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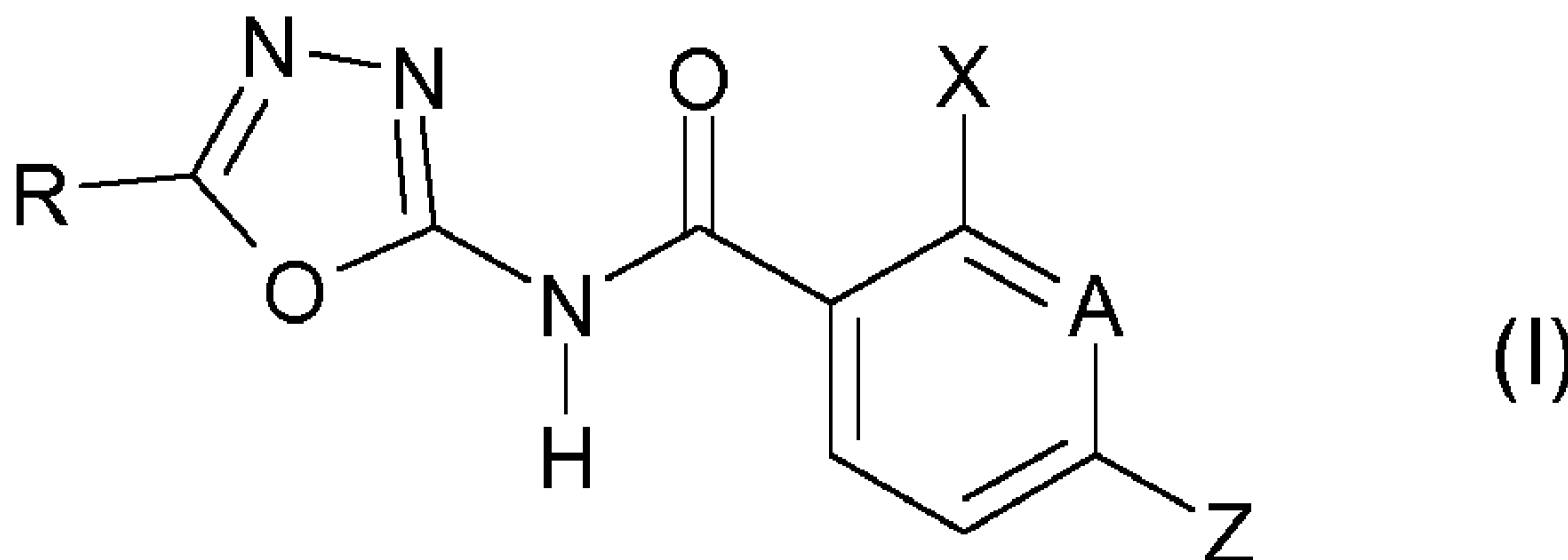
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(54) **Titre : UTILISATION DE N-(1,3,4-OXADIAZOL-2-YL)ARYLCARBOXAMIDES OU DE LEURS SELS POUR LUTTER CONTRE LES PLANTES INDESIRABLES DANS DES ZONES DE CULTURE DE PLANTES TRANSGENIQUES TOLERANTES AUX HERBICIDES INHIBITEURS DE LA HPPD**

(54) **Title: USE OF N-(1,3,4-OXADIAZOL-2-YL)ARYLCARBOXAMIDES OR THEIR SALTS FOR CONTROLLING UNWANTED PLANTS IN AREAS OF TRANSGENIC CROP PLANTS BEING TOLERANT TO HPPD INHIBITOR HERBICIDES**



(57) **Abrégé/Abstract:**

Use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides of formula (I) or salts thereof with R, X, A, and Z having the meaning as defined in the description, for controlling unwanted plants in areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides by



(57) Abrégé(suite)/Abstract(continued):

containing one or more chimeric gene(s) comprising (I) a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, (b) Pseudomonas, (c) Synechococcoideae, (d) Blepharismidae, (e) Rhodococcus, (f) Picrophilaceae, (g) Kordia, or (II) one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably from Pseudomonas, or (III) one or more DNA sequences encoding mutated maize (Zea mays) or soybean (Glycine max) HPPD each being mutated as described in WO 2012/021785.

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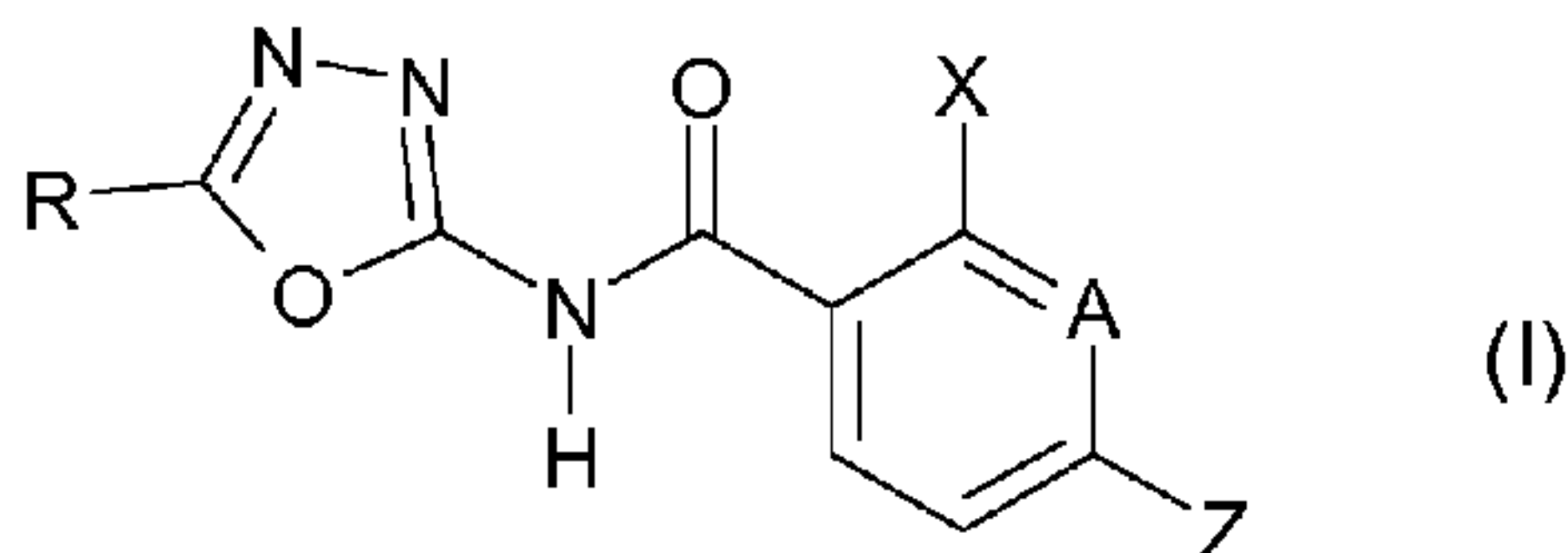
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(54) Title: USE OF N-(1,3,4-OXADIAZOL-2-YL)ARYLCARBOXAMIDES OR THEIR SALTS FOR CONTROLLING UNWANTED PLANTS IN AREAS OF TRANSGENIC CROP PLANTS BEING TOLERANT TO HPPD INHIBITOR HERBICIDES



(57) Abstract: Use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides of formula (I) or salts thereof with R, X, A, and Z having the meaning as defined in the description, for controlling unwanted plants in areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides by containing one or more chimeric gene(s) comprising (I) a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, (b) Pseudomonas, (c) Synechococcoideae, (d) Blepharismidae, (e) Rhodococcus, (f) Picrophilaceae, (g) Kordia, or (II) one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably from Pseudomonas, or (III) one or more DNA sequences encoding mutated maize (Zea mays) or soybean (Glycine max) HPPD each being mutated as described in WO 2012/021785.



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Use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides or their salts for controlling unwanted
5 plants in areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides

Description

The invention relates to the use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides or their salts
10 for controlling unwanted plants in areas of transgenic crop plants being tolerant to HPPD
inhibitor herbicides.

WO2012/126932 discloses several new N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides and
their use as HPPD inhibitor herbicides for weed control.

15 However, the herbicidal activity of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides might cause
damages on several crop plants which limit their use in such crop growing areas as
herbicides for weed control.

20 HPPD inhibitor herbicides can be used against grass and/or broad leaf weeds in crop
plants that display metabolic tolerance, such as maize (*Zea mays*) in which they are
rapidly degraded (Schulz et al., (1993). FEBS letters, 318, 162-166; Mitchell et al., (2001)
Pest Management Science, Vol 57, 120-128; Garcia et al., (2000) Biochem., 39, 7501-
7507; Pallett et al., (2001) Pest Management Science, Vol 57, 133-142). In order to extend
25 the scope of these HPPD inhibitor herbicides, several efforts have been developed in
order to confer to plants, particularly plants without or with an underperforming metabolic
tolerance, a tolerance level acceptable under agronomic field conditions.

Meanwhile transgenic plants have been engineered by by-passing HPPD-mediated
30 production of homogentisate (US 6,812,010), overexpressing the sensitive enzyme so as
to produce quantities of the target enzyme in the plant which are sufficient in relation to the
herbicide has been performed (WO96/38567).

Alternatively, transgenic plants have been generated expressing HPPD proteins that have
35 been mutated at various positions in order to obtain a target enzyme which, while retaining

its properties of catalysing the transformation of HPP into homogentisate, is less sensitive to HPPD inhibitor herbicides than is the native HPPD before mutation (for example see at EP496630, WO 99/24585).

- 5 More recently, the introduction of a *Pseudomonas* HPPD gene into the plastid genome of tobacco and soybean has shown to be more effective than nuclear transformation, conferring even tolerance to post-emergence application of at least one HPPD inhibitor (Dufourmantel et al., 2007, Plant Biotechnol J.5(1):118-33).
- 10 In WO 2009/144079, a nucleic acid sequence encoding a mutated hydroxyphenylpyruvate dioxygenase (HPPD) at position 336 of the *Pseudomonas fluorescens* HPPD protein and its use for obtaining plants which are tolerant to HPPD inhibitor herbicides is disclosed. Further mutants of the *Pseudomonas fluorescens* HPPD protein comprising mutations at various sites and their ability to confer resistance to certain HPPD inhibitor herbicides are
- 15 described in the PCT application filed (on September 13, 2013) under the PCT application number PCT/US2013/59598 and claiming priorities of US61/701,037 (filed on September 14, 2012), US 61/766,057 (filed on February 18, 2013), and US 61/790,404 (filed in March 15, 2013).
- Some of these mutants, i.e. mutants of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed herein under SEQ ID No:6 in PCT/US2013/59598), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID
- 25 No:8 in PCT/US2013/59598), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598) are hereby incorporated by reference concerning the production of the respective
- 30 transgenic plants conferring tolerance to HPPD inhibitor herbicides under its abbreviations PfHPPDEvo33, PfHPPDEvo40, and PfHPPDEvo41, respectively.

In the before, the amino acid named first characterizes the amino acid being present in the wild-type *Pseudomonas fluorescens* HPPD protein and the character given in the

brackets identifies the respective amino acid in the 3 letter code, whereas the character given in front of the brackets identifies the respective amino acid in the 1 letter code.

In WO 04/024928, the inventors have sought to increase the prenylquinone biosynthesis (e.g., synthesis of plastoquinones, tocopherols) in the cells of plants by increasing the flux of the HPP precursor into the cells of these plants. This has been done by connecting the synthesis of said precursor to the "shikimate" pathway by overexpression of the prephenate-dehydrogenase (PDH). They have also noted that the transformation of plants with a gene encoding a PDH enzyme makes it possible to increase the tolerance of said plants to HPPD inhibitors.

In WO 2002/046387, a gene obtained from *Avena sativa* encoding an HPPD was described to generate plants overexpressing such gene and thereby causing tolerance to various HPPD-inhibitor herbicides.

In WO 2008/150473, the combination of two distinct tolerance mechanisms – a modified *Avena sativa* gene coding for a mutant HPPD enzyme and a CYP450 Maize monooxygenase (nsf1 gene) – was exemplified in order to obtain an improved tolerance to HPPD inhibitor herbicides, but no data have been disclosed demonstrating the synergistic effects based on the combination of both proteins.

In WO 2010/085705, several mutants of the *Avena sativa* HPPD were described as well as plants comprising genes encoding such mutated HPPD and thereby causing an increased tolerance to various HPPD-inhibitor herbicides compared to non-mutated HPPD.

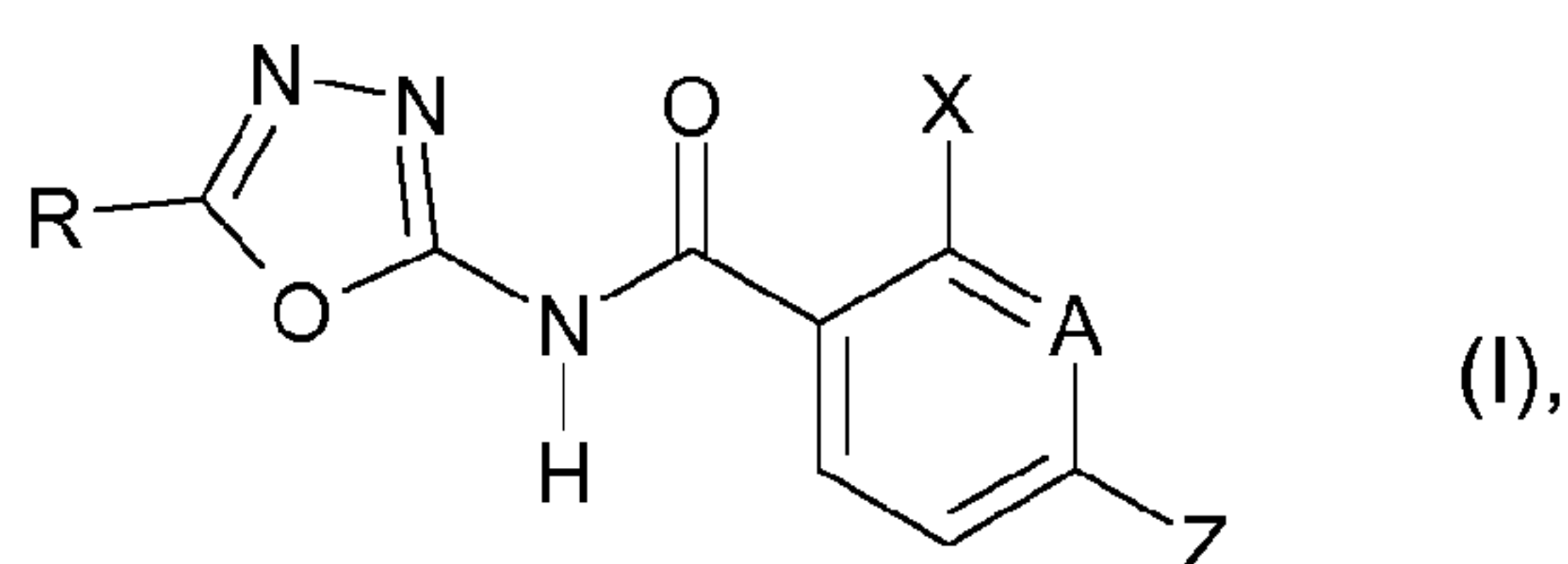
In WO 2012/021785, several mutants along HPPD proteins of various organisms, preferably HPPD obtained from maize were described. Data were obtained from such mutated HPPD enzymes in vitro as well as from plants comprising genes encoding such mutated HPPD and thereby causing an increased tolerance to various HPPD-inhibitor herbicides compared to non-mutated HPPD.

Recently, several new genes encoding HPPD enzymes from various organisms have been identified and employed for obtaining crop plants that show an agronomically useful level of tolerance concerning the application of various HPPD inhibitor herbicides, like such (i)

obtained from bacteria belonging to the subfamily Synechococcoideae and certain mutants thereof as disclosed in WO2011/076877(PCT/EP2010/070561), (ii) obtained from protists belonging to the family Blepharismidae as disclosed in WO2011/076882 (PCT/EP2010/070567); (iii) obtained from bacteria belonging to the genus Rhodococcus and certain mutants thereof as disclosed in WO2011/076892 (PCT/EP2010/070578); (iv) obtained from Euryarchaeota belonging to the family Picrophilaceae and certain mutants thereof as disclosed in WO2011/076885 (PCT/EP2010/070570); or (v) obtained from bacteria belonging to the genus Kordia and certain mutants thereof disclosed as in WO2011/076889 (PCT/EP2010/070575) and which are hereby incorporated by reference concerning the production of the respective transgenic plants conferring tolerance to HPPD inhibitor herbicides.

It has now been found that N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides or salts thereof can be employed on transgenic crop plants being tolerant to HPPD inhibitor herbicides by containing one or more genes conferring tolerance to HPPD inhibitor herbicides.

Subject matter of the present invention is the use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides of the formula (I) or their salts



in which the substituents are defined as follows:

A is N or CY,

R is hydrogen, (C₁–C₆)-alkyl, R¹O-(C₁–C₆)-alkyl, CH₂R⁶, (C₃–C₇)-cycloalkyl, halo-(C₁–C₆)-alkyl, (C₂–C₆)-alkenyl, halo-(C₂–C₆)-alkenyl, (C₂–C₆)-alkynyl, halo-(C₂–C₆)-alkynyl, OR¹, NHR¹, methoxycarbonyl, ethoxycarbonyl, methoxycarbonylmethyl, ethoxycarbonylmethyl, methylcarbonyl, trifluoromethylcarbonyl, dimethylamino, acetylamino, methylsulfenyl, methylsulfinyl, methylsulfonyl, or heteroaryl,

5

heterocyclyl, benzyl or phenyl each substituted by s radicals from the group of halogen, nitro, cyano, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl, S(O)_n-(C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, halo-(C₁-C₆)-alkoxy, (C₁-C₆)-alkoxy-(C₁-C₄)-alkyl,

- 5 X is nitro, halogen, cyano, formyl, thiocyanato, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, (C₂-C₆)-alkenyl, halo-(C₂-C₆)-alkenyl, (C₂-C₆)-alkynyl, halo-(C₃-C₆)-alkynyl, (C₃-C₆)-cycloalkyl, halo-(C₃-C₆)-cycloalkyl, (C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, halo-(C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, COR¹, COOR¹, OCOOR¹, NR¹COOR¹, C(O)N(R¹)₂, NR¹C(O)N(R¹)₂, OC(O)N(R¹)₂, C(O)NR¹OR¹, OR¹, OCOR¹, OSO₂R², S(O)_nR², SO₂OR¹, SO₂N(R¹)₂, NR¹SO₂R², NR¹COR¹, (C₁-C₆)-alkyl-S(O)_nR², (C₁-C₆)-alkyl-OR¹, (C₁-C₆)-alkyl-OCOR¹, (C₁-C₆)-alkyl-OSO₂R², (C₁-C₆)-alkyl-CO₂R¹, (C₁-C₆)-alkyl-SO₂OR¹, (C₁-C₆)-alkyl-CON(R¹)₂, (C₁-C₆)-alkyl-SO₂N(R¹)₂, (C₁-C₆)-alkyl-NR¹COR¹, (C₁-C₆)-alkyl-NR¹SO₂R², NR¹R², P(O)(OR⁵)₂, CH₂P(O)(OR⁵)₂, (C₁-C₆)-alkylheteroaryl, (C₁-C₆)-alkylheterocyclyl, where the two latter radicals are each substituted by s halogen, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, S(O)_n-(C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, halo-(C₁-C₆)-alkoxy radicals, and where heterocyclyl bears n oxo groups,
- 10
- 15
- 20 Y is hydrogen, nitro, halogen, cyano, thiocyanato, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, (C₂-C₆)-alkenyl, halo-(C₂-C₆)-alkenyl, (C₂-C₆)-alkynyl, halo-(C₂-C₆)-alkynyl, (C₃-C₆)-cycloalkyl, (C₃-C₆)-cycloalkenyl, halo-(C₃-C₆)-cycloalkyl, (C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, halo-(C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, COR¹, COOR¹, OCOOR¹, NR¹COOR¹, C(O)N(R¹)₂, NR¹C(O)N(R¹)₂, OC(O)N(R¹)₂, CO(NOR¹)R¹, NR¹SO₂R², NR¹COR¹, OR¹, OSO₂R², S(O)_nR², SO₂OR¹, SO₂N(R¹)₂, (C₁-C₆)-alkyl-S(O)_nR², (C₁-C₆)-alkyl-OR¹, (C₁-C₆)-alkyl-OCOR¹, (C₁-C₆)-alkyl-OSO₂R², (C₁-C₆)-alkyl-CO₂R¹, (C₁-C₆)-alkyl-CN, (C₁-C₆)-alkyl-SO₂OR¹, (C₁-C₆)-alkyl-CON(R¹)₂, (C₁-C₆)-alkyl-SO₂N(R¹)₂, (C₁-C₆)-alkyl-NR¹COR¹, (C₁-C₆)-alkyl-NR¹SO₂R², N(R¹)₂, P(O)(OR⁵)₂, CH₂P(O)(OR⁵)₂, (C₁-C₆)-alkylphenyl, (C₁-C₆)-alkylheteroaryl, (C₁-C₆)-alkylheterocyclyl, phenyl, heteroaryl or heterocyclyl, where the 6 latter radicals are each substituted by s radicals from the group of halogen, nitro, cyano, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl, S(O)_n-(C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, halo-(C₁-C₆)-alkoxy, (C₁-C₆)-alkoxy-(C₁-C₄)-alkyl and cyanomethyl, and where heterocyclyl bears n oxo groups,
- 25
- 30

