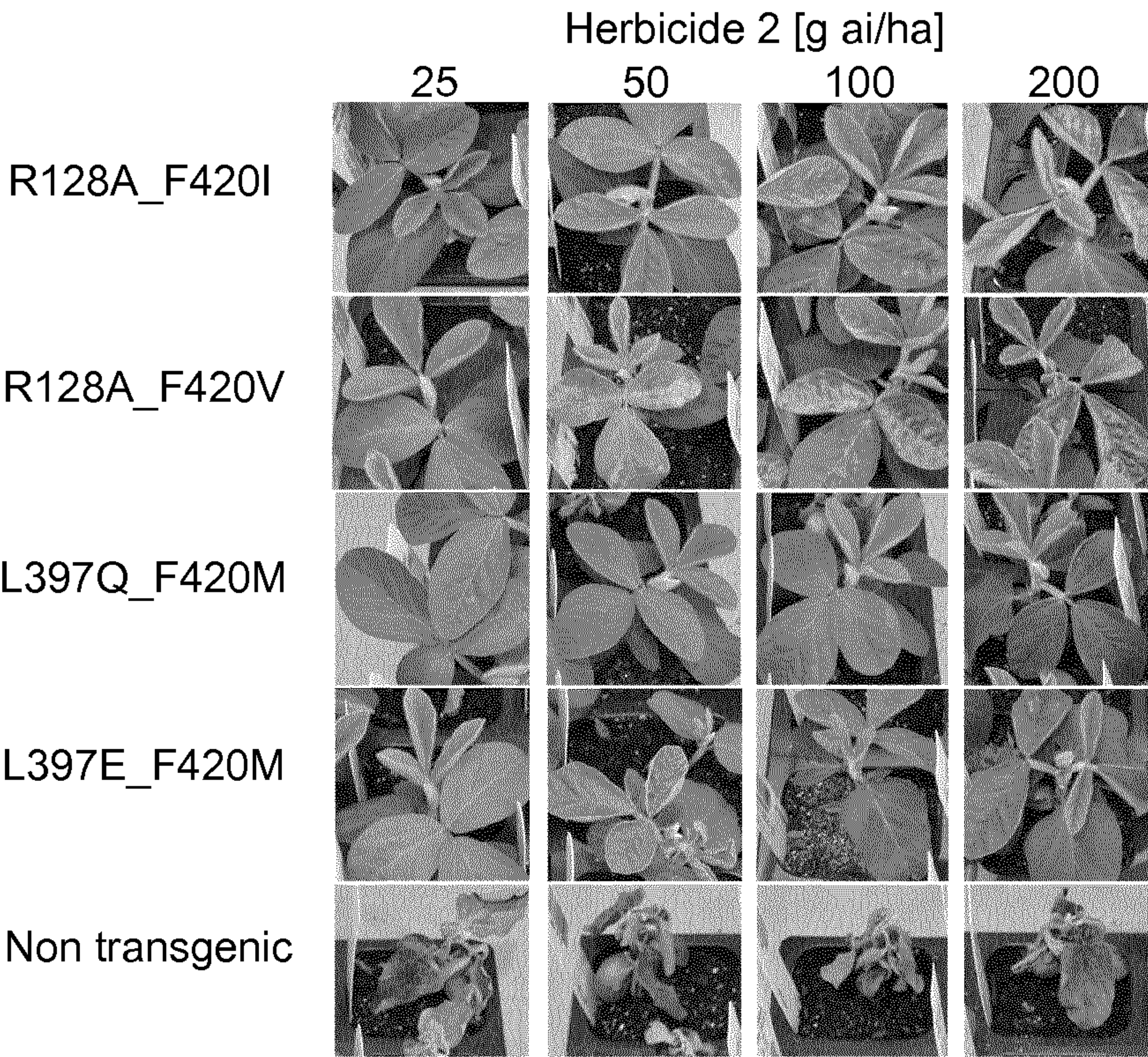


Figure 2 C