- Z is hydrogen, halogen, cyano, thiocyanato, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, halo-(C₁-C₆)-alkyl, (C₂-C₆)-alkenyl, halo-(C₂-C₆)-alkenyl, (C₂-C₆)-alkynyl, halo-(C₂-C₆)-alkynyl, (C₃-C₆)-cycloalkyl, halo-(C₃-C₆)-cycloalkyl, (C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, halo-(C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, COR¹, COOR¹, OCOOR¹, NR¹COOR¹, C(O)N(R¹)₂,
 5 NR¹C(O)N(R¹)₂, OC(O)N(R¹)₂, C(O)NR¹OR¹, OSO₂R², S(O)_nR², SO₂OR¹, SO₂N(R¹)₂, NR¹SO₂R², NR¹COR¹, (C₁-C₆)-alkyl-S(O)_nR², (C₁-C₆)-alkyl-OR¹, (C₁-C₆)-alkyl-OCOR¹, (C₁-C₆)-alkyl-OSO₂R², (C₁-C₆)-alkyl-CO₂R¹, (C₁-C₆)-alkyl-SO₂OR¹, (C₁-C₆)-alkyl-CON(R¹)₂, (C₁-C₆)-alkyl-SO₂N(R¹)₂, (C₁-C₆)-alkyl-NR¹COR¹, (C₁-C₆)-alkyl-NR¹SO₂R², N(R¹)₂, P(O)(OR⁵)₂, heteroaryl, heterocyclyl or phenyl,
 10 where the three latter radicals are each substituted by s radicals from the group of halogen, nitro, cyano, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl, S(O)_n-(C₁-C₆)-alkyl, (C₁-C₆)-alkoxy or halo-(C₁-C₆)-alkoxy, and where heterocyclyl bears n oxo groups,
- 15 R¹ is hydrogen, (C₁-C₆)-alkyl, (C₁-C₆)-haloalkyl, (C₂-C₆)-alkenyl, (C₂-C₆)-haloalkenyl, (C₂-C₆)-alkynyl, (C₂-C₆)-haloalkynyl, (C₃-C₆)-cycloalkyl, (C₃-C₆)-cycloalkenyl, (C₃-C₆)-halocycloalkyl, (C₁-C₆)-alkyl-O-(C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, phenyl, phenyl-(C₁-C₆)-alkyl, heteroaryl, (C₁-C₆)-alkylheteroaryl, heterocyclyl, (C₁-C₆)-alkylheterocyclyl, (C₁-C₆)-alkyl-O-heteroaryl, (C₁-C₆)-alkyl-O-heterocyclyl, (C₁-C₆)-alkyl-NR³-heteroaryl, (C₁-C₆)-alkyl-NR³-heterocyclyl, where the 21 latter radicals
 20 are substituted by s radicals from the group consisting of cyano, halogen, nitro, thiocyanato, OR³, S(O)_nR⁴, N(R³)₂, NR³OR³, COR³, OCOR³, SCOR⁴, NR³COR³, NR³SO₂R⁴, CO₂R³, COSR⁴, CON(R³)₂ and (C₁-C₄)-alkoxy-(C₂-C₆)-alkoxycarbonyl, and where heterocyclyl bears n oxo groups,
- 25 R² is (C₁-C₆)-alkyl, (C₁-C₆)-haloalkyl, (C₂-C₆)-alkenyl, (C₂-C₆)-haloalkenyl, (C₂-C₆)-alkynyl, (C₂-C₆)-haloalkynyl, (C₃-C₆)-cycloalkyl, (C₃-C₆)-cycloalkenyl, (C₃-C₆)-halocycloalkyl, (C₁-C₆)-alkyl-O-(C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, phenyl, phenyl-(C₁-C₆)-alkyl, heteroaryl, (C₁-C₆)-alkylheteroaryl, heterocyclyl, (C₁-C₆)-alkylheterocyclyl, (C₁-C₆)-alkyl-O-heteroaryl, (C₁-C₆)-alkyl-O-heterocyclyl, (C₁-C₆)-alkyl-NR³-heteroaryl, (C₁-C₆)-alkyl-NR³-heterocyclyl, where the 21 latter radicals are
 30 substituted by s radicals from the group consisting of cyano, halogen, nitro, thiocyanato, OR³, S(O)_nR⁴, N(R³)₂, NR³OR³, COR³, OCOR³, SCOR⁴, NR³COR³, NR³SO₂R⁴, CO₂R³, COSR⁴, CON(R³)₂ and (C₁-C₄)-alkoxy-(C₂-C₆)-alkoxycarbonyl,

and where heterocyclyl bears n oxo groups,

R³ is hydrogen, (C₁-C₆)-alkyl, (C₂-C₆)-alkenyl, (C₂-C₆)-alkynyl, (C₃-C₆)-cycloalkyl or (C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl,

5

R⁴ is (C₁-C₆)-alkyl, (C₂-C₆)-alkenyl or (C₂-C₆)-alkynyl,

R⁵ is methyl or ethyl,

10 R⁶ is acetoxy, acetamido, N-methylacetamido, benzoyloxy, benzamido, N-methylbenzamido, methoxycarbonyl, ethoxycarbonyl, benzoyl, methylcarbonyl, piperidinylcarbonyl, morpholinylcarbonyl, trifluoromethylcarbonyl, aminocarbonyl, methylaminocarbonyl, dimethylaminocarbonyl, (C₁-C₆)-alkoxy, (C₃-C₆)-cycloalkyl, or
15 heteroaryl, heterocyclyl or phenyl each substituted by s radicals from the group of methyl, ethyl, methoxy, trifluoromethyl and halogen,

n is 0, 1 or 2; and

s is 0, 1, 2 or 3.

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for controlling unwanted plants in areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides by containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d)
25 *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising

30

a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 ,
 (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA
 sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g)
Kordia, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical
 5 to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or
 more mutated DNA sequences of HPPD encoding genes of the before defined organisms,
 preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079,
 WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885,
 WO2011/076889, WO 2012/021785, according to the latter, comprising more especially
 10 one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea*
mays) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize
 (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598,
 more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i)
 comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp)
 15 replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID
 No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No.
 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser)
 replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named
 PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being
 20 disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P
 (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K
 (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at
 position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in
 PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or
 25 (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more
 specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD
 protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S
 (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356
 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in
 30 PCT/US2013/59598, and being disclosed in present application as the HPPD protein
 sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at
 position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala)
 replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named
 Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and

being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

In the formula (I) and all the formulae which follow, alkyl radicals having more than two carbon atoms may be straight-chain or branched. Alkyl radicals are, for example, methyl, ethyl, n- or isopropyl, n-, iso-, tert- or 2-butyl, pentyls, hexyls such as n-hexyl, isohexyl and 1,3,-dimethylbutyl. Halogen is fluorine, chlorine, bromine or iodine.

Heterocyclyl is a saturated, semi saturated or fully unsaturated cyclic radical containing 3 to 6 ring atoms, of which 1 to 4 are from the group of oxygen, nitrogen and sulfur, and which may additionally be fused by a benzo ring. For example, heterocyclyl is piperidinyl, pyrrolidinyl, tetrahydrofuranyl, dihydrofuranyl and oxetanyl,

Heteroaryl is an aromatic cyclic radical containing 3 to 6 ring atoms, of which 1 to 4 are from the group of oxygen, nitrogen and sulfur, and which may additionally be fused by a

benzo ring. For example, heteroaryl is benzimidazol-2-yl, furanyl, imidazolyl, isoxazolyl, isothiazolyl, oxazolyl, pyrazinyl, pyrimidinyl, pyridazinyl, pyridinyl, benzisoxazolyl, thiazolyl, pyrrolyl, pyrazolyl, thiophenyl, 1,2,3-oxadiazolyl, 1,2,4-oxadiazolyl, 1,2,5-oxadiazolyl, 1,3,4-oxadiazolyl, 1,2,4-triazolyl, 1,2,3-triazolyl, 1,2,5-triazolyl, 1,3,4-triazolyl, 1,2,4-triazolyl, 1,2,4-thiadiazolyl, 1,3,4-thiadiazolyl, 1,2,3-thiadiazolyl, 1,2,5-thiadiazolyl, 2H-1,2,3,4-tetrazolyl, 1H-1,2,3,4-tetrazolyl, 1,2,3,4-oxatriazolyl, 1,2,3,5-oxatriazolyl, 1,2,3,4-thiatrizolyl and 1,2,3,5-thiatrizolyl.

When a group is polysubstituted by radicals, this means that this group is substituted by one or more identical or different radicals from those mentioned.

According to the nature and the bonding of the substituents, the compounds of the general formula (I) may be present as stereoisomers. When, for example, one or more asymmetric carbon atoms are present, enantiomers and diastereomers may occur. Stereoisomers likewise occur when n is 1 (sulfoxides). Stereoisomers can be obtained from the mixtures obtained in the preparation by customary separation methods, for example by chromatographic separation processes. It is equally possible to selectively prepare stereoisomers by using stereo selective reactions using optically active starting materials and/or auxiliaries. The invention also relates to all stereoisomers and mixtures thereof which are encompassed by the general formula (I) but not defined specifically.

Preference is given to the inventive use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides of general formula (I), in which

A is N or CY,

R is hydrogen, (C₁–C₆)-alkyl, (C₃–C₇)-cycloalkyl, halo-(C₁–C₆)-alkyl, (C₃–C₇)-cycloalkylmethyl, methoxycarbonylmethyl, ethoxycarbonylmethyl, acetylmethyl, methoxymethyl, methoxyethyl, benzyl, pyrazin-2-yl, furan-2-yl, tetrahydrofuran-2-yl, morpholine, dimethylamino, or phenyl substituted by s radicals from the group of methyl, methoxy, trifluoromethyl and halogen;

- X is nitro, halogen, cyano, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl, OR¹, S(O)_nR², (C₁-C₆)-alkyl-S(O)_nR², (C₁-C₆)-alkyl-OR¹, (C₁-C₆)-alkyl-CON(R¹)₂, (C₁-C₆)-alkyl-SO₂N(R¹)₂, (C₁-C₆)-alkyl-NR¹COR¹, (C₁-C₆)-alkyl-NR¹SO₂R², (C₁-C₆)-alkylheteroaryl, (C₁-C₆)-alkylheterocyclyl, where the two latter radicals are each substituted by s halogen, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, S(O)_n-(C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, halo-(C₁-C₆)-alkoxy radicals, and where heterocyclyl bears n oxo groups,
- Y hydrogen, nitro, halogen, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-haloalkyl, OR¹, S(O)_nR², SO₂N(R¹)₂, N(R¹)₂, NR¹SO₂R², NR¹COR¹, (C₁-C₆)-alkyl-S(O)_nR², (C₁-C₆)-alkyl-OR¹, (C₁-C₆)-alkyl-CON(R¹)₂, (C₁-C₆)-alkyl-SO₂N(R¹)₂, (C₁-C₆)-alkyl-NR¹COR¹, (C₁-C₆)-alkyl-NR¹SO₂R², (C₁-C₆)-alkylphenyl, (C₁-C₆)-alkylheteroaryl, (C₁-C₆)-alkylheterocyclyl, phenyl, heteroaryl or heterocyclyl, where the 6 latter radicals are each substituted by s radicals from the group of halogen, nitro, cyano, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl, S(O)_n-(C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, halo-(C₁-C₆)-alkoxy, (C₁-C₆)-alkoxy-(C₁-C₄)-alkyl and cyanomethyl, and where heterocyclyl bears n oxo groups,
- Z is halogen, cyano, nitro, methyl, halo-(C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl, S(O)_nR², 1,2,4-triazol-1-yl, pyrazol-1-yl, or Z may also be hydrogen if Y is the S(O)_nR² radical,
- R¹ is hydrogen, (C₁-C₆)-alkyl, (C₂-C₆)-alkenyl, (C₂-C₆)-alkynyl, (C₃-C₆)-cycloalkyl, (C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, (C₁-C₆)-alkyl-O-(C₁-C₆)-alkyl, phenyl, phenyl-(C₁-C₆)-alkyl, heteroaryl, (C₁-C₆)-alkylheteroaryl, heterocyclyl, (C₁-C₆)-alkylheterocyclyl, (C₁-C₆)-alkyl-O-heteroaryl, (C₁-C₆)-alkyl-O-heterocyclyl, (C₁-C₆)-alkyl-NR³-heteroaryl or (C₁-C₆)-alkyl-NR³-heterocyclyl, where the 16 latter radicals are substituted by s radicals from the group consisting of cyano, halogen, nitro, OR³, S(O)_nR⁴, N(R³)₂, NR³OR³, COR³, OCOR³, NR³COR³, NR³SO₂R⁴, CO₂R³, CON(R³)₂ and (C₁-C₄)-alkoxy-(C₂-C₆)-alkoxycarbonyl, and where heterocyclyl bears n oxo groups,
- R² is (C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl or (C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, where these three aforementioned radicals are each substituted by s radicals from the group consisting of halogen and OR³,

R³ is hydrogen or (C₁-C₆)-alkyl,

R⁴ is (C₁-C₆)-alkyl,

5

n is 0, 1 or 2;

s is 0, 1, 2 or 3,

10 for controlling unwanted plants in areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides by containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID

15 No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA

20 sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 ,

25 (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms,

30 preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize

(Zea mays) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present

application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

Particular preference is given to the inventive use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides of general formula (I), in which

- A is N or CY,
- R is hydrogen, (C₁-C₄)-alkyl, cyclopropyl, halo-(C₁-C₄)-alkyl, (C₃-C₆)-cycloalkylmethyl, methoxymethyl, methoxyethyl, benzyl,;
- X is nitro, halogen, cyano, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, cyclopropyl, OR¹, S(O)_nR², (C₁-C₆)-alkyl-S(O)_nR², (C₁-C₆)-alkyl-OR¹, (C₁-C₂)-alkylheteroaryl, (C₁-C₂)-alkylheterocyclyl, where the two latter radicals are each substituted by s halogen, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, S(O)_n-(C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, halo-(C₁-C₆)-alkoxy radicals, and where heterocyclyl bears n oxo groups,
- Y hydrogen, nitro, halogen, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-haloalkyl, OR¹, S(O)_nR², SO₂N(R¹)₂, N(R¹)₂, NR¹SO₂R², NR¹COR¹, (C₁-C₆)-alkyl-S(O)_nR², (C₁-C₆)-alkyl-OR¹, (C₁-C₆)-alkyl-CON(R¹)₂, (C₁-C₆)-alkyl-SO₂N(R¹)₂, (C₁-C₆)-alkyl-NR¹COR¹, (C₁-C₆)-alkyl-NR¹SO₂R², (C₁-C₆)-alkylphenyl, (C₁-C₆)-alkylheteroaryl, (C₁-C₆)-alkylheterocyclyl, phenyl, heteroaryl or heterocyclyl, where the 6 latter radicals are each substituted by s radicals from the group of halogen, nitro, cyano, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl, S(O)_n-(C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, halo-(C₁-

C₆)-alkoxy, (C₁-C₆)-alkoxy-(C₁-C₄)-alkyl and cyanomethyl, and where heterocyclyl bears n oxo groups,

Z is halogen, cyano, nitro, methyl, halo-(C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl, S(O)_nR²,
 5 1,2,4-triazol-1-yl, pyrazol-1-yl,

R¹ is hydrogen, (C₁-C₆)-alkyl, (C₂-C₆)-alkenyl, (C₂-C₆)-alkynyl, (C₃-C₆)-cycloalkyl, (C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, (C₁-C₆)-alkyl-O-(C₁-C₆)-alkyl, phenyl, phenyl-(C₁-C₆)-alkyl, heteroaryl, (C₁-C₆)-alkylheteroaryl, heterocyclyl, (C₁-C₆)-alkylheterocyclyl, (C₁-C₆)-alkyl-O-heteroaryl, (C₁-C₆)-alkyl-O-heterocyclyl, (C₁-C₆)-alkyl-NR³-heteroaryl or
 10 (C₁-C₆)-alkyl-NR³-heterocyclyl, where the 16 latter radicals are substituted by s radicals from the group consisting of cyano, halogen, nitro, OR³, S(O)_nR⁴, N(R³)₂, NR³OR³, COR³, OCOR³, NR³COR³, NR³SO₂R⁴, CO₂R³, CON(R³)₂ and (C₁-C₄)-alkoxy-(C₂-C₆)-alkoxycarbonyl, and where heterocyclyl bears n oxo groups,

R² is (C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl or (C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, where these three aforementioned radicals are each substituted by s radicals from the group consisting of halogen and OR³,

R³ is hydrogen or (C₁-C₆)-alkyl,

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No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e)

5 *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 ,

10 (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079,

15 WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598,

20 more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser)

25 replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at

30 position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S

(Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

In all of the formulae below, the substituents and symbols have the same definition as described under formula (I), unless otherwise defined.

N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides to be used according to the invention can be prepared as described in detail in WO2012/126932 which is hereby incorporated by reference.

- 5 The compounds listed in the Tables 1 to 7, herein below, are very specially preferred used for controlling unwanted plants in areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides by containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) *Avena*, preferably *Avena sativa*, more preferably
- 10 comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d)
- 15 *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising
- 20 a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or
- 25 more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID
- 30

No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being

5 disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or

10 (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in

15 PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and

20 being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named

25 Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being

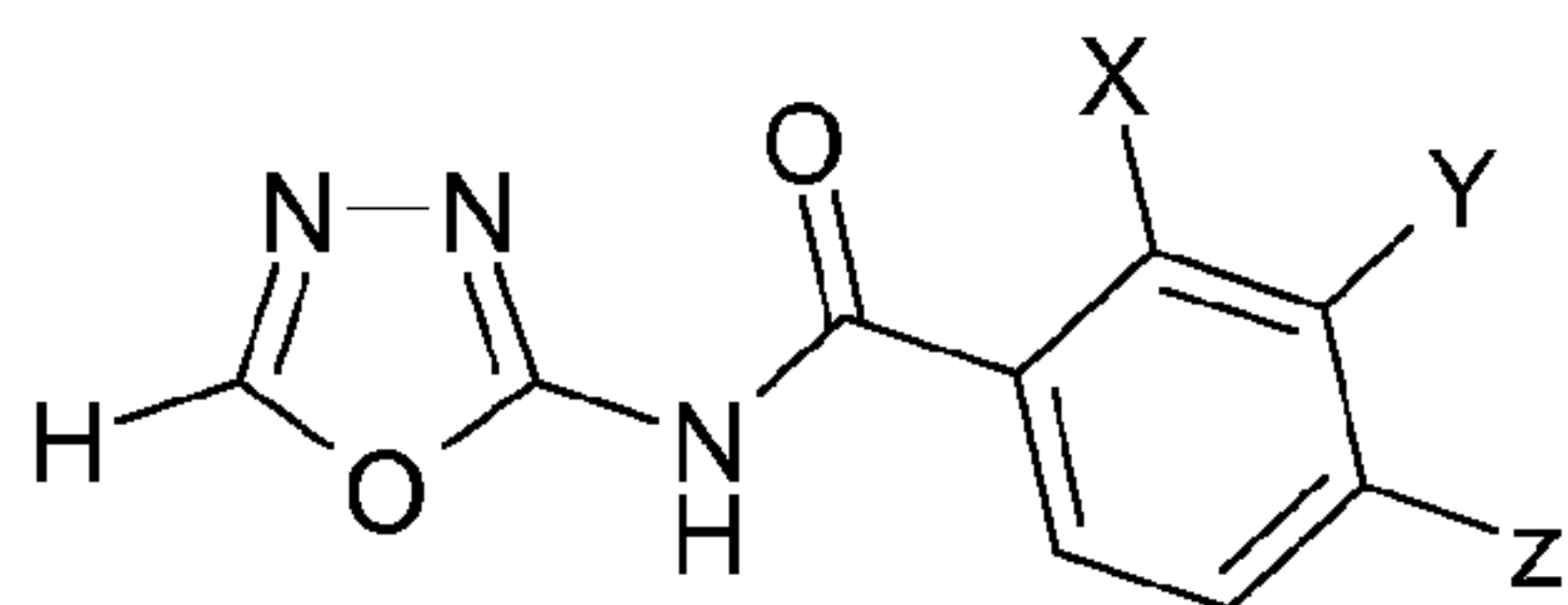
30 disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A

(Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

10 The abbreviations used mean:

Et = ethyl Me = methyl n-Pr = n-propyl i-Pr = isopropyl
c-Pr = cyclopropyl Ph = phenyl Ac = acetyl Bz = benzoyl

Table 1: Compounds of the general formula (I) in which A is CY and R is hydrogen and X, Y, and Z are as defined below.



No.	X	Y	Z
1-1	F	H	Cl
1-2	F	H	SO ₂ Me
1-3	F	H	SO ₂ Et
1-4	F	H	CF ₃
1-5	F	H	NO ₂
1-6	Cl	H	Br
1-7	Cl	H	SMe
1-8	Cl	H	SOMe
1-9	Cl	H	SO ₂ Me
1-10	Cl	H	SO ₂ CH ₂ Cl
1-11	Cl	H	SEt
1-12	Cl	H	SO ₂ Et
1-13	Cl	H	CF ₃
1-14	Cl	H	NO ₂

No.	X	Y	Z
1-15	Cl	H	pyrazol-1-yl
1-16	Cl	H	1H-1,2,4-triazol-1-yl
1-17	Br	H	Cl
1-18	Br	H	Br
1-19	Br	H	SO ₂ Me
1-20	Br	H	SO ₂ Et
1-21	Br	H	CF ₃
1-22	SO ₂ Me	H	Cl
1-23	SO ₂ Me	H	Br
1-24	SO ₂ Me	H	SMe
1-25	SO ₂ Me	H	SOMe
1-26	SO ₂ Me	H	SO ₂ Me
1-27	SO ₂ Me	H	SO ₂ Et
1-28	SO ₂ Me	H	CF ₃
1-29	SO ₂ Et	H	Cl
1-30	SO ₂ Et	H	Br
1-31	SO ₂ Et	H	SMe
1-32	SO ₂ Et	H	SOMe
1-33	SO ₂ Et	H	SO ₂ Me
1-34	SO ₂ Et	H	CF ₃
1-35	NO ₂	H	F
1-36	NO ₂	H	Cl
1-37	NO ₂	H	Br
1-38	NO ₂	H	I
1-39	NO ₂	H	CN
1-40	NO ₂	H	SO ₂ Me
1-41	NO ₂	H	SO ₂ Et
1-42	NO ₂	H	CF ₃
1-43	Me	H	Cl
1-44	Me	H	Br
1-45	Me	H	SMe
1-46	Me	H	SO ₂ Me
1-47	Me	H	SO ₂ CH ₂ Cl
1-48	Me	H	SEt
1-49	Me	H	SO ₂ Et
1-50	Me	H	CF ₃
1-51	CH ₂ SO ₂ Me	H	CF ₃
1-52	Et	H	Cl
1-53	Et	H	Br
1-54	Et	H	SMe

No.	X	Y	Z
1-55	Et	H	SO ₂ Me
1-56	Et	H	SO ₂ CH ₂ Cl
1-57	Et	H	SEt
1-58	Et	H	SO ₂ Et
1-59	Et	H	CF ₃
1-60	CF ₃	H	Cl
1-61	CF ₃	H	Br
1-62	CF ₃	H	SO ₂ Me
1-63	CF ₃	H	SO ₂ Et
1-64	CF ₃	H	CF ₃
1-65	NO ₂	NH ₂	F
1-66	NO ₂	NHMe	F
1-67	NO ₂	NMe ₂	F
1-68	NO ₂	Me	Cl
1-69	NO ₂	NH ₂	Cl
1-70	NO ₂	NHMe	Cl
1-71	NO ₂	NMe ₂	Cl
1-72	NO ₂	NH ₂	Br
1-73	NO ₂	NHMe	Br
1-74	NO ₂	NMe ₂	Br
1-75	NO ₂	NH ₂	CF ₃
1-76	NO ₂	NMe ₂	CF ₃
1-77	NO ₂	NH ₂	SO ₂ Me
1-78	NO ₂	NH ₂	SO ₂ Et
1-79	NO ₂	NHMe	SO ₂ Me
1-80	NO ₂	NMe ₂	SO ₂ Me
1-81	NO ₂	NMe ₂	SO ₂ Et
1-82	NO ₂	NH ₂	1H-1,2,4-triazol-1-yl
1-83	NO ₂	NHMe	1H-1,2,4-triazol-1-yl
1-84	NO ₂	NMe ₂	1H-1,2,4-triazol-1-yl
1-85	Me	SMe	H
1-86	Me	SOMe	H
1-87	Me	SO ₂ Me	H
1-88	Me	SEt	H
1-89	Me	SOEt	H
1-90	Me	SO ₂ Et	H
1-91	Me	S(CH ₂) ₂ OMe	H
1-92	Me	SO(CH ₂) ₂ OMe	H
1-93	Me	SO ₂ (CH ₂) ₂ OMe	H

No.	X	Y	Z
1-94	Me	F	F
1-95	Me	F	Cl
1-96	Me	SEt	F
1-97	Me	SOEt	F
1-98	Me	SO ₂ Et	F
1-99	Me	Me	Cl
1-100	Me	F	Cl
1-101	Me	Cl	Cl
1-102	Me	NH ₂	Cl
1-103	Me	NHMe	Cl
1-104	Me	NMe ₂	Cl
1-105	Me	O(CH ₂) ₂ OMe	Cl
1-106	Me	O(CH ₂) ₃ OMe	Cl
1-107	Me	O(CH ₂) ₄ OMe	Cl
1-108	Me	OCH ₂ CONMe ₂	Cl
1-109	Me	O(CH ₂) ₂ -CO-NMe ₂	Cl
1-110	Me	O(CH ₂) ₂ - NH(CO)NMe ₂	Cl
1-111	Me	O(CH ₂) ₂ - NH(CO)NHCO ₂ Et	Cl
1-112	Me	O(CH ₂) ₂ -NHCO ₂ Me	Cl
1-113	Me	OCH ₂ -NHSO ₂ cPr	Cl
1-114	Me	O(CH ₂)-5-2,4- dimethyl-2,4- dihydro-3H-1,2,4- triazol-3-one	Cl
1-115	Me	O(CH ₂)-3,5- dimethyl-1,2-oxazol- 4-yl	Cl
1-116	Me	SMe	Cl
1-117	Me	SOMe	Cl
1-118	Me	SO ₂ Me	Cl
1-119	Me	SEt	Cl
1-120	Me	SOEt	Cl
1-121	Me	SO ₂ Et	Cl
1-122	Me	S(CH ₂) ₂ OMe	Cl
1-123	Me	SO(CH ₂) ₂ OMe	Cl
1-124	Me	SO ₂ (CH ₂) ₂ OMe	Cl
1-125	Me	NH ₂	Br
1-126	Me	NHMe	Br
1-127	Me	NMe ₂	Br
1-128	Me	OCH ₂ (CO)NMe ₂	Br
1-129	Me	O(CH ₂)-5-pyrrolidin-	Br

No.	X	Y	Z
		2-one	
1-130	Me	SMe	Br
1-131	Me	SOMe	Br
1-132	Me	SO ₂ Me	Br
1-133	Me	SEt	Br
1-134	Me	SOEt	Br
1-135	Me	SO ₂ Et	Br
1-136	Me	SMe	I
1-137	Me	SOMe	I
1-138	Me	SO ₂ Me	I
1-139	Me	SEt	I
1-140	Me	SOEt	I
1-141	Me	SO ₂ Et	I
1-142	Me	Cl	CF ₃
1-143	Me	SMe	CF ₃
1-144	Me	SOMe	CF ₃
1-145	Me	SO ₂ Me	CF ₃
1-146	Me	SEt	CF ₃
1-147	Me	SOEt	CF ₃
1-148	Me	SO ₂ Et	CF ₃
1-149	Me	S(CH ₂) ₂ OMe	CF ₃
1-150	Me	SO(CH ₂) ₂ OMe	CF ₃
1-151	Me	SO ₂ (CH ₂) ₂ OMe	CF ₃
1-152	Me	Me	SO ₂ Me
1-153	Me	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
1-154	Me	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
1-155	Me	5-cyanomethyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
1-156	Me	5-cyanomethyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
1-157	Me	NH ₂	SO ₂ Me
1-158	Me	NHMe	SO ₂ Me
1-159	Me	NMe ₂	SO ₂ Me
1-160	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
1-161	Me	pyrazol-1-yl	SO ₂ Me
1-162	Me	OH	SO ₂ Me
1-163	Me	OMe	SO ₂ Me
1-164	Me	OMe	SO ₂ Et
1-165	Me	OEt	SO ₂ Me

No.	X	Y	Z
1-166	Me	OEt	SO ₂ Et
1-167	Me	OiPr	SO ₂ Me
1-168	Me	OiPr	SO ₂ Et
1-169	Me	O(CH ₂) ₂ OMe	SO ₂ Me
1-170	Me	O(CH ₂) ₂ OMe	SO ₂ Et
1-171	Me	O(CH ₂) ₃ OMe	SO ₂ Me
1-172	Me	O(CH ₂) ₃ OMe	SO ₂ Et
1-173	Me	O(CH ₂) ₄ OMe	SO ₂ Me
1-174	Me	O(CH ₂) ₄ OMe	SO ₂ Et
1-175	Me	O(CH ₂) ₂ NHSO ₂ Me	SO ₂ Me
1-176	Me	O(CH ₂) ₂ NHSO ₂ Me	SO ₂ Et
1-177	Me	OCH ₂ (CO)NMe ₂	SO ₂ Me
1-178	Me	OCH ₂ (CO)NMe ₂	SO ₂ Et
1-179	Me	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
1-180	Me	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
1-181	Me	O(CH ₂) ₂ -O-(3,5-dimethoxypyrimidin-2-yl)	SO ₂ Me
1-182	Me	Cl	SO ₂ Me
1-183	Me	SMe	SO ₂ Me
1-184	Me	SOMe	SO ₂ Me
1-185	Me	SO ₂ Me	SO ₂ Me
1-186	Me	SO ₂ Me	SO ₂ Et
1-187	Me	SEt	SO ₂ Me
1-188	Me	SOEt	SO ₂ Me
1-189	Me	SO ₂ Et	SO ₂ Me
1-190	Me	S(CH ₂) ₂ OMe	SO ₂ Me
1-191	Me	SO(CH ₂) ₂ OMe	SO ₂ Me
1-192	Me	SO ₂ (CH ₂) ₂ OMe	SO ₂ Me
1-193	CH ₂ SMe	OMe	SO ₂ Me
1-194	CH ₂ OMe	OMe	SO ₂ Me
1-195	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₂ OEt	SO ₂ Me
1-196	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₃ OEt	SO ₂ Me
1-197	CH ₂ O(CH ₂) ₃ OMe	OMe	SO ₂ Me
1-198	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₂ OMe	SO ₂ Me
1-199	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₃ OMe	SO ₂ Me
1-200	Et	SMe	Cl
1-201	Et	SO ₂ Me	Cl
1-202	Et	SMe	CF ₃
1-203	Et	SO ₂ Me	CF ₃

No.	X	Y	Z
1-204	Et	F	SO ₂ Me
1-205	Et	NH(CH ₂) ₂ OMe	SO ₂ Me
1-206	iPr	SO ₂ Me	CF ₃
1-207	cPr	SO ₂ Me	CF ₃
1-208	CF ₃	O(CH ₂) ₂ OMe	F
1-209	CF ₃	O(CH ₂) ₃ OMe	F
1-210	CF ₃	OCH ₂ CONMe ₂	F
1-211	CF ₃	[1,4]dioxan-2-yl-methoxy	F
1-212	CF ₃	O(CH ₂) ₂ OMe	Cl
1-213	CF ₃	O(CH ₂) ₃ OMe	Cl
1-214	CF ₃	OCH ₂ CONMe ₂	Cl
1-215	CF ₃	[1,4]dioxan-2-yl-methoxy	Cl
1-216	CF ₃	O(CH ₂) ₂ OMe	Br
1-217	CF ₃	O(CH ₂) ₃ OMe	Br
1-218	CF ₃	OCH ₂ CONMe ₂	Br
1-219	CF ₃	[1,4]dioxan-2-yl-methoxy	Br
1-220	CF ₃	O(CH ₂) ₂ OMe	I
1-221	CF ₃	O(CH ₂) ₃ OMe	I
1-222	CF ₃	OCH ₂ CONMe ₂	I
1-223	CF ₃	[1,4]dioxan-2-yl-methoxy	I
1-224	CF ₃	F	SO ₂ Me
1-225	CF ₃	F	SO ₂ Et
1-226	CF ₃	O(CH ₂) ₂ OMe	SO ₂ Me
1-227	CF ₃	O(CH ₂) ₂ OMe	SO ₂ Et
1-228	CF ₃	O(CH ₂) ₃ OMe	SO ₂ Me
1-229	CF ₃	O(CH ₂) ₃ OMe	SO ₂ Et
1-230	CF ₃	OCH ₂ CONMe ₂	SO ₂ Me
1-231	CF ₃	OCH ₂ CONMe ₂	SO ₂ Et
1-232	CF ₃	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
1-233	CF ₃	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
1-234	F	SMe	CF ₃
1-235	F	SOMe	CF ₃
1-236	Cl	Me	Cl
1-237	Cl	OCH ₂ CHCH ₂	Cl
1-238	Cl	OCH ₂ CHF ₂	Cl
1-239	Cl	O(CH ₂) ₂ OMe	Cl

27

No.	X	Y	Z
1-240	Cl	OCH ₂ CONMe ₂	Cl
1-241	Cl	O(CH ₂)-5-pyrrolidin-2-one	Cl
1-242	Cl	SMe	Cl
1-243	Cl	SOMe	Cl
1-244	Cl	SO ₂ Me	Cl
1-245	Cl	F	SMe
1-246	Cl	Cl	SO ₂ Me
1-247	Cl	COOMe	SO ₂ Me
1-248	Cl	CONMe ₂	SO ₂ Me
1-249	Cl	CONMe(OMe)	SO ₂ Me
1-250	Cl	CH ₂ OMe	SO ₂ Me
1-251	Cl	CH ₂ OMe	SO ₂ Et
1-252	Cl	CH ₂ OEt	SO ₂ Me
1-253	Cl	CH ₂ OEt	SO ₂ Et
1-254	Cl	CH ₂ OCH ₂ CHF ₂	SO ₂ Me
1-255	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
1-256	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Et
1-257	Cl	CH ₂ OCH ₂ CF ₂ CHF ₂	SO ₂ Me
1-258	Cl	CH ₂ OcPentyl	SO ₂ Me
1-259	Cl	CH ₂ PO(OMe) ₂	SO ₂ Me
1-260	Cl	4,5-dihydro-1,2-oxazol-3-yl	SMe
1-261	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
1-262	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
1-263	Cl	5-cyanomethyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
1-264	Cl	5-cyanomethyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
1-265	Cl	5-(methoxymethyl)-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
1-266	Cl	5-(methoxymethyl)-5-methyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
1-267	Cl	CH ₂ O-tetrahydrofuran-3-yl	SO ₂ Me
1-268	Cl	CH ₂ O-tetrahydrofuran-3-yl	SO ₂ Et
1-269	Cl	CH ₂ OCH ₂ -	SO ₂ Me

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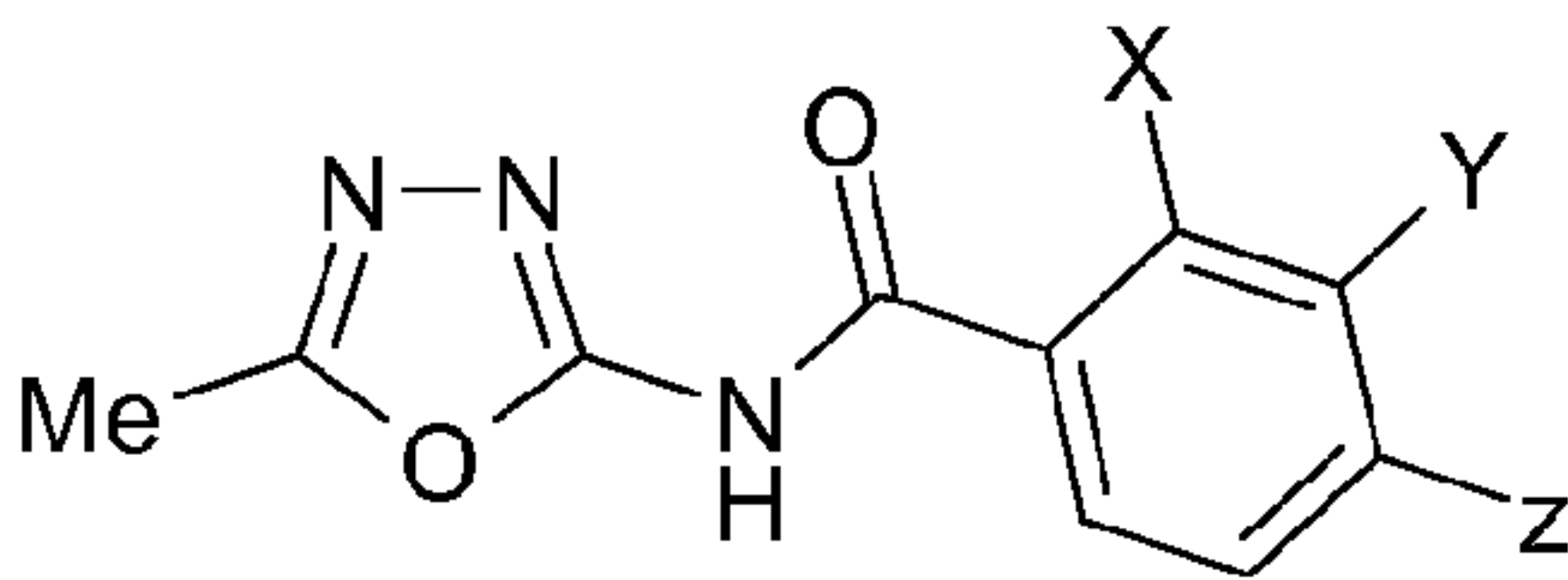
No.	X	Y	Z
		tetrahydrofuran-2-yl	
1-270	Cl	CH ₂ OCH ₂ - tetrahydrofuran-2-yl	SO ₂ Et
1-271	Cl	CH ₂ OCH ₂ - tetrahydrofuran-3-yl	SO ₂ Me
1-272	Cl	CH ₂ OCH ₂ - tetrahydrofuran-3-yl	SO ₂ Et
1-273	Cl	OMe	SO ₂ Me
1-274	Cl	OMe	SO ₂ Et
1-275	Cl	OEt	SO ₂ Me
1-276	Cl	OEt	SO ₂ Et
1-277	Cl	OiPr	SO ₂ Me
1-278	Cl	OiPr	SO ₂ Et
1-279	Cl	O(CH ₂) ₂ OMe	SO ₂ Me
1-280	Cl	O(CH ₂) ₄ OMe	SO ₂ Me
1-281	Cl	O(CH ₂) ₄ OMe	SO ₂ Et
1-282	Cl	O(CH ₂) ₃ OMe	SO ₂ Me
1-283	Cl	O(CH ₂) ₃ OMe	SO ₂ Et
1-284	Cl	O(CH ₂) ₂ OMe	SO ₂ Me
1-285	Cl	O(CH ₂) ₂ OMe	SO ₂ Et
1-286	Cl	[1,4]dioxan-2-yl- methoxy	SO ₂ Me
1-287	Cl	[1,4]dioxan-2-yl- methoxy	SO ₂ Et
1-288	Cl	OCH ₂ (CO)NMe ₂	SO ₂ Me
1-289	Cl	OCH ₂ (CO)NMe ₂	SO ₂ Et
1-290	Cl	SMe	SO ₂ Me
1-291	Cl	SOMe	SO ₂ Me
1-292	Br	OMe	Br
1-293	Br	O(CH ₂) ₂ OMe	Br
1-294	Br	O(CH ₂) ₂ OMe	SO ₂ Me
1-295	Br	O(CH ₂) ₂ OMe	SO ₂ Et
1-296	Br	O(CH ₂) ₃ OMe	SO ₂ Me
1-297	Br	O(CH ₂) ₃ OMe	SO ₂ Et
1-298	Br	O(CH ₂) ₄ OMe	SO ₂ Me
1-299	Br	O(CH ₂) ₄ OMe	SO ₂ Et
1-300	Br	[1,4]dioxan-2-yl- methoxy	SO ₂ Me
1-301	Br	[1,4]dioxan-2-yl- methoxy	SO ₂ Et
1-302	I	O(CH ₂) ₂ OMe	SO ₂ Me
1-303	I	O(CH ₂) ₂ OMe	SO ₂ Et
1-304	I	O(CH ₂) ₃ OMe	SO ₂ Me

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No.	X	Y	Z
1-305	I	O(CH ₂) ₃ OMe	SO ₂ Et
1-306	I	O(CH ₂) ₄ OMe	SO ₂ Me
1-307	I	O(CH ₂) ₄ OMe	SO ₂ Et
1-308	I	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
1-309	I	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
1-310	OMe	SMe	CF ₃
1-311	OMe	SOMe	CF ₃
1-312	OMe	SO ₂ Me	CF ₃
1-313	OMe	SOEt	CF ₃
1-314	OMe	SO ₂ Et	CF ₃
1-315	OMe	S(CH ₂) ₂ OMe	CF ₃
1-316	OMe	SO(CH ₂) ₂ OMe	CF ₃
1-317	OMe	SO ₂ (CH ₂) ₂ OMe	CF ₃
1-318	OMe	SMe	Cl
1-319	OMe	SOMe	Cl
1-320	OMe	SO ₂ Me	Cl
1-321	OMe	SEt	Cl
1-322	OMe	SOEt	Cl
1-323	OMe	SO ₂ Et	Cl
1-324	OMe	S(CH ₂) ₂ OMe	Cl
1-325	OMe	SO(CH ₂) ₂ OMe	Cl
1-326	OMe	SO ₂ (CH ₂) ₂ OMe	Cl
1-327	OCH ₂ c-Pr	SMe	CF ₃
1-328	OCH ₂ c-Pr	SOMe	CF ₃
1-329	OCH ₂ c-Pr	SO ₂ Me	CF ₃
1-330	OCH ₂ c-Pr	SEt	CF ₃
1-331	OCH ₂ c-Pr	SOEt	CF ₃
1-332	OCH ₂ c-Pr	SO ₂ Et	CF ₃
1-333	OCH ₂ c-Pr	S(CH ₂) ₂ OMe	CF ₃
1-334	OCH ₂ c-Pr	SO(CH ₂) ₂ OMe	CF ₃
1-335	OCH ₂ c-Pr	SO ₂ (CH ₂) ₂ OMe	CF ₃
1-336	OCH ₂ c-Pr	SMe	Cl
1-337	OCH ₂ c-Pr	SOMe	Cl
1-338	OCH ₂ c-Pr	SO ₂ Me	Cl
1-339	OCH ₂ c-Pr	SEt	Cl
1-340	OCH ₂ c-Pr	SOEt	Cl
1-341	OCH ₂ c-Pr	SO ₂ Et	Cl
1-342	OCH ₂ c-Pr	S(CH ₂) ₂ OMe	Cl
1-343	OCH ₂ c-Pr	SO(CH ₂) ₂ OMe	Cl

No.	X	Y	Z
1-344	OCH ₂ c-Pr	SO ₂ (CH ₂) ₂ OMe	Cl
1-345	OCH ₂ c-Pr	SMe	SO ₂ Me
1-346	OCH ₂ c-Pr	SOMe	SO ₂ Me
1-347	OCH ₂ c-Pr	SO ₂ Me	SO ₂ Me
1-348	OCH ₂ c-Pr	SEt	SO ₂ Me
1-349	OCH ₂ c-Pr	SOEt	SO ₂ Me
1-350	OCH ₂ c-Pr	SO ₂ Et	SO ₂ Me
1-351	OCH ₂ c-Pr	S(CH ₂) ₂ OMe	SO ₂ Me
1-352	OCH ₂ c-Pr	SO(CH ₂) ₂ OMe	SO ₂ Me
1-353	OCH ₂ c-Pr	SO ₂ (CH ₂) ₂ OMe	SO ₂ Me
1-354	SO ₂ Me	F	CF ₃
1-355	SO ₂ Me	NH ₂	CF ₃
1-356	SO ₂ Me	NHEt	Cl
1-357	SMe	SEt	F
1-358	SMe	SMe	F
1-359	Cl	SMe	CF ₃
1-360	Cl	S(O)Me	CF ₃
1-361	Cl	CF ₃	CF ₃
1-362	Cl	CF ₃	CF ₃

Table 2: Compounds of the general formula (I) in which A is CY and R is methyl, and X, Y, and Z are as defined below.