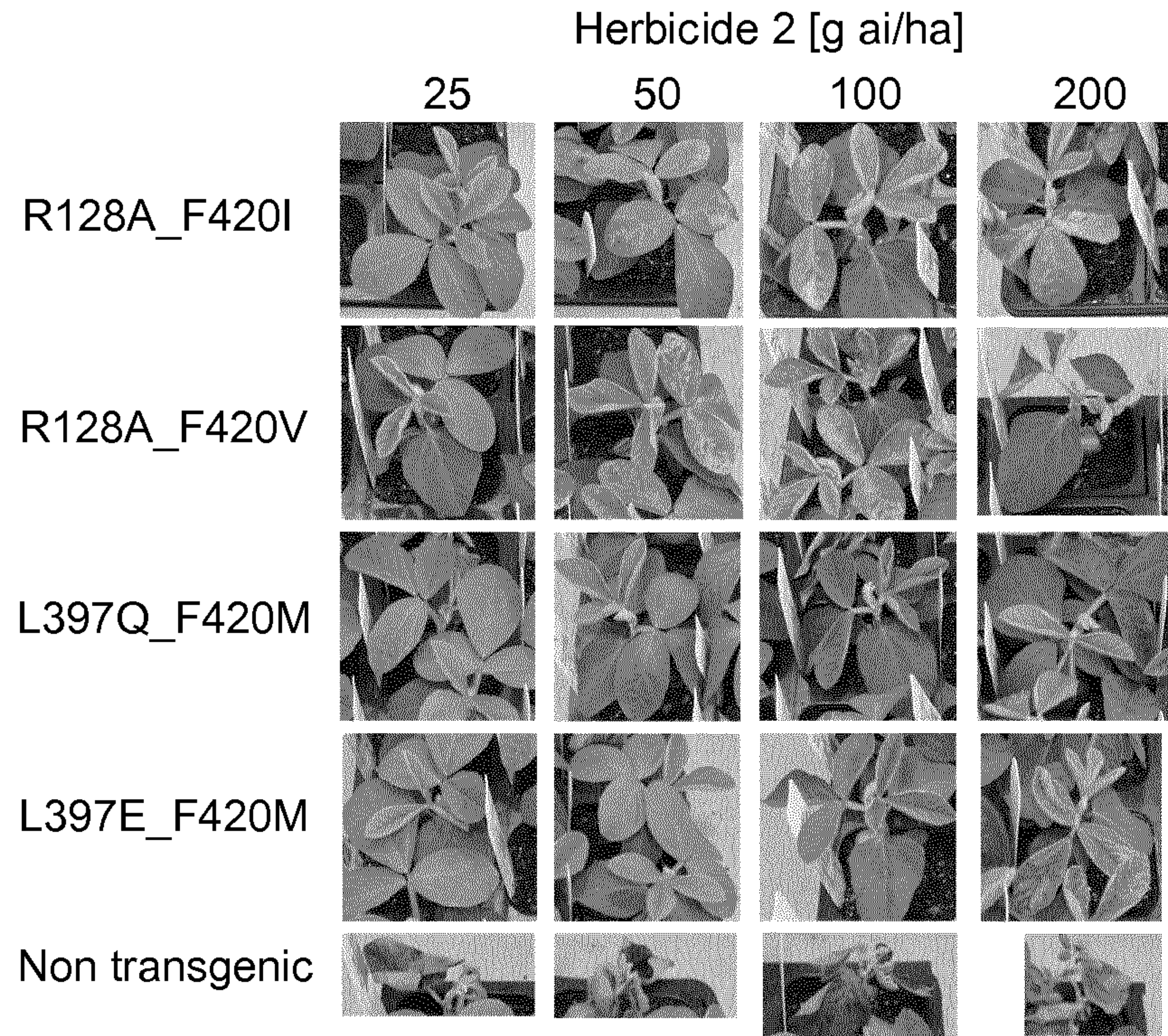


Figure 2 D