No.	X	Y	Z
2-1	F	H	Cl
2-2	F	H	SO ₂ Me
2-3	F	H	SO ₂ Et
2-4	F	H	CF ₃
2-5	F	H	NO ₂
2-6	Cl	H	Br
2-7	Cl	H	SMe
2-8	Cl	H	SOMe
2-9	Cl	H	SO ₂ Me
2-10	Cl	H	SO ₂ CH ₂ Cl
2-11	Cl	H	SEt

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No.	X	Y	Z
2-12	Cl	H	SO ₂ Et
2-13	Cl	H	CF ₃
2-14	Cl	H	NO ₂
2-15	Cl	H	pyrazol-1-yl
2-16	Cl	H	1H-1,2,4-triazol-1-yl
2-17	Br	H	Cl
2-18	Br	H	Br
2-19	Br	H	SO ₂ Me
2-20	Br	H	SO ₂ Et
2-21	Br	H	CF ₃
2-22	SO ₂ Me	H	Cl
2-23	SO ₂ Me	H	Br
2-24	SO ₂ Me	H	SMe
2-25	SO ₂ Me	H	SOMe
2-26	SO ₂ Me	H	SO ₂ Me
2-27	SO ₂ Me	H	SO ₂ Et
2-28	SO ₂ Me	H	CF ₃
2-29	SO ₂ Et	H	Cl
2-30	SO ₂ Et	H	Br
2-31	SO ₂ Et	H	SMe
2-32	SO ₂ Et	H	SOMe
2-33	SO ₂ Et	H	SO ₂ Me
2-34	SO ₂ Et	H	CF ₃
2-35	NO ₂	H	F
2-36	NO ₂	H	Cl
2-37	NO ₂	H	Br
2-38	NO ₂	H	I
2-39	NO ₂	H	CN
2-40	NO ₂	H	SO ₂ Me
2-41	NO ₂	H	SO ₂ Et
2-42	NO ₂	H	CF ₃
2-43	Me	H	Cl
2-44	Me	H	Br
2-45	Me	H	SMe
2-46	Me	H	SO ₂ Me
2-47	Me	H	SO ₂ CH ₂ Cl
2-48	Me	H	SEt
2-49	Me	H	SO ₂ Et
2-50	Me	H	CF ₃
2-51	CH ₂ SO ₂ Me	H	CF ₃
2-52	Et	H	Cl

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No.	X	Y	Z
2-53	Et	H	Br
2-54	Et	H	SMe
2-55	Et	H	SO ₂ Me
2-56	Et	H	SO ₂ CH ₂ Cl
2-57	Et	H	SEt
2-58	Et	H	SO ₂ Et
2-59	Et	H	CF ₃
2-60	CF ₃	H	Cl
2-61	CF ₃	H	Br
2-62	CF ₃	H	SO ₂ Me
2-63	CF ₃	H	SO ₂ Et
2-64	CF ₃	H	CF ₃
2-65	NO ₂	NH ₂	F
2-66	NO ₂	NHMe	F
2-67	NO ₂	NMe ₂	F
2-68	NO ₂	Me	Cl
2-69	NO ₂	NH ₂	Cl
2-70	NO ₂	NHMe	Cl
2-71	NO ₂	NMe ₂	Cl
2-72	NO ₂	NH ₂	Br
2-73	NO ₂	NHMe	Br
2-74	NO ₂	NMe ₂	Br
2-75	NO ₂	NH ₂	CF ₃
2-76	NO ₂	NMe ₂	CF ₃
2-77	NO ₂	NH ₂	SO ₂ Me
2-78	NO ₂	NH ₂	SO ₂ Et
2-79	NO ₂	NHMe	SO ₂ Me
2-80	NO ₂	NMe ₂	SO ₂ Me
2-81	NO ₂	NMe ₂	SO ₂ Et
2-82	NO ₂	NH ₂	1H-1,2,4-triazol-1-yl
2-83	NO ₂	NHMe	1H-1,2,4-triazol-1-yl
2-84	NO ₂	NMe ₂	1H-1,2,4-triazol-1-yl
2-85	Me	SMe	H
2-86	Me	SOMe	H
2-87	Me	SO ₂ Me	H
2-88	Me	SEt	H
2-89	Me	SOEt	H
2-90	Me	SO ₂ Et	H
2-91	Me	S(CH ₂) ₂ OMe	H
2-92	Me	SO(CH ₂) ₂ OMe	H
2-93	Me	SO ₂ (CH ₂) ₂ OMe	H

33

No.	X	Y	Z
2-94	Me	F	F
2-95	Me	F	Cl
2-96	Me	SEt	F
2-97	Me	SOEt	F
2-98	Me	SO ₂ Et	F
2-99	Me	Me	Cl
2-100	Me	F	Cl
2-101	Me	Cl	Cl
2-102	Me	NH ₂	Cl
2-103	Me	NHMe	Cl
2-104	Me	NMe ₂	Cl
2-105	Me	O(CH ₂) ₂ OMe	Cl
2-106	Me	O(CH ₂) ₃ OMe	Cl
2-107	Me	O(CH ₂) ₄ OMe	Cl
2-108	Me	OCH ₂ CONMe ₂	Cl
2-109	Me	O(CH ₂) ₂ -CO-NMe ₂	Cl
2-110	Me	O(CH ₂) ₂ - NH(CO)NMe ₂	Cl
2-111	Me	O(CH ₂) ₂ - NH(CO)NHCO ₂ Et	Cl
2-112	Me	O(CH ₂) ₂ -NHCO ₂ Me	Cl
2-113	Me	O-CH ₂ -NHSO ₂ cPr	Cl
2-114	Me	O(CH ₂)-5-2,4- dimethyl-2,4- dihydro-3H-1,2,4- triazol-3-one	Cl
2-115	Me	O(CH ₂)-3,5- dimethyl-1,2-oxazol- 4-yl	Cl
2-116	Me	SMe	Cl
2-117	Me	SOMe	Cl
2-118	Me	SO ₂ Me	Cl
2-119	Me	SEt	Cl
2-120	Me	SOEt	Cl
2-121	Me	SO ₂ Et	Cl
2-122	Me	S(CH ₂) ₂ OMe	Cl
2-123	Me	SO(CH ₂) ₂ OMe	Cl
2-124	Me	SO ₂ (CH ₂) ₂ OMe	Cl
2-125	Me	NH ₂	Br
2-126	Me	NHMe	Br
2-127	Me	NMe ₂	Br
2-128	Me	O(CH ₂)CONEt ₂	Br
2-129	Me	O(CH ₂)-5-pyrrolidin-	Br

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No.	X	Y	Z
		2-one	
2-130	Me	SMe	Br
2-131	Me	SOMe	Br
2-132	Me	SO ₂ Me	Br
2-133	Me	SEt	Br
2-134	Me	SOEt	Br
2-135	Me	SO ₂ Et	Br
2-136	Me	SMe	I
2-137	Me	SOMe	I
2-138	Me	SO ₂ Me	I
2-139	Me	SEt	I
2-140	Me	SOEt	I
2-141	Me	SO ₂ Et	I
2-142	Me	Cl	CF ₃
2-143	Me	SMe	CF ₃
2-144	Me	SOMe	CF ₃
2-145	Me	SO ₂ Me	CF ₃
2-146	Me	SEt	CF ₃
2-147	Me	SOEt	CF ₃
2-148	Me	SO ₂ Et	CF ₃
2-149	Me	S(CH ₂) ₂ OMe	CF ₃
2-150	Me	SO(CH ₂) ₂ OMe	CF ₃
2-151	Me	SO ₂ (CH ₂) ₂ OMe	CF ₃
2-152	Me	Me	SO ₂ Me
2-153	Me	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
2-154	Me	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
2-155	Me	5-cyanomethyl- 4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
2-156	Me	5-cyanomethyl- 4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
2-157	Me	NH ₂	SO ₂ Me
2-158	Me	NHMe	SO ₂ Me
2-159	Me	NMe ₂	SO ₂ Me
2-160	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
2-161	Me	pyrazol-1-yl	SO ₂ Me
2-162	Me	OH	SO ₂ Me
2-163	Me	OMe	SO ₂ Me
2-164	Me	OMe	SO ₂ Et
2-165	Me	OEt	SO ₂ Me

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No.	X	Y	Z
2-166	Me	OEt	SO ₂ Et
2-167	Me	OiPr	SO ₂ Me
2-168	Me	OiPr	SO ₂ Et
2-169	Me	O(CH ₂) ₂ OMe	SO ₂ Me
2-170	Me	O(CH ₂) ₂ OMe	SO ₂ Et
2-171	Me	O(CH ₂) ₃ OMe	SO ₂ Me
2-172	Me	O(CH ₂) ₃ OMe	SO ₂ Et
2-173	Me	O(CH ₂) ₄ OMe	SO ₂ Me
2-174	Me	O(CH ₂) ₄ OMe	SO ₂ Et
2-175	Me	O(CH ₂) ₂ NHSO ₂ Me	SO ₂ Me
2-176	Me	O(CH ₂) ₂ NHSO ₂ Me	SO ₂ Et
2-177	Me	OCH ₂ (CO)NMe ₂	SO ₂ Me
2-178	Me	OCH ₂ (CO)NMe ₂	SO ₂ Et
2-179	Me	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
2-180	Me	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
2-181	Me	O(CH ₂) ₂ -O-(3,5-dimethoxypyrimidin-2-yl)	SO ₂ Me
2-182	Me	Cl	SO ₂ Me
2-183	Me	SMe	SO ₂ Me
2-184	Me	SOMe	SO ₂ Me
2-185	Me	SO ₂ Me	SO ₂ Me
2-186	Me	SO ₂ Me	SO ₂ Et
2-187	Me	SEt	SO ₂ Me
2-188	Me	SOEt	SO ₂ Me
2-189	Me	SO ₂ Et	SO ₂ Me
2-190	Me	S(CH ₂) ₂ OMe	SO ₂ Me
2-191	Me	SO(CH ₂) ₂ OMe	SO ₂ Me
2-192	Me	SO ₂ (CH ₂) ₂ OMe	SO ₂ Me
2-193	CH ₂ SMe	OMe	SO ₂ Me
2-194	CH ₂ OMe	OMe	SO ₂ Me
2-195	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₂ OEt	SO ₂ Me
2-196	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₃ OEt	SO ₂ Me
2-197	CH ₂ O(CH ₂) ₃ OMe	OMe	SO ₂ Me
2-198	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₂ OMe	SO ₂ Me
2-199	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₃ OMe	SO ₂ Me

36

No.	X	Y	Z
2-200	Et	SMe	Cl
2-201	Et	SO ₂ Me	Cl
2-202	Et	SMe	CF ₃
2-203	Et	SO ₂ Me	CF ₃
2-204	Et	F	SO ₂ Me
2-205	Et	NH(CH ₂) ₂ OMe	SO ₂ Me
2-206	iPr	SO ₂ Me	CF ₃
2-207	cPr	SO ₂ Me	CF ₃
2-208	CF ₃	O(CH ₂) ₂ OMe	F
2-209	CF ₃	O(CH ₂) ₃ OMe	F
2-210	CF ₃	OCH ₂ CONMe ₂	F
2-211	CF ₃	[1,4]dioxan-2-yl-methoxy	F
2-212	CF ₃	O(CH ₂) ₂ OMe	Cl
2-213	CF ₃	O(CH ₂) ₃ OMe	Cl
2-214	CF ₃	OCH ₂ CONMe ₂	Cl
2-215	CF ₃	[1,4]dioxan-2-yl-methoxy	Cl
2-216	CF ₃	O(CH ₂) ₂ OMe	Br
2-217	CF ₃	O(CH ₂) ₃ OMe	Br
2-218	CF ₃	OCH ₂ CONMe ₂	Br
2-219	CF ₃	[1,4]dioxan-2-yl-methoxy	Br
2-220	CF ₃	O(CH ₂) ₂ OMe	I
2-221	CF ₃	O(CH ₂) ₃ OMe	I
2-222	CF ₃	OCH ₂ CONMe ₂	I
2-223	CF ₃	[1,4]dioxan-2-yl-methoxy	I
2-224	CF ₃	F	SO ₂ Me
2-225	CF ₃	F	SO ₂ Et
2-226	CF ₃	O(CH ₂) ₂ OMe	SO ₂ Me
2-227	CF ₃	O(CH ₂) ₂ OMe	SO ₂ Et
2-228	CF ₃	O(CH ₂) ₃ OMe	SO ₂ Me
2-229	CF ₃	O(CH ₂) ₃ OMe	SO ₂ Et
2-230	CF ₃	OCH ₂ CONMe ₂	SO ₂ Me
2-231	CF ₃	OCH ₂ CONMe ₂	SO ₂ Et
2-232	CF ₃	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
2-233	CF ₃	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
2-234	F	SMe	CF ₃
2-235	F	SOMe	CF ₃

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No.	X	Y	Z
2-236	Cl	Me	Cl
2-237	Cl	OCH ₂ CHCH ₂	Cl
2-238	Cl	OCH ₂ CHF ₂	Cl
2-239	Cl	O(CH ₂) ₂ OMe	Cl
2-240	Cl	OCH ₂ (CO)NMe ₂	Cl
2-241	Cl	O(CH ₂)-5-pyrrolidin-2-one	Cl
2-242	Cl	SMe	Cl
2-243	Cl	SOMe	Cl
2-244	Cl	SO ₂ Me	Cl
2-245	Cl	F	SMe
2-246	Cl	Cl	SO ₂ Me
2-247	Cl	COOMe	SO ₂ Me
2-248	Cl	CONMe ₂	SO ₂ Me
2-249	Cl	CONMe(OMe)	SO ₂ Me
2-250	Cl	CH ₂ OMe	SO ₂ Me
2-251	Cl	CH ₂ OMe	SO ₂ Et
2-252	Cl	CH ₂ OEt	SO ₂ Me
2-253	Cl	CH ₂ OEt	SO ₂ Et
2-254	Cl	CH ₂ OCH ₂ CHF ₂	SO ₂ Me
2-255	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
2-256	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Et
2-257	Cl	CH ₂ OCH ₂ CF ₂ CHF ₂	SO ₂ Me
2-258	Cl	CH ₂ OcPentyl	SO ₂ Me
2-259	Cl	CH ₂ PO(OMe) ₂	SO ₂ Me
2-260	Cl	4,5-dihydro-1,2-oxazol-3-yl	SMe
2-261	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
2-262	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
2-263	Cl	5-cyanomethyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
2-264	Cl	5-cyanomethyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
2-265	Cl	5-(methoxymethyl)-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et

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No.	X	Y	Z
2-266	Cl	5-(methoxymethyl)- 5-methyl-4,5- dihydro-1,2-oxazol- 3-yl	SO ₂ Et
2-267	Cl	CH ₂ O- tetrahydrofuran-3-yl	SO ₂ Me
2-268	Cl	CH ₂ O- tetrahydrofuran-3-yl	SO ₂ Et
2-269	Cl	CH ₂ OCH ₂ - tetrahydrofuran-2-yl	SO ₂ Me
2-270	Cl	CH ₂ OCH ₂ - tetrahydrofuran-2-yl	SO ₂ Et
2-271	Cl	CH ₂ OCH ₂ - tetrahydrofuran-3-yl	SO ₂ Me
2-272	Cl	CH ₂ OCH ₂ - tetrahydrofuran-3-yl	SO ₂ Et
2-273	Cl	OMe	SO ₂ Me
2-274	Cl	OMe	SO ₂ Et
2-275	Cl	OEt	SO ₂ Me
2-276	Cl	OEt	SO ₂ Et
2-277	Cl	OiPr	SO ₂ Me
2-278	Cl	OiPr	SO ₂ Et
2-279	Cl	O(CH ₂) ₂ OMe	SO ₂ Me
2-280	Cl	O(CH ₂) ₄ OMe	SO ₂ Me
2-281	Cl	O(CH ₂) ₄ OMe	SO ₂ Et
2-282	Cl	O(CH ₂) ₃ OMe	SO ₂ Me
2-283	Cl	O(CH ₂) ₃ OMe	SO ₂ Et
2-284	Cl	O(CH ₂) ₂ OMe	SO ₂ Me
2-285	Cl	O(CH ₂) ₂ OMe	SO ₂ Et
2-286	Cl	[1,4]dioxan-2-yl- methoxy	SO ₂ Me
2-287	Cl	[1,4]dioxan-2-yl- methoxy	SO ₂ Et
2-288	Cl	OCH ₂ (CO)NMe ₂	SO ₂ Me
2-289	Cl	OCH ₂ (CO)NMe ₂	SO ₂ Et
2-290	Cl	SMe	SO ₂ Me
2-291	Cl	SOMe	SO ₂ Me
2-292	Br	OMe	Br
2-293	Br	O(CH ₂) ₂ OMe	Br
2-294	Br	O(CH ₂) ₂ OMe	SO ₂ Me
2-295	Br	O(CH ₂) ₂ OMe	SO ₂ Et
2-296	Br	O(CH ₂) ₃ OMe	SO ₂ Me
2-297	Br	O(CH ₂) ₃ OMe	SO ₂ Et
2-298	Br	O(CH ₂) ₄ OMe	SO ₂ Me

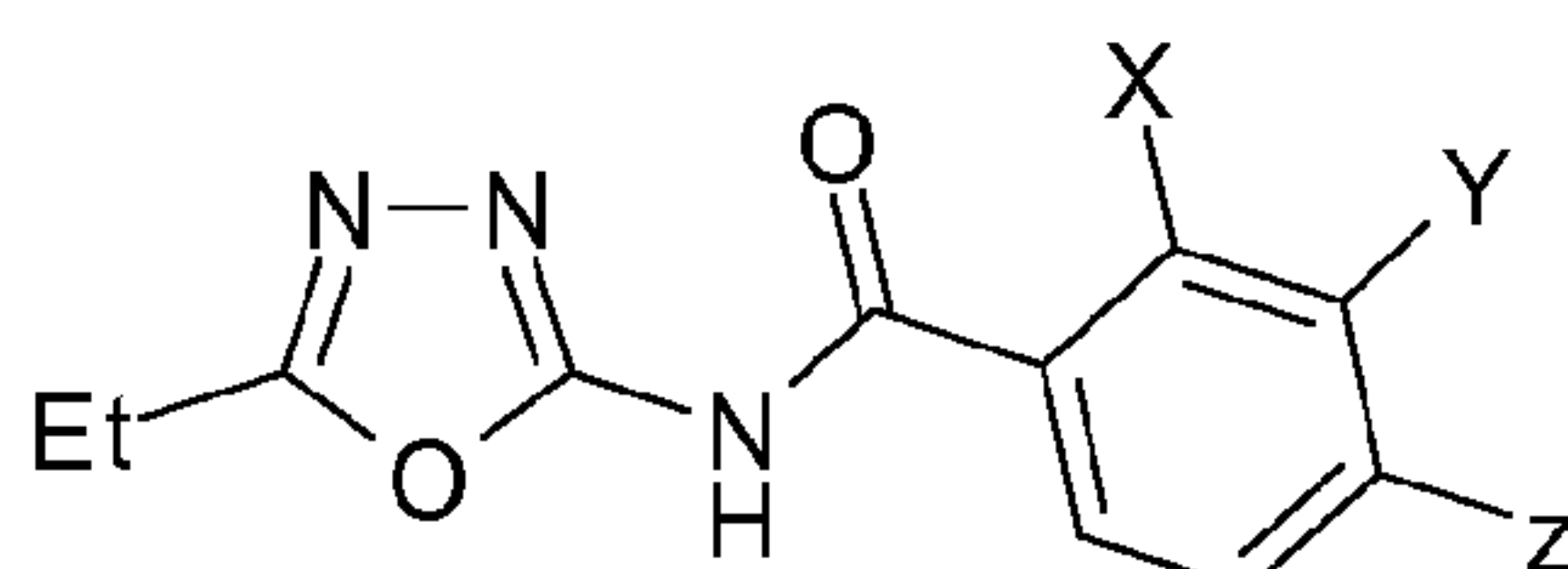
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No.	X	Y	Z
2-299	Br	O(CH ₂) ₄ OMe	SO ₂ Et
2-300	Br	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
2-301	Br	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
2-302	I	O(CH ₂) ₂ OMe	SO ₂ Me
2-303	I	O(CH ₂) ₂ OMe	SO ₂ Et
2-304	I	O(CH ₂) ₃ OMe	SO ₂ Me
2-305	I	O(CH ₂) ₃ OMe	SO ₂ Et
2-306	I	O(CH ₂) ₄ OMe	SO ₂ Me
2-307	I	O(CH ₂) ₄ OMe	SO ₂ Et
2-308	I	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
2-309	I	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
2-310	OMe	SMe	CF ₃
2-311	OMe	SOMe	CF ₃
2-312	OMe	SO ₂ Me	CF ₃
2-313	OMe	SOEt	CF ₃
2-314	OMe	SO ₂ Et	CF ₃
2-315	OMe	S(CH ₂) ₂ OMe	CF ₃
2-316	OMe	SO(CH ₂) ₂ OMe	CF ₃
2-317	OMe	SO ₂ (CH ₂) ₂ OMe	CF ₃
2-318	OMe	SMe	Cl
2-319	OMe	SOMe	Cl
2-320	OMe	SO ₂ Me	Cl
2-321	OMe	SEt	Cl
2-322	OMe	SOEt	Cl
2-323	OMe	SO ₂ Et	Cl
2-324	OMe	S(CH ₂) ₂ OMe	Cl
2-325	OMe	SO(CH ₂) ₂ OMe	Cl
2-326	OMe	SO ₂ (CH ₂) ₂ OMe	Cl
2-327	OCH ₂ c-Pr	SMe	CF ₃
2-328	OCH ₂ c-Pr	SOMe	CF ₃
2-329	OCH ₂ c-Pr	SO ₂ Me	CF ₃
2-330	OCH ₂ c-Pr	SEt	CF ₃
2-331	OCH ₂ c-Pr	SOEt	CF ₃
2-332	OCH ₂ c-Pr	SO ₂ Et	CF ₃
2-333	OCH ₂ c-Pr	S(CH ₂) ₂ OMe	CF ₃
2-334	OCH ₂ c-Pr	SO(CH ₂) ₂ OMe	CF ₃
2-335	OCH ₂ c-Pr	SO ₂ (CH ₂) ₂ OMe	CF ₃
2-336	OCH ₂ c-Pr	SMe	Cl

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No.	X	Y	Z
2-337	OCH ₂ c-Pr	SOMe	Cl
2-338	OCH ₂ c-Pr	SO ₂ Me	Cl
2-339	OCH ₂ c-Pr	SEt	Cl
2-340	OCH ₂ c-Pr	SOEt	Cl
2-341	OCH ₂ c-Pr	SO ₂ Et	Cl
2-342	OCH ₂ c-Pr	S(CH ₂) ₂ OMe	Cl
2-343	OCH ₂ c-Pr	SO(CH ₂) ₂ OMe	Cl
2-344	OCH ₂ c-Pr	SO ₂ (CH ₂) ₂ OMe	Cl
2-345	OCH ₂ c-Pr	SMe	SO ₂ Me
2-346	OCH ₂ c-Pr	SOMe	SO ₂ Me
2-347	OCH ₂ c-Pr	SO ₂ Me	SO ₂ Me
2-348	OCH ₂ c-Pr	SEt	SO ₂ Me
2-349	OCH ₂ c-Pr	SOEt	SO ₂ Me
2-350	OCH ₂ c-Pr	SO ₂ Et	SO ₂ Me
2-351	OCH ₂ c-Pr	S(CH ₂) ₂ OMe	SO ₂ Me
2-352	OCH ₂ c-Pr	SO(CH ₂) ₂ OMe	SO ₂ Me
2-353	OCH ₂ c-Pr	SO ₂ (CH ₂) ₂ OMe	SO ₂ Me
2-354	SO ₂ Me	F	CF ₃
2-355	SO ₂ Me	NH ₂	CF ₃
2-356	SO ₂ Me	NHEt	Cl
2-357	SMe	SEt	F
2-358	SMe	SMe	F
2-359	Cl	SMe	CF ₃
2-360	Cl	S(O)Me	CF ₃
2-361	Cl	SO ₂ Me	CF ₃
2-362	Cl	SO ₂ Me	SO ₂ Me
2-363	Cl	1H-pyrazol-1-yl	CF ₃
2-364	Cl	O(CH ₂) ₂ F	CF ₃

Table 3: Compounds of the general formula (I) in which A is CY and R is ethyl, and X, Y, and Z are as defined below.



No.	X	Y	Z
3-1	F	H	Cl
3-2	F	H	SO ₂ Me
3-3	F	H	SO ₂ Et

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No.	X	Y	Z
3-4	F	H	CF ₃
3-5	F	H	NO ₂
3-6	Cl	H	Br
3-7	Cl	H	SMe
3-8	Cl	H	SOMe
3-9	Cl	H	SO ₂ Me
3-10	Cl	H	SO ₂ CH ₂ Cl
3-11	Cl	H	SEt
3-12	Cl	H	SO ₂ Et
3-13	Cl	H	CF ₃
3-14	Cl	H	NO ₂
3-15	Cl	H	pyrazol-1-yl
3-16	Cl	H	1H-1,2,4-triazol-1-yl
3-17	Br	H	Cl
3-18	Br	H	Br
3-19	Br	H	SO ₂ Me
3-20	Br	H	SO ₂ Et
3-21	Br	H	CF ₃
3-22	SO ₂ Me	H	Cl
3-23	SO ₂ Me	H	Br
3-24	SO ₂ Me	H	SMe
3-25	SO ₂ Me	H	SOMe
3-26	SO ₂ Me	H	SO ₂ Me
3-27	SO ₂ Me	H	SO ₂ Et
3-28	SO ₂ Me	H	CF ₃
3-29	SO ₂ Et	H	Cl
3-30	SO ₂ Et	H	Br
3-31	SO ₂ Et	H	SMe
3-32	SO ₂ Et	H	SOMe
3-33	SO ₂ Et	H	SO ₂ Me
3-34	SO ₂ Et	H	CF ₃
3-35	NO ₂	H	F
3-36	NO ₂	H	Cl
3-37	NO ₂	H	Br
3-38	NO ₂	H	I
3-39	NO ₂	H	CN
3-40	NO ₂	H	SO ₂ Me
3-41	NO ₂	H	SO ₂ Et
3-42	NO ₂	H	CF ₃
3-43	Me	H	Cl

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No.	X	Y	Z
3-44	Me	H	Br
3-45	Me	H	SMe
3-46	Me	H	SO ₂ Me
3-47	Me	H	SO ₂ CH ₂ Cl
3-48	Me	H	SEt
3-49	Me	H	SO ₂ Et
3-50	Me	H	CF ₃
3-51	CH ₂ SO ₂ Me	H	CF ₃
3-52	Et	H	Cl
3-53	Et	H	Br
3-54	Et	H	SMe
3-55	Et	H	SO ₂ Me
3-56	Et	H	SO ₂ CH ₂ Cl
3-57	Et	H	SEt
3-58	Et	H	SO ₂ Et
3-59	Et	H	CF ₃
3-60	CF ₃	H	Cl
3-61	CF ₃	H	Br
3-62	CF ₃	H	SO ₂ Me
3-63	CF ₃	H	SO ₂ Et
3-64	CF ₃	H	CF ₃
3-65	NO ₂	NH ₂	F
3-66	NO ₂	NHMe	F
3-67	NO ₂	NMe ₂	F
3-68	NO ₂	Me	Cl
3-69	NO ₂	NH ₂	Cl
3-70	NO ₂	NHMe	Cl
3-71	NO ₂	NMe ₂	Cl
3-72	NO ₂	NH ₂	Br
3-73	NO ₂	NHMe	Br
3-74	NO ₂	NMe ₂	Br
3-75	NO ₂	NH ₂	CF ₃
3-76	NO ₂	NMe ₂	CF ₃
3-77	NO ₂	NH ₂	SO ₂ Me
3-78	NO ₂	NH ₂	SO ₂ Et
3-79	NO ₂	NHMe	SO ₂ Me
3-80	NO ₂	NMe ₂	SO ₂ Me
3-81	NO ₂	NMe ₂	SO ₂ Et
3-82	NO ₂	NH ₂	1H-1,2,4-triazol-1-yl

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No.	X	Y	Z
3-83	NO ₂	NHMe	1H-1,2,4-triazol-1-yl
3-84	NO ₂	NMe ₂	1H-1,2,4-triazol-1-yl
3-85	Me	SMe	H
3-86	Me	SOMe	H
3-87	Me	SO ₂ Me	H
3-88	Me	SEt	H
3-89	Me	SOEt	H
3-90	Me	SO ₂ Et	H
3-91	Me	S(CH ₂) ₂ OMe	H
3-92	Me	SO(CH ₂) ₂ OMe	H
3-93	Me	SO ₂ (CH ₂) ₂ OMe	H
3-94	Me	F	F
3-95	Me	F	Cl
3-96	Me	SEt	F
3-97	Me	SOEt	F
3-98	Me	SO ₂ Et	F
3-99	Me	Me	Cl
3-100	Me	F	Cl
3-101	Me	Cl	Cl
3-102	Me	NH ₂	Cl
3-103	Me	NHMe	Cl
3-104	Me	NMe ₂	Cl
3-105	Me	O(CH ₂) ₂ OMe	Cl
3-106	Me	O(CH ₂) ₃ OMe	Cl
3-107	Me	O(CH ₂) ₄ OMe	Cl
3-108	Me	OCH ₂ CONMe ₂	Cl
3-109	Me	O(CH ₂) ₂ -CONMe ₂	Cl
3-110	Me	O(CH ₂) ₂ -NH(CO)NMe ₂	Cl
3-111	Me	O(CH ₂) ₂ -NH(CO)NHCO ₂ Et	Cl
3-112	Me	O(CH ₂) ₂ NHCO ₂ Me	Cl
3-113	Me	OCH ₂ NHSO ₂ cPr	Cl
3-114	Me	O(CH ₂)-5-2,4-dimethyl-2,4-dihydro-3H-1,2,4-triazol-3-one	Cl
3-115	Me	O(CH ₂)-3,5-dimethyl-1,2-oxazol-4-yl	Cl
3-116	Me	SMe	Cl

No.	X	Y	Z
3-117	Me	SOMe	Cl
3-118	Me	SO ₂ Me	Cl
3-119	Me	SEt	Cl
3-120	Me	SOEt	Cl
3-121	Me	SO ₂ Et	Cl
3-122	Me	S(CH ₂) ₂ OMe	Cl
3-123	Me	SO(CH ₂) ₂ OMe	Cl
3-124	Me	SO ₂ (CH ₂) ₂ OMe	Cl
3-125	Me	NH ₂	Br
3-126	Me	NHMe	Br
3-127	Me	NMe ₂	Br
3-128	Me	OCH ₂ CONMe ₂	Br
3-129	Me	O(CH ₂)-5-pyrrolidin- 2-one	Br
3-130	Me	SMe	Br
3-131	Me	SOMe	Br
3-132	Me	SO ₂ Me	Br
3-133	Me	SEt	Br
3-134	Me	SOEt	Br
3-135	Me	SO ₂ Et	Br
3-136	Me	SMe	I
3-137	Me	SOMe	I
3-138	Me	SO ₂ Me	I
3-139	Me	SEt	I
3-140	Me	SOEt	I
3-141	Me	SO ₂ Et	I
3-142	Me	Cl	CF ₃
3-143	Me	SMe	CF ₃
3-144	Me	SOMe	CF ₃
3-145	Me	SO ₂ Me	CF ₃
3-146	Me	SEt	CF ₃
3-147	Me	SOEt	CF ₃
3-148	Me	SO ₂ Et	CF ₃
3-149	Me	S(CH ₂) ₂ OMe	CF ₃
3-150	Me	SO(CH ₂) ₂ OMe	CF ₃
3-151	Me	SO ₂ (CH ₂) ₂ OMe	CF ₃
3-152	Me	Me	SO ₂ Me
3-153	Me	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
3-154	Me	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et

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No.	X	Y	Z
3-155	Me	5-cyanomethyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
3-156	Me	5-cyanomethyl- 4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
3-157	Me	NH ₂	SO ₂ Me
3-158	Me	NHMe	SO ₂ Me
3-159	Me	NMe ₂	SO ₂ Me
3-160	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
3-161	Me	pyrazol-1-yl	SO ₂ Me
3-162	Me	OH	SO ₂ Me
3-163	Me	OMe	SO ₂ Me
3-164	Me	OMe	SO ₂ Et
3-165	Me	OEt	SO ₂ Me
3-166	Me	OEt	SO ₂ Et
3-167	Me	OiPr	SO ₂ Me
3-168	Me	OiPr	SO ₂ Et
3-169	Me	O(CH ₂) ₂ OMe	SO ₂ Me
3-170	Me	O(CH ₂) ₂ OMe	SO ₂ Et
3-171	Me	O(CH ₂) ₃ OMe	SO ₂ Me
3-172	Me	O(CH ₂) ₃ OMe	SO ₂ Et
3-173	Me	O(CH ₂) ₄ OMe	SO ₂ Me
3-174	Me	O(CH ₂) ₄ OMe	SO ₂ Et
3-175	Me	O(CH ₂) ₂ NHSO ₂ Me	SO ₂ Me
3-176	Me	O(CH ₂) ₂ NHSO ₂ Me	SO ₂ Et
3-177	Me	OCH ₂ (CO)NMe ₂	SO ₂ Me
3-178	Me	OCH ₂ (CO)NMe ₂	SO ₂ Et
3-179	Me	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
3-180	Me	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
3-181	Me	O(CH ₂) ₂ -O-(3,5-dimethoxypyrimidin-2-yl)	SO ₂ Me
3-182	Me	Cl	SO ₂ Me
3-183	Me	SMe	SO ₂ Me
3-184	Me	SOMe	SO ₂ Me
3-185	Me	SO ₂ Me	SO ₂ Me
3-186	Me	SO ₂ Me	SO ₂ Et
3-187	Me	SEt	SO ₂ Me
3-188	Me	SOEt	SO ₂ Me
3-189	Me	SO ₂ Et	SO ₂ Me

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No.	X	Y	Z
3-190	Me	S(CH ₂) ₂ OMe	SO ₂ Me
3-191	Me	SO(CH ₂) ₂ OMe	SO ₂ Me
3-192	Me	SO ₂ (CH ₂) ₂ OMe	SO ₂ Me
3-193	CH ₂ SMe	OMe	SO ₂ Me
3-194	CH ₂ OMe	OMe	SO ₂ Me
3-195	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₂ OEt	SO ₂ Me
3-196	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₃ OEt	SO ₂ Me
3-197	CH ₂ O(CH ₂) ₃ OMe	OMe	SO ₂ Me
3-198	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₂ OMe	SO ₂ Me
3-199	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₃ OMe	SO ₂ Me
3-200	Et	SMe	Cl
3-201	Et	SO ₂ Me	Cl
3-202	Et	SMe	CF ₃
3-203	Et	SO ₂ Me	CF ₃
3-204	Et	F	SO ₂ Me
3-205	Et	NH(CH ₂) ₂ OMe	SO ₂ Me
3-206	iPr	SO ₂ Me	CF ₃
3-207	cPr	SO ₂ Me	CF ₃
3-208	CF ₃	O(CH ₂) ₂ OMe	F
3-209	CF ₃	O(CH ₂) ₃ OMe	F
3-210	CF ₃	OCH ₂ CONMe ₂	F
3-211	CF ₃	[1,4]dioxan-2-yl- methoxy	F
3-212	CF ₃	O(CH ₂) ₂ OMe	Cl
3-213	CF ₃	O(CH ₂) ₃ OMe	Cl
3-214	CF ₃	OCH ₂ CONMe ₂	Cl
3-215	CF ₃	[1,4]dioxan-2-yl- methoxy	Cl
3-216	CF ₃	O(CH ₂) ₂ OMe	Br
3-217	CF ₃	O(CH ₂) ₃ OMe	Br
3-218	CF ₃	OCH ₂ CONMe ₂	Br
3-219	CF ₃	[1,4]dioxan-2-yl- methoxy	Br
3-220	CF ₃	O(CH ₂) ₂ OMe	I
3-221	CF ₃	O(CH ₂) ₃ OMe	I
3-222	CF ₃	OCH ₂ CONMe ₂	I
3-223	CF ₃	[1,4]dioxan-2-yl- methoxy	I

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No.	X	Y	Z
3-224	CF ₃	F	SO ₂ Me
3-225	CF ₃	F	SO ₂ Et
3-226	CF ₃	O(CH ₂) ₂ OMe	SO ₂ Me
3-227	CF ₃	O(CH ₂) ₂ OMe	SO ₂ Et
3-228	CF ₃	O(CH ₂) ₃ OMe	SO ₂ Me
3-229	CF ₃	O(CH ₂) ₃ OMe	SO ₂ Et
3-230	CF ₃	OCH ₂ CONMe ₂	SO ₂ Me
3-231	CF ₃	OCH ₂ CONMe ₂	SO ₂ Et
3-232	CF ₃	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
3-233	CF ₃	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
3-234	F	SMe	CF ₃
3-235	F	SOMe	CF ₃
3-236	Cl	Me	Cl
3-237	Cl	OCH ₂ CHCH ₂	Cl
3-238	Cl	OCH ₂ CHF ₂	Cl
3-239	Cl	O(CH ₂) ₂ OMe	Cl
3-240	Cl	OCH ₂ (CO)NMe ₂	Cl
3-241	Cl	O(CH ₂)-5-pyrrolidin-2-one	Cl
3-242	Cl	SMe	Cl
3-243	Cl	SOMe	Cl
3-244	Cl	SO ₂ Me	Cl
3-245	Cl	F	SMe
3-246	Cl	Cl	SO ₂ Me
3-247	Cl	COOMe	SO ₂ Me
3-248	Cl	CONMe ₂	SO ₂ Me
3-249	Cl	CONMe(OMe)	SO ₂ Me
3-250	Cl	CH ₂ OMe	SO ₂ Me
3-251	Cl	CH ₂ OMe	SO ₂ Et
3-252	Cl	CH ₂ OEt	SO ₂ Me
3-253	Cl	CH ₂ OEt	SO ₂ Et
3-254	Cl	CH ₂ OCH ₂ CHF ₂	SO ₂ Me
3-255	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
3-256	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Et
3-257	Cl	CH ₂ OCH ₂ CF ₂ CHF ₂	SO ₂ Me
3-258	Cl	CH ₂ OcPentyl	SO ₂ Me
3-259	Cl	CH ₂ PO(OMe) ₂	SO ₂ Me
3-260	Cl	4,5-dihydro-1,2-oxazol-3-yl	SMe

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No.	X	Y	Z
3-261	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
3-262	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
3-263	Cl	5-cyanomethyl- 4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
3-264	Cl	5-cyanomethyl- 4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
3-265	Cl	5-(methoxymethyl)-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
3-266	Cl	5-(methoxymethyl)-5-methyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
3-267	Cl	CH ₂ O-tetrahydrofuran-3-yl	SO ₂ Me
3-268	Cl	CH ₂ O-tetrahydrofuran-3-yl	SO ₂ Et
3-269	Cl	CH ₂ OCH ₂ -tetrahydrofuran-2-yl	SO ₂ Me
3-270	Cl	CH ₂ OCH ₂ -tetrahydrofuran-2-yl	SO ₂ Et
3-271	Cl	CH ₂ OCH ₂ -tetrahydrofuran-3-yl	SO ₂ Me
3-272	Cl	CH ₂ OCH ₂ -tetrahydrofuran-3-yl	SO ₂ Et
3-273	Cl	OMe	SO ₂ Me
3-274	Cl	OMe	SO ₂ Et
3-275	Cl	OEt	SO ₂ Me
3-276	Cl	OEt	SO ₂ Et
3-277	Cl	OiPr	SO ₂ Me
3-278	Cl	OiPr	SO ₂ Et
3-279	Cl	O(CH ₂) ₂ OMe	SO ₂ Me
3-280	Cl	O(CH ₂) ₄ OMe	SO ₂ Me
3-281	Cl	O(CH ₂) ₄ OMe	SO ₂ Et
3-282	Cl	O(CH ₂) ₃ OMe	SO ₂ Me
3-283	Cl	O(CH ₂) ₃ OMe	SO ₂ Et
3-284	Cl	O(CH ₂) ₂ OMe	SO ₂ Me
3-285	Cl	O(CH ₂) ₂ OMe	SO ₂ Et
3-286	Cl	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
3-287	Cl	[1,4]dioxan-2-yl-methoxy	SO ₂ Et

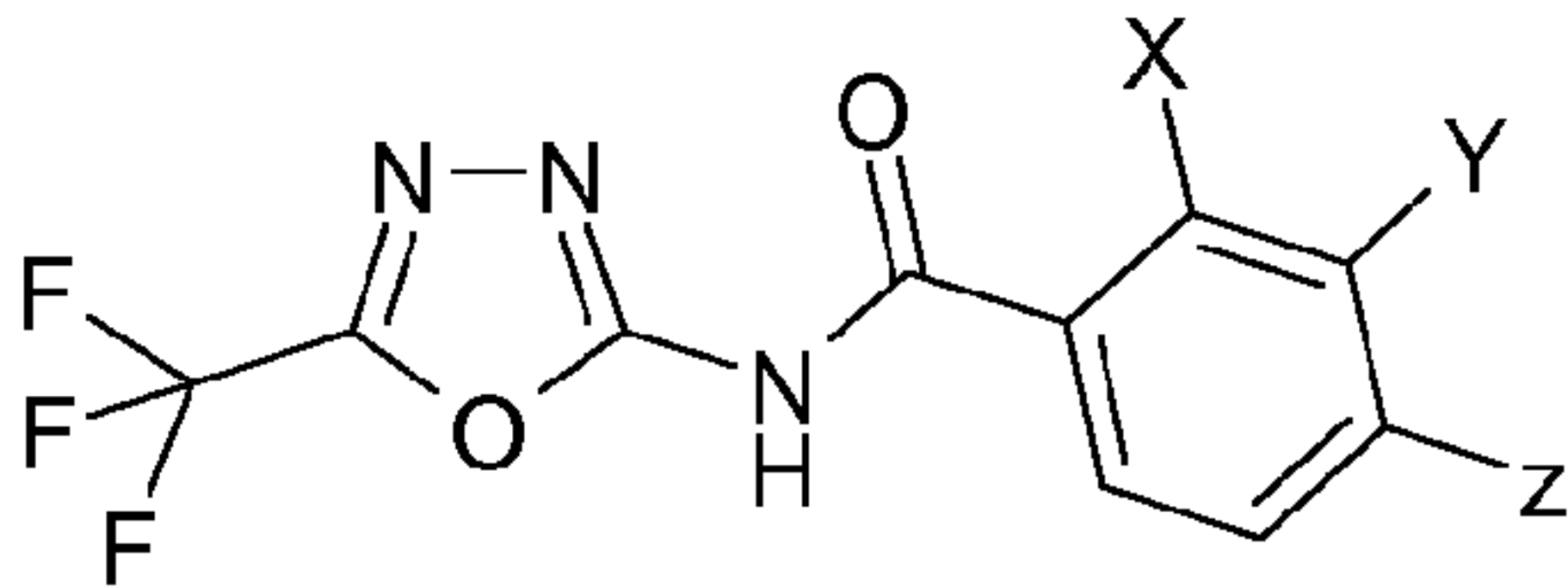
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No.	X	Y	Z
3-288	Cl	OCH ₂ (CO)NMe ₂	SO ₂ Me
3-289	Cl	OCH ₂ (CO)NMe ₂	SO ₂ Et
3-290	Cl	SMe	SO ₂ Me
3-291	Cl	SOMe	SO ₂ Me
3-292	Br	OMe	Br
3-293	Br	O(CH ₂) ₂ OMe	Br
3-294	Br	O(CH ₂) ₂ OMe	SO ₂ Me
3-295	Br	O(CH ₂) ₂ OMe	SO ₂ Et
3-296	Br	O(CH ₂) ₃ OMe	SO ₂ Me
3-297	Br	O(CH ₂) ₃ OMe	SO ₂ Et
3-298	Br	O(CH ₂) ₄ OMe	SO ₂ Me
3-299	Br	O(CH ₂) ₄ OMe	SO ₂ Et
3-300	Br	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
3-301	Br	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
3-302	I	O(CH ₂) ₂ OMe	SO ₂ Me
3-303	I	O(CH ₂) ₂ OMe	SO ₂ Et
3-304	I	O(CH ₂) ₃ OMe	SO ₂ Me
3-305	I	O(CH ₂) ₃ OMe	SO ₂ Et
3-306	I	O(CH ₂) ₄ OMe	SO ₂ Me
3-307	I	O(CH ₂) ₄ OMe	SO ₂ Et
3-308	I	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
3-309	I	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
3-310	OMe	SMe	CF ₃
3-311	OMe	SOMe	CF ₃
3-312	OMe	SO ₂ Me	CF ₃
3-313	OMe	SOEt	CF ₃
3-314	OMe	SO ₂ Et	CF ₃
3-315	OMe	S(CH ₂) ₂ OMe	CF ₃
3-316	OMe	SO(CH ₂) ₂ OMe	CF ₃
3-317	OMe	SO ₂ (CH ₂) ₂ OMe	CF ₃
3-318	OMe	SMe	Cl
3-319	OMe	SOMe	Cl
3-320	OMe	SO ₂ Me	Cl
3-321	OMe	SEt	Cl
3-322	OMe	SOEt	Cl
3-323	OMe	SO ₂ Et	Cl
3-324	OMe	S(CH ₂) ₂ OMe	Cl
3-325	OMe	SO(CH ₂) ₂ OMe	Cl

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No.	X	Y	Z
3-326	OMe	SO ₂ (CH ₂) ₂ OMe	Cl
3-327	OCH ₂ c-Pr	SMe	CF ₃
3-328	OCH ₂ c-Pr	SOMe	CF ₃
3-329	OCH ₂ c-Pr	SO ₂ Me	CF ₃
3-330	OCH ₂ c-Pr	SEt	CF ₃
3-331	OCH ₂ c-Pr	SOEt	CF ₃
3-332	OCH ₂ c-Pr	SO ₂ Et	CF ₃
3-333	OCH ₂ c-Pr	S(CH ₂) ₂ OMe	CF ₃
3-334	OCH ₂ c-Pr	SO(CH ₂) ₂ OMe	CF ₃
3-335	OCH ₂ c-Pr	SO ₂ (CH ₂) ₂ OMe	CF ₃
3-336	OCH ₂ c-Pr	SMe	Cl
3-337	OCH ₂ c-Pr	SOMe	Cl
3-338	OCH ₂ c-Pr	SO ₂ Me	Cl
3-339	OCH ₂ c-Pr	SEt	Cl
3-340	OCH ₂ c-Pr	SOEt	Cl
3-341	OCH ₂ c-Pr	SO ₂ Et	Cl
3-342	OCH ₂ c-Pr	S(CH ₂) ₂ OMe	Cl
3-343	OCH ₂ c-Pr	SO(CH ₂) ₂ OMe	Cl
3-344	OCH ₂ c-Pr	SO ₂ (CH ₂) ₂ OMe	Cl
3-345	OCH ₂ c-Pr	SMe	SO ₂ Me
3-346	OCH ₂ c-Pr	SOMe	SO ₂ Me
3-347	OCH ₂ c-Pr	SO ₂ Me	SO ₂ Me
3-348	OCH ₂ c-Pr	SEt	SO ₂ Me
3-349	OCH ₂ c-Pr	SOEt	SO ₂ Me
3-350	OCH ₂ c-Pr	SO ₂ Et	SO ₂ Me
3-351	OCH ₂ c-Pr	S(CH ₂) ₂ OMe	SO ₂ Me
3-352	OCH ₂ c-Pr	SO(CH ₂) ₂ OMe	SO ₂ Me
3-353	OCH ₂ c-Pr	SO ₂ (CH ₂) ₂ OMe	SO ₂ Me
3-354	SO ₂ Me	F	CF ₃
3-355	SO ₂ Me	NH ₂	CF ₃
3-356	SO ₂ Me	NHEt	Cl
3-357	SMe	SEt	F
3-358	SMe	SMe	F
3-359	Cl	SMe	CF ₃
3-360	Cl	S(O)Me	CF ₃
3-361	Cl	SO ₂ Me	CF ₃
3-362	Cl	SO ₂ Me	SO ₂ Me

Table 4: Compounds of the general formula (I) in which A is CY and R is trifluoromethyl, and X, Y, and Z are as defined below.



No.	X	Y	Z
4-1	F	H	Cl
4-2	F	H	SO ₂ Me
4-3	F	H	SO ₂ Et
4-4	F	H	CF ₃
4-5	F	H	NO ₂
4-6	Cl	H	Br
4-7	Cl	H	SMe
4-8	Cl	H	SOMe
4-9	Cl	H	SO ₂ Me
4-10	Cl	H	SO ₂ CH ₂ Cl
4-11	Cl	H	SEt
4-12	Cl	H	SO ₂ Et
4-13	Cl	H	CF ₃
4-14	Cl	H	NO ₂
4-15	Cl	H	pyrazol-1-yl
4-16	Cl	H	1H-1,2,4-triazol-1-yl
4-17	Br	H	Cl
4-18	Br	H	Br
4-19	Br	H	SO ₂ Me
4-20	Br	H	SO ₂ Et
4-21	Br	H	CF ₃
4-22	SO ₂ Me	H	Cl
4-23	SO ₂ Me	H	Br
4-24	SO ₂ Me	H	SMe
4-25	SO ₂ Me	H	SOMe
4-26	SO ₂ Me	H	SO ₂ Me
4-27	SO ₂ Me	H	SO ₂ Et
4-28	SO ₂ Me	H	CF ₃
4-29	SO ₂ Et	H	Cl
4-30	SO ₂ Et	H	Br
4-31	SO ₂ Et	H	SMe
4-32	SO ₂ Et	H	SOMe

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No.	X	Y	Z
4-33	SO ₂ Et	H	SO ₂ Me
4-34	SO ₂ Et	H	CF ₃
4-35	NO ₂	H	F
4-36	NO ₂	H	Cl
4-37	NO ₂	H	Br
4-38	NO ₂	H	I
4-39	NO ₂	H	CN
4-40	NO ₂	H	SO ₂ Me
4-41	NO ₂	H	SO ₂ Et
4-42	NO ₂	H	CF ₃
4-43	Me	H	Cl
4-44	Me	H	Br
4-45	Me	H	SMe
4-46	Me	H	SO ₂ Me
4-47	Me	H	SO ₂ CH ₂ Cl
4-48	Me	H	SEt
4-49	Me	H	SO ₂ Et
4-50	Me	H	CF ₃
4-51	CH ₂ SO ₂ Me	H	CF ₃
4-52	Et	H	Cl
4-53	Et	H	Br
4-54	Et	H	SMe
4-55	Et	H	SO ₂ Me
4-56	Et	H	SO ₂ CH ₂ Cl
4-57	Et	H	SEt
4-58	Et	H	SO ₂ Et
4-59	Et	H	CF ₃
4-60	CF ₃	H	Cl
4-61	CF ₃	H	Br
4-62	CF ₃	H	SO ₂ Me
4-63	CF ₃	H	SO ₂ Et
4-64	CF ₃	H	CF ₃
4-65	NO ₂	NH ₂	F
4-66	NO ₂	NHMe	F
4-67	NO ₂	NMe ₂	F
4-68	NO ₂	Me	Cl
4-69	NO ₂	NH ₂	Cl
4-70	NO ₂	NHMe	Cl
4-71	NO ₂	NMe ₂	Cl
4-72	NO ₂	NH ₂	Br
4-73	NO ₂	NHMe	Br

53

No.	X	Y	Z
4-74	NO ₂	NMe ₂	Br
4-75	NO ₂	NH ₂	CF ₃
4-76	NO ₂	NMe ₂	CF ₃
4-77	NO ₂	NH ₂	SO ₂ Me
4-78	NO ₂	NH ₂	SO ₂ Et
4-79	NO ₂	NHMe	SO ₂ Me
4-80	NO ₂	NMe ₂	SO ₂ Me
4-81	NO ₂	NMe ₂	SO ₂ Et
4-82	NO ₂	NH ₂	1H-1,2,4-triazol-1-yl
4-83	NO ₂	NHMe	1H-1,2,4-triazol-1-yl
4-84	NO ₂	NMe ₂	1H-1,2,4-triazol-1-yl
4-85	Me	SMe	H
4-86	Me	SOMe	H
4-87	Me	SO ₂ Me	H
4-88	Me	SEt	H
4-89	Me	SOEt	H
4-90	Me	SO ₂ Et	H
4-91	Me	S(CH ₂) ₂ OMe	H
4-92	Me	SO(CH ₂) ₂ OMe	H
4-93	Me	SO ₂ (CH ₂) ₂ OMe	H
4-94	Me	F	F
4-95	Me	F	Cl
4-96	Me	SEt	F
4-97	Me	SOEt	F
4-98	Me	SO ₂ Et	F
4-99	Me	Me	Cl
4-100	Me	F	Cl
4-101	Me	Cl	Cl
4-102	Me	NH ₂	Cl
4-103	Me	NHMe	Cl
4-104	Me	NMe ₂	Cl
4-105	Me	O(CH ₂) ₂ OMe	Cl
4-106	Me	O(CH ₂) ₃ OMe	Cl
4-107	Me	O(CH ₂) ₄ OMe	Cl
4-108	Me	OCH ₂ CONMe ₂	Cl
4-109	Me	O(CH ₂) ₂ -CO-NMe ₂	Cl
4-110	Me	O(CH ₂) ₂ -NH(CO)NMe ₂	Cl
4-111	Me	O(CH ₂) ₂ -NH(CO)NHCO ₂ Et	Cl

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No.	X	Y	Z
4-112	Me	O(CH ₂) ₂ -NHCO ₂ Me	Cl
4-113	Me	OCH ₂ -NHSO ₂ cPr	Cl
4-114	Me	O(CH ₂)-5-2,4-dimethyl- 2,4-dihydro-3H-1,2,4- triazol-3-one	Cl
4-115	Me	O(CH ₂)-3,5-dimethyl- 1,2-oxazol-4-yl	Cl
4-116	Me	SMe	Cl
4-117	Me	SOMe	Cl
4-118	Me	SO ₂ Me	Cl
4-119	Me	SEt	Cl
4-120	Me	SOEt	Cl
4-121	Me	SO ₂ Et	Cl
4-122	Me	S(CH ₂) ₂ OMe	Cl
4-123	Me	SO(CH ₂) ₂ OMe	Cl
4-124	Me	SO ₂ (CH ₂) ₂ OMe	Cl
4-125	Me	NH ₂	Br
4-126	Me	NHMe	Br
4-127	Me	NMe ₂	Br
4-128	Me	OCH ₂ (CO)NMe ₂	Br
4-129	Me	O(CH ₂)-5-pyrrolidin-2- one	Br
4-130	Me	SMe	Br
4-131	Me	SOMe	Br
4-132	Me	SO ₂ Me	Br
4-133	Me	SEt	Br
4-134	Me	SOEt	Br
4-135	Me	SO ₂ Et	Br
4-136	Me	SMe	I
4-137	Me	SOMe	I
4-138	Me	SO ₂ Me	I
4-139	Me	SEt	I
4-140	Me	SOEt	I
4-141	Me	SO ₂ Et	I
4-142	Me	Cl	CF ₃
4-143	Me	SMe	CF ₃
4-144	Me	SOMe	CF ₃
4-145	Me	SO ₂ Me	CF ₃
4-146	Me	SEt	CF ₃
4-147	Me	SOEt	CF ₃
4-148	Me	SO ₂ Et	CF ₃
4-149	Me	S(CH ₂) ₂ OMe	CF ₃

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No.	X	Y	Z
4-150	Me	SO(CH ₂) ₂ OMe	CF ₃
4-151	Me	SO ₂ (CH ₂) ₂ OMe	CF ₃
4-152	Me	Me	SO ₂ Me
4-153	Me	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
4-154	Me	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
4-155	Me	5-cyanomethyl- 4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
4-156	Me	5-cyanomethyl- 4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
4-157	Me	NH ₂	SO ₂ Me
4-158	Me	NHMe	SO ₂ Me
4-159	Me	NMe ₂	SO ₂ Me
4-160	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
4-161	Me	pyrazol-1-yl	SO ₂ Me
4-162	Me	OH	SO ₂ Me
4-163	Me	OMe	SO ₂ Me
4-164	Me	OMe	SO ₂ Et
4-165	Me	OEt	SO ₂ Me
4-166	Me	OEt	SO ₂ Et
4-167	Me	OiPr	SO ₂ Me
4-168	Me	OiPr	SO ₂ Et
4-169	Me	O(CH ₂) ₂ OMe	SO ₂ Me
4-170	Me	O(CH ₂) ₂ OMe	SO ₂ Et
4-171	Me	O(CH ₂) ₃ OMe	SO ₂ Me
4-172	Me	O(CH ₂) ₃ OMe	SO ₂ Et
4-173	Me	O(CH ₂) ₄ OMe	SO ₂ Me
4-174	Me	O(CH ₂) ₄ OMe	SO ₂ Et
4-175	Me	O(CH ₂) ₂ NHSO ₂ Me	SO ₂ Me
4-176	Me	O(CH ₂) ₂ NHSO ₂ Me	SO ₂ Et
4-177	Me	OCH ₂ (CO)NMe ₂	SO ₂ Me
4-178	Me	OCH ₂ (CO)NMe ₂	SO ₂ Et
4-179	Me	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
4-180	Me	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
4-181	Me	O(CH ₂) ₂ -O-(3,5-dimethoxypyrimidin-2-yl)	SO ₂ Me
4-182	Me	Cl	SO ₂ Me
4-183	Me	SMe	SO ₂ Me
4-184	Me	SOMe	SO ₂ Me
4-185	Me	SO ₂ Me	SO ₂ Me

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No.	X	Y	Z
4-186	Me	SO ₂ Me	SO ₂ Et
4-187	Me	SEt	SO ₂ Me
4-188	Me	SOEt	SO ₂ Me
4-189	Me	SO ₂ Et	SO ₂ Me
4-190	Me	S(CH ₂) ₂ OMe	SO ₂ Me
4-191	Me	SO(CH ₂) ₂ OMe	SO ₂ Me
4-192	Me	SO ₂ (CH ₂) ₂ OMe	SO ₂ Me
4-193	CH ₂ SMe	OMe	SO ₂ Me
4-194	CH ₂ OMe	OMe	SO ₂ Me
4-195	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₂ OEt	SO ₂ Me
4-196	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₃ OEt	SO ₂ Me
4-197	CH ₂ O(CH ₂) ₃ OMe	OMe	SO ₂ Me
4-198	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₂ OMe	SO ₂ Me
4-199	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₃ OMe	SO ₂ Me
4-200	Et	SMe	Cl
4-201	Et	SO ₂ Me	Cl
4-202	Et	SMe	CF ₃
4-203	Et	SO ₂ Me	CF ₃
4-204	Et	F	SO ₂ Me
4-205	Et	NH(CH ₂) ₂ OMe	SO ₂ Me
4-206	iPr	SO ₂ Me	CF ₃
4-207	cPr	SO ₂ Me	CF ₃
4-208	CF ₃	O(CH ₂) ₂ OMe	F
4-209	CF ₃	O(CH ₂) ₃ OMe	F
4-210	CF ₃	OCH ₂ CONMe ₂	F
4-211	CF ₃	[1,4]dioxan-2-yl-methoxy	F
4-212	CF ₃	O(CH ₂) ₂ OMe	Cl
4-213	CF ₃	O(CH ₂) ₃ OMe	Cl
4-214	CF ₃	OCH ₂ CONMe ₂	Cl
4-215	CF ₃	[1,4]dioxan-2-yl-methoxy	Cl
4-216	CF ₃	O(CH ₂) ₂ OMe	Br
4-217	CF ₃	O(CH ₂) ₃ OMe	Br
4-218	CF ₃	OCH ₂ CONMe ₂	Br
4-219	CF ₃	[1,4]dioxan-2-yl-methoxy	Br
4-220	CF ₃	O(CH ₂) ₂ OMe	I

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No.	X	Y	Z
4-221	CF ₃	O(CH ₂) ₃ OMe	I
4-222	CF ₃	OCH ₂ CONMe ₂	I
4-223	CF ₃	[1,4]dioxan-2-yl-methoxy	I
4-224	CF ₃	F	SO ₂ Me
4-225	CF ₃	F	SO ₂ Et
4-226	CF ₃	O(CH ₂) ₂ OMe	SO ₂ Me
4-227	CF ₃	O(CH ₂) ₂ OMe	SO ₂ Et
4-228	CF ₃	O(CH ₂) ₃ OMe	SO ₂ Me
4-229	CF ₃	O(CH ₂) ₃ OMe	SO ₂ Et
4-230	CF ₃	OCH ₂ CONMe ₂	SO ₂ Me
4-231	CF ₃	OCH ₂ CONMe ₂	SO ₂ Et
4-232	CF ₃	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
4-233	CF ₃	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
4-234	F	SMe	CF ₃
4-235	F	SOMe	CF ₃
4-236	Cl	Me	Cl
4-237	Cl	OCH ₂ CHCH ₂	Cl
4-238	Cl	OCH ₂ CHF ₂	Cl
4-239	Cl	O(CH ₂) ₂ OMe	Cl
4-240	Cl	OCH ₂ CONMe ₂	Cl
4-241	Cl	O(CH ₂)-5-pyrrolidin-2-one	Cl
4-242	Cl	SMe	Cl
4-243	Cl	SOMe	Cl
4-244	Cl	SO ₂ Me	Cl
4-245	Cl	F	SMe
4-246	Cl	Cl	SO ₂ Me
4-247	Cl	COOMe	SO ₂ Me
4-248	Cl	CONMe ₂	SO ₂ Me
4-249	Cl	CONMe(OMe)	SO ₂ Me
4-250	Cl	CH ₂ OMe	SO ₂ Me
4-251	Cl	CH ₂ OMe	SO ₂ Et
4-252	Cl	CH ₂ OEt	SO ₂ Me
4-253	Cl	CH ₂ OEt	SO ₂ Et
4-254	Cl	CH ₂ OCH ₂ CHF ₂	SO ₂ Me
4-255	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
4-256	Cl	CH ₂ OCH ₂ CF ₃	SMe
4-257	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Et

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No.	X	Y	Z
4-258	Cl	CH ₂ OCH ₂ CF ₂ CHF ₂	SO ₂ Me
4-259	Cl	CH ₂ OcPentyl	SO ₂ Me
4-260	Cl	CH ₂ PO(OMe) ₂	SO ₂ Me
4-261	Cl	4,5-dihydro-1,2-oxazol-3-yl	SMe
4-262	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
4-263	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
4-264	Cl	5-cyanomethyl- 4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
4-265	Cl	5-cyanomethyl- 4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
4-266	Cl	5-(methoxymethyl)-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
4-267	Cl	5-(methoxymethyl)-5-methyl- 4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
4-268	Cl	CH ₂ O-tetrahydrofuran-3-yl	SO ₂ Me
4-269	Cl	CH ₂ O-tetrahydrofuran-3-yl	SO ₂ Et
4-270	Cl	CH ₂ OCH ₂ -tetrahydrofuran-2-yl	SO ₂ Me
4-271	Cl	CH ₂ OCH ₂ -tetrahydrofuran-2-yl	SO ₂ Et
4-272	Cl	CH ₂ OCH ₂ -tetrahydrofuran-3-yl	SO ₂ Me
4-273	Cl	CH ₂ OCH ₂ -tetrahydrofuran-3-yl	SO ₂ Et
4-274	Cl	OMe	SO ₂ Me
4-275	Cl	OMe	SO ₂ Et
4-276	Cl	OEt	SO ₂ Me
4-277	Cl	OEt	SO ₂ Et
4-278	Cl	OiPr	SO ₂ Me
4-279	Cl	OiPr	SO ₂ Et
4-280	Cl	O(CH ₂) ₂ OMe	SO ₂ Me
4-281	Cl	O(CH ₂) ₄ OMe	SO ₂ Me
4-282	Cl	O(CH ₂) ₄ OMe	SO ₂ Et
4-283	Cl	O(CH ₂) ₃ OMe	SO ₂ Me
4-284	Cl	O(CH ₂) ₃ OMe	SO ₂ Et
4-285	Cl	O(CH ₂) ₂ OMe	SO ₂ Me
4-286	Cl	O(CH ₂) ₂ OMe	SO ₂ Et
4-287	Cl	[1,4]dioxan-2-yl-methoxy	SO ₂ Me

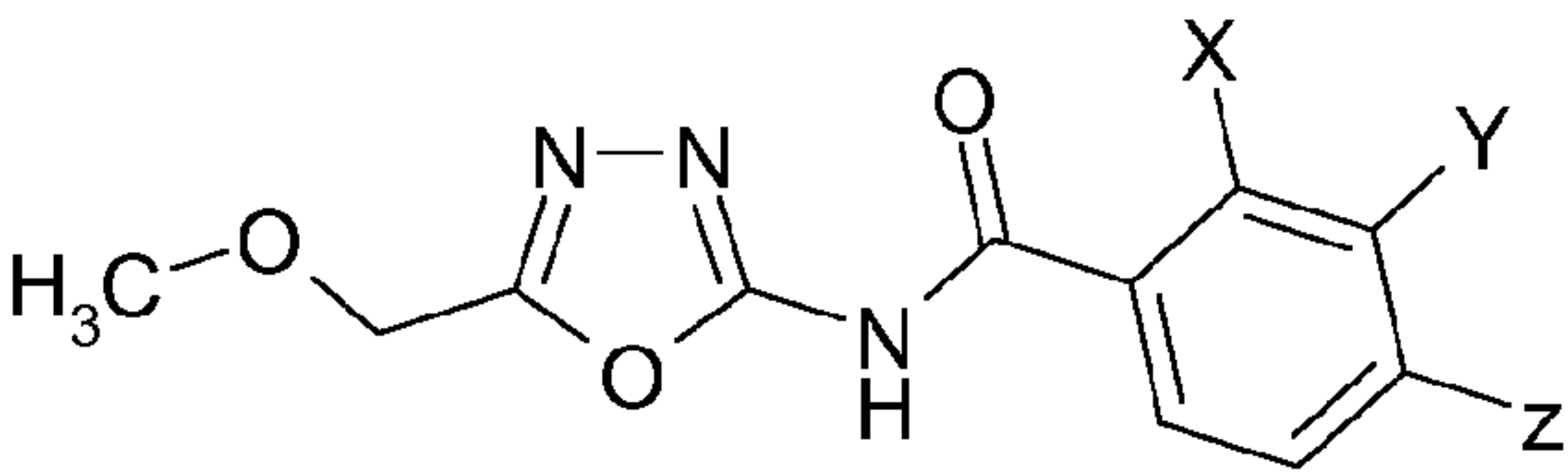
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No.	X	Y	Z
4-288	Cl	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
4-289	Cl	OCH ₂ (CO)NMe ₂	SO ₂ Me
4-290	Cl	OCH ₂ (CO)NMe ₂	SO ₂ Et
4-291	Cl	SMe	SO ₂ Me
4-292	Cl	SOMe	SO ₂ Me
4-293	Br	OMe	Br
4-294	Br	O(CH ₂) ₂ OMe	Br
4-295	Br	O(CH ₂) ₂ OMe	SO ₂ Me
4-296	Br	O(CH ₂) ₂ OMe	SO ₂ Et
4-297	Br	O(CH ₂) ₃ OMe	SO ₂ Me
4-298	Br	O(CH ₂) ₃ OMe	SO ₂ Et
4-299	Br	O(CH ₂) ₄ OMe	SO ₂ Me
4-300	Br	O(CH ₂) ₄ OMe	SO ₂ Et
4-301	Br	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
4-302	Br	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
4-303	I	O(CH ₂) ₂ OMe	SO ₂ Me
4-304	I	O(CH ₂) ₂ OMe	SO ₂ Et
4-305	I	O(CH ₂) ₃ OMe	SO ₂ Me
4-306	I	O(CH ₂) ₃ OMe	SO ₂ Et
4-307	I	O(CH ₂) ₄ OMe	SO ₂ Me
4-308	I	O(CH ₂) ₄ OMe	SO ₂ Et
4-309	I	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
4-310	I	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
4-311	OMe	SMe	CF ₃
4-312	OMe	SOMe	CF ₃
4-313	OMe	SO ₂ Me	CF ₃
4-314	OMe	SOEt	CF ₃
4-315	OMe	SO ₂ Et	CF ₃
4-316	OMe	S(CH ₂) ₂ OMe	CF ₃
4-317	OMe	SO(CH ₂) ₂ OMe	CF ₃
4-318	OMe	SO ₂ (CH ₂) ₂ OMe	CF ₃
4-319	OMe	SMe	Cl
4-320	OMe	SOMe	Cl
4-321	OMe	SO ₂ Me	Cl
4-322	OMe	SEt	Cl
4-323	OMe	SOEt	Cl
4-324	OMe	SO ₂ Et	Cl

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No.	X	Y	Z
4-325	OMe	S(CH ₂) ₂ OMe	Cl
4-326	OMe	SO(CH ₂) ₂ OMe	Cl
4-327	OMe	SO ₂ (CH ₂) ₂ OMe	Cl
4-328	OCH ₂ c-Pr	SMe	CF ₃
4-329	OCH ₂ c-Pr	SOMe	CF ₃
4-330	OCH ₂ c-Pr	SO ₂ Me	CF ₃
4-331	OCH ₂ c-Pr	SEt	CF ₃
4-332	OCH ₂ c-Pr	SOEt	CF ₃
4-333	OCH ₂ c-Pr	SO ₂ Et	CF ₃
4-334	OCH ₂ c-Pr	S(CH ₂) ₂ OMe	CF ₃
4-335	OCH ₂ c-Pr	SO(CH ₂) ₂ OMe	CF ₃
4-336	OCH ₂ c-Pr	SO ₂ (CH ₂) ₂ OMe	CF ₃
4-337	OCH ₂ c-Pr	SMe	Cl
4-338	OCH ₂ c-Pr	SOMe	Cl
4-339	OCH ₂ c-Pr	SO ₂ Me	Cl
4-340	OCH ₂ c-Pr	SEt	Cl
4-341	OCH ₂ c-Pr	SOEt	Cl
4-342	OCH ₂ c-Pr	SO ₂ Et	Cl
4-343	OCH ₂ c-Pr	S(CH ₂) ₂ OMe	Cl
4-344	OCH ₂ c-Pr	SO(CH ₂) ₂ OMe	Cl
4-345	OCH ₂ c-Pr	SO ₂ (CH ₂) ₂ OMe	Cl
4-346	OCH ₂ c-Pr	SMe	SO ₂ Me
4-347	OCH ₂ c-Pr	SOMe	SO ₂ Me
4-348	OCH ₂ c-Pr	SO ₂ Me	SO ₂ Me
4-349	OCH ₂ c-Pr	SEt	SO ₂ Me
4-350	OCH ₂ c-Pr	SOEt	SO ₂ Me
4-351	OCH ₂ c-Pr	SO ₂ Et	SO ₂ Me
4-352	OCH ₂ c-Pr	S(CH ₂) ₂ OMe	SO ₂ Me
4-353	OCH ₂ c-Pr	SO(CH ₂) ₂ OMe	SO ₂ Me
4-354	OCH ₂ c-Pr	SO ₂ (CH ₂) ₂ OMe	SO ₂ Me
4-355	SO ₂ Me	F	CF ₃
4-356	SO ₂ Me	NH ₂	CF ₃
4-357	SO ₂ Me	NHEt	Cl
4-358	SMe	SEt	F
4-359	SMe	SMe	F
4-360	Cl	SMe	CF ₃
4-361	Cl	S(O)Me	CF ₃
4-362	Cl	SO ₂ Me	CF ₃
4-363	Cl	SO ₂ Me	SO ₂ Me

Table 5: Compounds of the general formula (I) in which A is CY and R is CH₂OMe, and X, Y, and Z are as defined below.



5

No.	X	Y	Z
5-1	F	H	Cl
5-2	F	H	SO ₂ Me
5-3	F	H	SO ₂ Et
5-4	F	H	CF ₃
5-5	F	H	NO ₂
5-6	Cl	H	Br
5-7	Cl	H	SMe
5-8	Cl	H	SOMe
5-9	Cl	H	SO ₂ Me
5-10	Cl	H	SO ₂ CH ₂ Cl
5-11	Cl	H	SEt
5-12	Cl	H	SO ₂ Et
5-13	Cl	H	CF ₃
5-14	Cl	H	NO ₂
5-15	Cl	H	pyrazol-1-yl
5-16	Cl	H	1H-1,2,4-triazol-1-yl
5-17	Br	H	Cl
5-18	Br	H	Br
5-19	Br	H	SO ₂ Me
5-20	Br	H	SO ₂ Et
5-21	Br	H	CF ₃
5-22	SO ₂ Me	H	Cl
5-23	SO ₂ Me	H	Br
5-24	SO ₂ Me	H	SMe
5-25	SO ₂ Me	H	SOMe
5-26	SO ₂ Me	H	SO ₂ Me
5-27	SO ₂ Me	H	SO ₂ Et
5-28	SO ₂ Me	H	CF ₃
5-29	SO ₂ Et	H	Cl
5-30	SO ₂ Et	H	Br
5-31	SO ₂ Et	H	SMe
5-32	SO ₂ Et	H	SOMe

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No.	X	Y	Z
5-33	SO ₂ Et	H	SO ₂ Me
5-34	SO ₂ Et	H	CF ₃
5-35	NO ₂	H	F
5-36	NO ₂	H	Cl
5-37	NO ₂	H	Br
5-38	NO ₂	H	I
5-39	NO ₂	H	CN
5-40	NO ₂	H	SO ₂ Me
5-41	NO ₂	H	SO ₂ Et
5-42	NO ₂	H	CF ₃
5-43	Me	H	Cl
5-44	Me	H	Br
5-45	Me	H	SMe
5-46	Me	H	SO ₂ Me
5-47	Me	H	SO ₂ CH ₂ Cl
5-48	Me	H	SEt
5-49	Me	H	SO ₂ Et
5-50	Me	H	CF ₃
5-51	CH ₂ SO ₂ Me	H	CF ₃
5-52	Et	H	Cl
5-53	Et	H	Br
5-54	Et	H	SMe
5-55	Et	H	SO ₂ Me
5-56	Et	H	SO ₂ CH ₂ Cl
5-57	Et	H	SEt
5-58	Et	H	SO ₂ Et
5-59	Et	H	CF ₃
5-60	CF ₃	H	Cl
5-61	CF ₃	H	Br
5-62	CF ₃	H	SO ₂ Me
5-63	CF ₃	H	SO ₂ Et
5-64	CF ₃	H	CF ₃
5-65	NO ₂	NH ₂	F
5-66	NO ₂	NHMe	F
5-67	NO ₂	NMe ₂	F
5-68	NO ₂	Me	Cl
5-69	NO ₂	NH ₂	Cl
5-70	NO ₂	NHMe	Cl
5-71	NO ₂	NMe ₂	Cl
5-72	NO ₂	NH ₂	Br
5-73	NO ₂	NHMe	Br

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No.	X	Y	Z
5-74	NO ₂	NMe ₂	Br
5-75	NO ₂	NH ₂	CF ₃
5-76	NO ₂	NMe ₂	CF ₃
5-77	NO ₂	NH ₂	SO ₂ Me
5-78	NO ₂	NH ₂	SO ₂ Et
5-79	NO ₂	NHMe	SO ₂ Me
5-80	NO ₂	NMe ₂	SO ₂ Me
5-81	NO ₂	NMe ₂	SO ₂ Et
5-82	NO ₂	NH ₂	1H-1,2,4-triazol-1-yl
5-83	NO ₂	NHMe	1H-1,2,4-triazol-1-yl
5-84	NO ₂	NMe ₂	1H-1,2,4-triazol-1-yl
5-85	Me	SMe	H
5-86	Me	SOMe	H
5-87	Me	SO ₂ Me	H
5-88	Me	SEt	H
5-89	Me	SOEt	H
5-90	Me	SO ₂ Et	H
5-91	Me	S(CH ₂) ₂ OMe	H
5-92	Me	SO(CH ₂) ₂ OMe	H
5-93	Me	SO ₂ (CH ₂) ₂ OMe	H
5-94	Me	F	F
5-95	Me	F	Cl
5-96	Me	SEt	F
5-97	Me	SOEt	F
5-98	Me	SO ₂ Et	F
5-99	Me	Me	Cl
5-100	Me	F	Cl
5-101	Me	Cl	Cl
5-102	Me	NH ₂	Cl
5-103	Me	NHMe	Cl
5-104	Me	NMe ₂	Cl
5-105	Me	O(CH ₂) ₂ OMe	Cl
5-106	Me	O(CH ₂) ₃ OMe	Cl
5-107	Me	O(CH ₂) ₄ OMe	Cl
5-108	Me	OCH ₂ CONMe ₂	Cl
5-109	Me	O(CH ₂) ₂ -CO-NMe ₂	Cl
5-110	Me	O(CH ₂) ₂ -NH(CO)NMe ₂	Cl
5-111	Me	O(CH ₂) ₂ - NH(CO)NHCO ₂ Et	Cl
5-112	Me	O(CH ₂) ₂ -NHCO ₂ Me	Cl
5-113	Me	OCH ₂ -NHSO ₂ cPr	Cl

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No.	X	Y	Z
5-114	Me	O(CH ₂)-5-2,4-dimethyl-2,4-dihydro-3H-1,2,4-triazol-3-one	Cl
5-115	Me	O(CH ₂)-3,5-dimethyl-1,2-oxazol-4-yl	Cl
5-116	Me	SMe	Cl
5-117	Me	SOMe	Cl
5-118	Me	SO ₂ Me	Cl
5-119	Me	SEt	Cl
5-120	Me	SOEt	Cl
5-121	Me	SO ₂ Et	Cl
5-122	Me	S(CH ₂) ₂ OMe	Cl
5-123	Me	SO(CH ₂) ₂ OMe	Cl
5-124	Me	SO ₂ (CH ₂) ₂ OMe	Cl
5-125	Me	NH ₂	Br
5-126	Me	NHMe	Br
5-127	Me	NMe ₂	Br
5-128	Me	OCH ₂ (CO)NMe ₂	Br
5-129	Me	O(CH ₂)-5-pyrrolidin-2-one	Br
5-130	Me	SMe	Br
5-131	Me	SOMe	Br
5-132	Me	SO ₂ Me	Br
5-133	Me	SEt	Br
5-134	Me	SOEt	Br
5-135	Me	SO ₂ Et	Br
5-136	Me	SMe	I
5-137	Me	SOMe	I
5-138	Me	SO ₂ Me	I
5-139	Me	SEt	I
5-140	Me	SOEt	I
5-141	Me	SO ₂ Et	I
5-142	Me	Cl	CF ₃
5-143	Me	SMe	CF ₃
5-144	Me	SOMe	CF ₃
5-145	Me	SO ₂ Me	CF ₃
5-146	Me	SEt	CF ₃
5-147	Me	SOEt	CF ₃
5-148	Me	SO ₂ Et	CF ₃
5-149	Me	S(CH ₂) ₂ OMe	CF ₃
5-150	Me	SO(CH ₂) ₂ OMe	CF ₃
5-151	Me	SO ₂ (CH ₂) ₂ OMe	CF ₃

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No.	X	Y	Z
5-152	Me	Me	SO ₂ Me
5-153	Me	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
5-154	Me	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
5-155	Me	5-cyanomethyl- 4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
5-156	Me	5-cyanomethyl- 4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
5-157	Me	NH ₂	SO ₂ Me
5-158	Me	NHMe	SO ₂ Me
5-159	Me	NMe ₂	SO ₂ Me
5-160	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
5-161	Me	pyrazol-1-yl	SO ₂ Me
5-162	Me	OH	SO ₂ Me
5-163	Me	OMe	SO ₂ Me
5-164	Me	OMe	SO ₂ Et
5-165	Me	OEt	SO ₂ Me
5-166	Me	OEt	SO ₂ Et
5-167	Me	OiPr	SO ₂ Me
5-168	Me	OiPr	SO ₂ Et
5-169	Me	O(CH ₂) ₂ OMe	SO ₂ Me
5-170	Me	O(CH ₂) ₂ OMe	SO ₂ Et
5-171	Me	O(CH ₂) ₃ OMe	SO ₂ Me
5-172	Me	O(CH ₂) ₃ OMe	SO ₂ Et
5-173	Me	O(CH ₂) ₄ OMe	SO ₂ Me
5-174	Me	O(CH ₂) ₄ OMe	SO ₂ Et
5-175	Me	O(CH ₂) ₂ NHSO ₂ Me	SO ₂ Me
5-176	Me	O(CH ₂) ₂ NHSO ₂ Me	SO ₂ Et
5-177	Me	OCH ₂ (CO)NMe ₂	SO ₂ Me
5-178	Me	OCH ₂ (CO)NMe ₂	SO ₂ Et
5-179	Me	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
5-180	Me	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
5-181	Me	O(CH ₂) ₂ -O-(3,5-dimethoxypyrimidin-2-yl)	SO ₂ Me
5-182	Me	Cl	SO ₂ Me
5-183	Me	SMe	SO ₂ Me
5-184	Me	SOMe	SO ₂ Me
5-185	Me	SO ₂ Me	SO ₂ Me
5-186	Me	SO ₂ Me	SO ₂ Et
5-187	Me	SEt	SO ₂ Me
5-188	Me	SOEt	SO ₂ Me

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No.	X	Y	Z
5-189	Me	SO ₂ Et	SO ₂ Me
5-190	Me	S(CH ₂) ₂ OMe	SO ₂ Me
5-191	Me	SO(CH ₂) ₂ OMe	SO ₂ Me
5-192	Me	SO ₂ (CH ₂) ₂ OMe	SO ₂ Me
5-193	CH ₂ SMe	OMe	SO ₂ Me
5-194	CH ₂ OMe	OMe	SO ₂ Me
5-195	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₂ OEt	SO ₂ Me
5-196	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₃ OEt	SO ₂ Me
5-197	CH ₂ O(CH ₂) ₃ OMe	OMe	SO ₂ Me
5-198	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₂ OMe	SO ₂ Me
5-199	CH ₂ O(CH ₂) ₂ OMe	NH(CH ₂) ₃ OMe	SO ₂ Me
5-200	Et	SMe	Cl
5-201	Et	SO ₂ Me	Cl
5-202	Et	SMe	CF ₃
5-203	Et	SO ₂ Me	CF ₃
5-204	Et	F	SO ₂ Me
5-205	Et	NH(CH ₂) ₂ OMe	SO ₂ Me
5-206	iPr	SO ₂ Me	CF ₃
5-207	cPr	SO ₂ Me	CF ₃
5-208	CF ₃	O(CH ₂) ₂ OMe	F
5-209	CF ₃	O(CH ₂) ₃ OMe	F
5-210	CF ₃	OCH ₂ CONMe ₂	F
5-211	CF ₃	[1,4]dioxan-2-yl-methoxy	F
5-212	CF ₃	O(CH ₂) ₂ OMe	Cl
5-213	CF ₃	O(CH ₂) ₃ OMe	Cl
5-214	CF ₃	OCH ₂ CONMe ₂	Cl
5-215	CF ₃	[1,4]dioxan-2-yl-methoxy	Cl
5-216	CF ₃	O(CH ₂) ₂ OMe	Br
5-217	CF ₃	O(CH ₂) ₃ OMe	Br
5-218	CF ₃	OCH ₂ CONMe ₂	Br
5-219	CF ₃	[1,4]dioxan-2-yl-methoxy	Br
5-220	CF ₃	O(CH ₂) ₂ OMe	I
5-221	CF ₃	O(CH ₂) ₃ OMe	I
5-222	CF ₃	OCH ₂ CONMe ₂	I
5-223	CF ₃	[1,4]dioxan-2-yl-methoxy	I
5-224	CF ₃	F	SO ₂ Me
5-225	CF ₃	F	SO ₂ Et

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No.	X	Y	Z
5-226	CF ₃	O(CH ₂) ₂ OMe	SO ₂ Me
5-227	CF ₃	O(CH ₂) ₂ OMe	SO ₂ Et
5-228	CF ₃	O(CH ₂) ₃ OMe	SO ₂ Me
5-229	CF ₃	O(CH ₂) ₃ OMe	SO ₂ Et
5-230	CF ₃	OCH ₂ CONMe ₂	SO ₂ Me
5-231	CF ₃	OCH ₂ CONMe ₂	SO ₂ Et
5-232	CF ₃	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
5-233	CF ₃	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
5-234	F	SMe	CF ₃
5-235	F	SOMe	CF ₃
5-236	Cl	Me	Cl
5-237	Cl	OCH ₂ CHCH ₂	Cl
5-238	Cl	OCH ₂ CHF ₂	Cl
5-239	Cl	O(CH ₂) ₂ OMe	Cl
5-240	Cl	OCH ₂ CONMe ₂	Cl
5-241	Cl	O(CH ₂)-5-pyrrolidin-2-one	Cl
5-242	Cl	SMe	Cl
5-243	Cl	SOMe	Cl
5-244	Cl	SO ₂ Me	Cl
5-245	Cl	F	SMe
5-246	Cl	Cl	SO ₂ Me
5-247	Cl	COOMe	SO ₂ Me
5-248	Cl	CONMe ₂	SO ₂ Me
5-249	Cl	CONMe(OMe)	SO ₂ Me
5-250	Cl	CH ₂ OMe	SO ₂ Me
5-251	Cl	CH ₂ OMe	SO ₂ Et
5-252	Cl	CH ₂ OEt	SO ₂ Me
5-253	Cl	CH ₂ OEt	SO ₂ Et
5-254	Cl	CH ₂ OCH ₂ CHF ₂	SO ₂ Me
5-255	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
5-256	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Et
5-257	Cl	CH ₂ OCH ₂ CF ₂ CHF ₂	SO ₂ Me
5-258	Cl	CH ₂ OcPentyl	SO ₂ Me
5-259	Cl	CH ₂ PO(OMe) ₂	SO ₂ Me
5-260	Cl	4,5-dihydro-1,2-oxazol-3-yl	SMe
5-261	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
5-262	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et

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No.	X	Y	Z
5-263	Cl	5-cyanomethyl- 4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Me
5-264	Cl	5-cyanomethyl- 4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
5-265	Cl	5-(methoxymethyl)-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
5-266	Cl	5-(methoxymethyl)-5-methyl- 4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
5-267	Cl	CH ₂ O-tetrahydrofuran-3-yl	SO ₂ Me
5-268	Cl	CH ₂ O-tetrahydrofuran-3-yl	SO ₂ Et
5-269	Cl	CH ₂ OCH ₂ -tetrahydrofuran-2-yl	SO ₂ Me
5-270	Cl	CH ₂ OCH ₂ -tetrahydrofuran-2-yl	SO ₂ Et
5-271	Cl	CH ₂ OCH ₂ -tetrahydrofuran-3-yl	SO ₂ Me
5-272	Cl	CH ₂ OCH ₂ -tetrahydrofuran-3-yl	SO ₂ Et
5-273	Cl	OMe	SO ₂ Me
5-274	Cl	OMe	SO ₂ Et
5-275	Cl	OEt	SO ₂ Me
5-276	Cl	OEt	SO ₂ Et
5-277	Cl	OiPr	SO ₂ Me
5-278	Cl	OiPr	SO ₂ Et
5-279	Cl	O(CH ₂) ₂ OMe	SO ₂ Me
5-280	Cl	O(CH ₂) ₄ OMe	SO ₂ Me
5-281	Cl	O(CH ₂) ₄ OMe	SO ₂ Et
5-282	Cl	O(CH ₂) ₃ OMe	SO ₂ Me
5-283	Cl	O(CH ₂) ₃ OMe	SO ₂ Et
5-284	Cl	O(CH ₂) ₂ OMe	SO ₂ Me
5-285	Cl	O(CH ₂) ₂ OMe	SO ₂ Et
5-286	Cl	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
5-287	Cl	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
5-288	Cl	OCH ₂ (CO)NMe ₂	SO ₂ Me
5-289	Cl	OCH ₂ (CO)NMe ₂	SO ₂ Et
5-290	Cl	SMe	SO ₂ Me
5-291	Cl	SOMe	SO ₂ Me
5-292	Br	OMe	Br
5-293	Br	O(CH ₂) ₂ OMe	Br
5-294	Br	O(CH ₂) ₂ OMe	SO ₂ Me
5-295	Br	O(CH ₂) ₂ OMe	SO ₂ Et

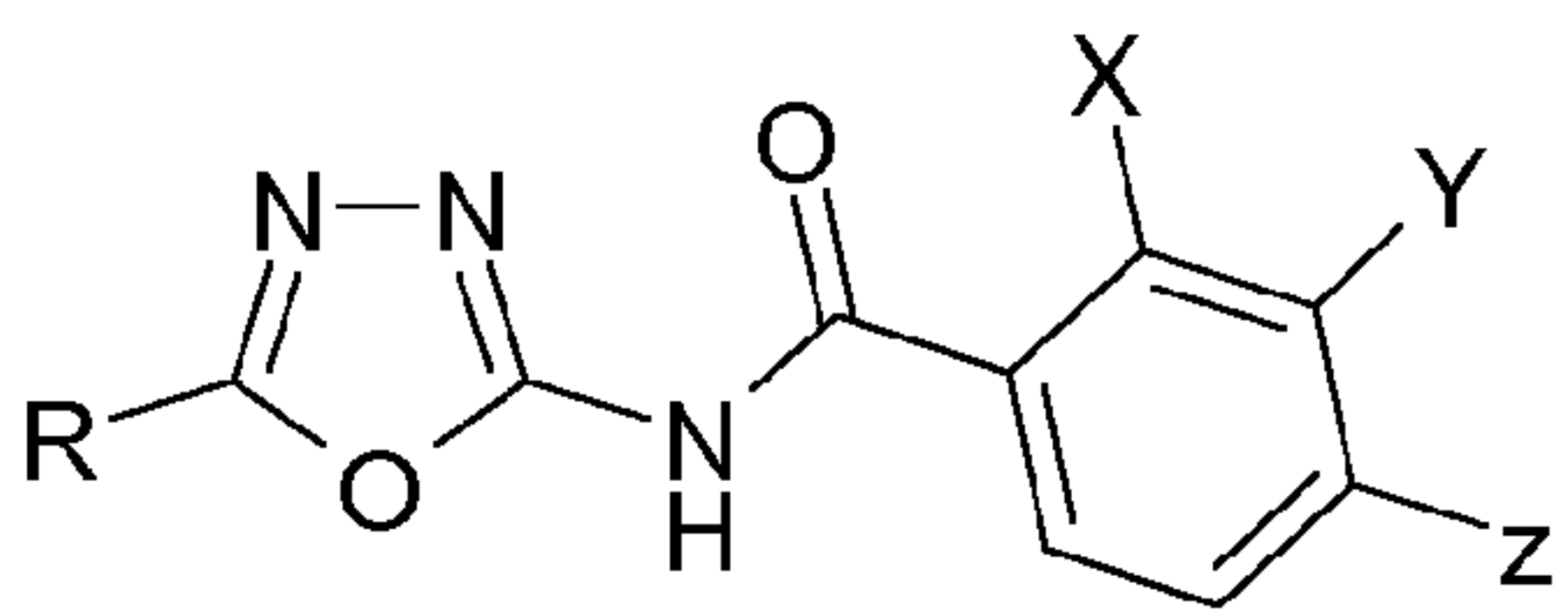
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No.	X	Y	Z
5-296	Br	O(CH ₂) ₃ OMe	SO ₂ Me
5-297	Br	O(CH ₂) ₃ OMe	SO ₂ Et
5-298	Br	O(CH ₂) ₄ OMe	SO ₂ Me
5-299	Br	O(CH ₂) ₄ OMe	SO ₂ Et
5-300	Br	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
5-301	Br	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
5-302	I	O(CH ₂) ₂ OMe	SO ₂ Me
5-303	I	O(CH ₂) ₂ OMe	SO ₂ Et
5-304	I	O(CH ₂) ₃ OMe	SO ₂ Me
5-305	I	O(CH ₂) ₃ OMe	SO ₂ Et
5-306	I	O(CH ₂) ₄ OMe	SO ₂ Me
5-307	I	O(CH ₂) ₄ OMe	SO ₂ Et
5-308	I	[1,4]dioxan-2-yl-methoxy	SO ₂ Me
5-309	I	[1,4]dioxan-2-yl-methoxy	SO ₂ Et
5-310	OMe	SMe	CF ₃
5-311	OMe	SOMe	CF ₃
5-312	OMe	SO ₂ Me	CF ₃
5-313	OMe	SOEt	CF ₃
5-314	OMe	SO ₂ Et	CF ₃
5-315	OMe	S(CH ₂) ₂ OMe	CF ₃
5-316	OMe	SO(CH ₂) ₂ OMe	CF ₃
5-317	OMe	SO ₂ (CH ₂) ₂ OMe	CF ₃
5-318	OMe	SMe	Cl
5-319	OMe	SOMe	Cl
5-320	OMe	SO ₂ Me	Cl
5-321	OMe	SEt	Cl
5-322	OMe	SOEt	Cl
5-323	OMe	SO ₂ Et	Cl
5-324	OMe	S(CH ₂) ₂ OMe	Cl
5-325	OMe	SO(CH ₂) ₂ OMe	Cl
5-326	OMe	SO ₂ (CH ₂) ₂ OMe	Cl
5-327	OMe	H	SO ₂ Me
5-328	OCH ₂ -c-Pr	SMe	CF ₃
5-329	OCH ₂ -c-Pr	SOMe	CF ₃
5-330	OCH ₂ -c-Pr	SO ₂ Me	CF ₃
5-331	OCH ₂ -c-Pr	SEt	CF ₃
5-332	OCH ₂ -c-Pr	SOEt	CF ₃
5-333	OCH ₂ -c-Pr	SO ₂ Et	CF ₃
5-334	OCH ₂ -c-Pr	S(CH ₂) ₂ OMe	CF ₃
5-335	OCH ₂ -c-Pr	SO(CH ₂) ₂ OMe	CF ₃
5-336	OCH ₂ -c-Pr	SO ₂ (CH ₂) ₂ OMe	CF ₃

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No.	X	Y	Z
5-337	OCH ₂ -c-Pr	SMe	Cl
5-338	OCH ₂ -c-Pr	SOMe	Cl
5-339	OCH ₂ -c-Pr	SO ₂ Me	Cl
5-340	OCH ₂ -c-Pr	SEt	Cl
5-341	OCH ₂ -c-Pr	SOEt	Cl
5-342	OCH ₂ -c-Pr	SO ₂ Et	Cl
5-343	OCH ₂ -c-Pr	S(CH ₂) ₂ OMe	Cl
5-344	OCH ₂ -c-Pr	SO(CH ₂) ₂ OMe	Cl
5-345	OCH ₂ -c-Pr	SO ₂ (CH ₂) ₂ OMe	Cl
5-346	OCH ₂ -c-Pr	SMe	SO ₂ Me
5-347	OCH ₂ -c-Pr	SOMe	SO ₂ Me
5-348	OCH ₂ -c-Pr	SO ₂ Me	SO ₂ Me
5-349	OCH ₂ -c-Pr	SEt	SO ₂ Me
5-350	OCH ₂ -c-Pr	SOEt	SO ₂ Me
5-351	OCH ₂ -c-Pr	SO ₂ Et	SO ₂ Me
5-352	OCH ₂ -c-Pr	S(CH ₂) ₂ OMe	SO ₂ Me
5-353	OCH ₂ -c-Pr	SO(CH ₂) ₂ OMe	SO ₂ Me
5-354	OCH ₂ -c-Pr	SO ₂ (CH ₂) ₂ OMe	SO ₂ Me
5-355	SO ₂ Me	F	CF ₃
5-356	SO ₂ Me	NH ₂	CF ₃
5-357	SO ₂ Me	NHEt	Cl
5-358	SMe	SEt	F
5-359	SMe	SMe	F
5-360	F	SO ₂ Me	CF ₃
5-361	Cl	SMe	CF ₃
5-362	Cl	S(O)Me	CF ₃
5-363	Cl	SO ₂ Me	CF ₃
5-364	Cl	SO ₂ Me	SO ₂ Me

Table 6: Compounds of the general formula (I) in which A is CY, and R, X, Y, and Z are as defined below.



No.	R	X	Y	Z
6-1	c-Pr	NO ₂	H	SO ₂ Me
6-2	c-Pr	Cl	H	SO ₂ Me
6-3	c-Pr	SO ₂ Me	H	CF ₃

No.	R	X	Y	Z
6-4	c-Pr	NO ₂	H	OMe
6-5	c-Pr	NO ₂	H	Br
6-6	c-Pr	NO ₂	H	Cl
6-7	c-Pr	NO ₂	H	CF ₃
6-8	c-Pr	NO ₂	H	NO ₂
6-9	c-Pr	NO ₂	H	Me
6-10	c-Pr	NO ₂	H	F
6-11	c-Pr	OMe	H	SO ₂ Me
6-12	c-Pr	CF ₃	H	NO ₂
6-13	c-Pr	CF ₃	H	Cl
6-14	c-Pr	CH ₂ SO ₂ Me	H	Br
6-15	c-Pr	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-16	c-Pr	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-17	c-Pr	Cl	5-cyanomethyl- 4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-18	c-Pr	Cl	4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-19	c-Pr	Cl	CH ₂ OCH ₂ - tetrahydrofuran-2- yl	SO ₂ Me
6-20	c-Pr	Cl	SMe	Cl
6-21	c-Pr	Cl	SMe	SO ₂ Me
6-22	c-Pr	Cl	Me	SO ₂ Et
6-23	c-Pr	Cl	O(CH ₂) ₂ OMe	Cl
6-24	c-Pr	Cl	OCH ₂ -cyclopropyl	Cl
6-25	c-Pr	Cl	OMe	Cl
6-26	c-Pr	Cl	NHAc	Cl
6-27	c-Pr	Cl	OCH ₂ C(O)NMe ₂	Cl
6-28	c-Pr	Cl	Cl	SO ₂ Me
6-29	c-Pr	Cl	pyrazol-1-yl	SO ₂ Me
6-30	c-Pr	Cl	4-methoxy- pyrazol-1-yl	SO ₂ Me
6-31	c-Pr	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-32	c-Pr	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-33	c-Pr	Cl	F	SO ₂ Me
6-34	c-Pr	Me	SO ₂ Me	SO ₂ Me
6-35	c-Pr	Me	SO ₂ Me	CF ₃
6-36	c-Pr	Me	NMe ₂	SO ₂ Me
6-37	c-Pr	Me	S(O)Me	CF ₃
6-38	c-Pr	Me	SMe	CF ₃
6-39	c-Pr	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃

No.	R	X	Y	Z
6-40	c-Pr	Me	pyrazol-1-yl	SO ₂ Me
6-41	c-Pr	Me	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-42	c-Pr	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-43	c-Pr	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-44	c-Pr	Me	Cl	SO ₂ Me
6-45	c-Pr	Me	Me	SO ₂ Me
6-46	c-Pr	Me	F	Cl
6-47	c-Pr	Me	SO ₂ Me	Cl
6-48	c-Pr	Me	NMe ₂	SO ₂ Me
6-49	c-Pr	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-50	c-Pr	CF ₃	F	SO ₂ CH ₃
6-51	c-Pr	CF ₃	SMe	SO ₂ CH ₃
6-52	c-Pr	CF ₃	SEt	SO ₂ CH ₃
6-53	c-Pr	CF ₃	S(O)Et	SO ₂ CH ₃
6-54	c-Pr	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-55	c-Pr	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-56	c-Pr	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-57	c-Pr	CF ₃	CH ₂ O-tetrahydrofuran-2-yl	SO ₂ Et
6-58	c-Pr	SMe	SMe	F
6-59	c-Pr	SMe	SEt	F
6-60	c-Pr	SO ₂ CH ₃	F	Cl
6-61	c-Pr	F	S(O)Me	CF ₃
6-62	c-Pr	F	SMe	CF ₃
6-63	CO ₂ Et	NO ₂	H	SO ₂ Me
6-64	CO ₂ Et	Cl	H	SO ₂ Me
6-65	CO ₂ Et	SO ₂ Me	H	CF ₃
6-66	CO ₂ Et	NO ₂	H	OMe
6-67	CO ₂ Et	NO ₂	H	Br
6-68	CO ₂ Et	NO ₂	H	CF ₃
6-69	CO ₂ Et	NO ₂	H	NO ₂
6-70	CO ₂ Et	NO ₂	H	Cl
6-71	CO ₂ Et	NO ₂	H	Me
6-72	CO ₂ Et	NO ₂	H	F
6-73	CO ₂ Et	OMe	H	SO ₂ Me
6-74	CO ₂ Et	CF ₃	H	NO ₂
6-75	CO ₂ Et	CH ₂ SO ₂ Me	H	Br
6-76	CO ₂ Et	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-77	CO ₂ Et	Cl	CH ₂ OCH ₂ CF ₃	SMe

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No.	R	X	Y	Z
6-78	CO ₂ Et	Cl	5-cyanomethyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
6-79	CO ₂ Et	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
6-80	CO ₂ Et	Cl	CH ₂ OCH ₂ -tetrahydrofuran-2-yl	SO ₂ Me
6-81	CO ₂ Et	Cl	SMe	Cl
6-82	CO ₂ Et	Cl	SMe	SO ₂ Me
6-83	CO ₂ Et	Cl	Me	SO ₂ Et
6-84	CO ₂ Et	Cl	O(CH ₂) ₂ OMe	Cl
6-85	CO ₂ Et	Cl	OCH ₂ -cyclopropyl	Cl
6-86	CO ₂ Et	Cl	OMe	Cl
6-87	CO ₂ Et	Cl	NHAc	Cl
6-88	CO ₂ Et	Cl	OCH ₂ C(O)NMe ₂	Cl
6-89	CO ₂ Et	Cl	Cl	SO ₂ Me
6-90	CO ₂ Et	Cl	pyrazol-1-yl	SO ₂ Me
6-91	CO ₂ Et	Cl	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-92	CO ₂ Et	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-93	CO ₂ Et	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-94	CO ₂ Et	Cl	F	SO ₂ Me
6-95	CO ₂ Et	Me	SO ₂ Me	SO ₂ Me
6-96	CO ₂ Et	Me	SO ₂ Me	CF ₃
6-97	CO ₂ Et	Me	NMe ₂	SO ₂ Me
6-98	CO ₂ Et	Me	S(O)Me	CF ₃
6-99	CO ₂ Et	Me	SMe	CF ₃
6-100	CO ₂ Et	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-101	CO ₂ Et	Me	pyrazol-1-yl	SO ₂ Me
6-102	CO ₂ Et	Me	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-103	CO ₂ Et	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-104	CO ₂ Et	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-105	CO ₂ Et	Me	Cl	SO ₂ Me
6-106	CO ₂ Et	Me	Me	SO ₂ Me
6-107	CO ₂ Et	Me	Me	SMe
6-108	CO ₂ Et	Me	SO ₂ Me	Cl
6-109	CO ₂ Et	Me	NMe ₂	SO ₂ Me
6-110	CO ₂ Et	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-111	CO ₂ Et	CF ₃	F	SO ₂ CH ₃
6-112	CO ₂ Et	CF ₃	SMe	SO ₂ CH ₃

No.	R	X	Y	Z
6-113	CO ₂ Et	CF ₃	SEt	SO ₂ CH ₃
6-114	CO ₂ Et	CF ₃	S(O)Et	SO ₂ CH ₃
6-115	CO ₂ Et	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-116	CO ₂ Et	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-117	CO ₂ Et	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-118	CO ₂ Et	CF ₃	CH ₂ O- tetrahydrofuran-2- yl	SO ₂ Et
6-119	CO ₂ Et	SMe	SMe	F
6-120	CO ₂ Et	SMe	SEt	F
6-121	CO ₂ Et	SO ₂ CH ₃	F	Cl
6-122	CO ₂ Et	F	S(O)Me	CF ₃
6-123	CO ₂ Et	F	SMe	CF ₃
6-124	CO ₂ Me	NO ₂	H	SO ₂ Me
6-125	CO ₂ Me	Cl	H	SO ₂ Me
6-126	CO ₂ Me	SO ₂ Me	H	CF ₃
6-127	CO ₂ Me	NO ₂	H	OMe
6-128	CO ₂ Me	NO ₂	H	Br
6-129	CO ₂ Me	NO ₂	H	CF ₃
6-130	CO ₂ Me	NO ₂	H	NO ₂
6-131	CO ₂ Me	NO ₂	H	Cl
6-132	CO ₂ Me	NO ₂	H	Me
6-133	CO ₂ Me	NO ₂	H	F
6-134	CO ₂ Me	OMe	H	SO ₂ Me
6-135	CO ₂ Me	CF ₃	H	NO ₂
6-136	CO ₂ Me	CH ₂ SO ₂ Me	H	Br
6-137	CO ₂ Me	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-138	CO ₂ Me	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-139	CO ₂ Me	Cl	5-cyanomethyl- 4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-140	CO ₂ Me	Cl	4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-141	CO ₂ Me	Cl	CH ₂ OCH ₂ - tetrahydrofuran-2- yl	SO ₂ Me
6-142	CO ₂ Me	Cl	SMe	Cl
6-143	CO ₂ Me	Cl	SMe	SO ₂ Me
6-144	CO ₂ Me	Cl	Me	SO ₂ Et
6-145	CO ₂ Me	Cl	O(CH ₂) ₂ OMe	Cl
6-146	CO ₂ Me	Cl	OCH ₂ -cyclopropyl	Cl
6-147	CO ₂ Me	Cl	OMe	Cl
6-148	CO ₂ Me	Cl	NHAc	Cl

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No.	R	X	Y	Z
6-149	CO ₂ Me	Cl	OCH ₂ C(O)NMe ₂	Cl
6-150	CO ₂ Me	Cl	Cl	SO ₂ Me
6-151	CO ₂ Me	Cl	pyrazol-1-yl	SO ₂ Me
6-152	CO ₂ Me	Cl	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-153	CO ₂ Me	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-154	CO ₂ Me	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-155	CO ₂ Me	Cl	F	SO ₂ Me
6-156	CO ₂ Me	Me	SO ₂ Me	SO ₂ Me
6-157	CO ₂ Me	Me	SO ₂ Me	CF ₃
6-158	CO ₂ Me	Me	NMe ₂	SO ₂ Me
6-159	CO ₂ Me	Me	S(O)Me	CF ₃
6-160	CO ₂ Me	Me	SMe	CF ₃
6-161	CO ₂ Me	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-162	CO ₂ Me	Me	pyrazol-1-yl	SO ₂ Me
6-163	CO ₂ Me	Me	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-164	CO ₂ Me	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-165	CO ₂ Me	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-166	CO ₂ Me	Me	Cl	SO ₂ Me
6-167	CO ₂ Me	Me	Me	SO ₂ Me
6-168	CO ₂ Me	Me	Me	SMe
6-169	CO ₂ Me	Me	SO ₂ Me	Cl
6-170	CO ₂ Me	Me	NMe ₂	SO ₂ Me
6-171	CO ₂ Me	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-172	CO ₂ Me	CF ₃	F	SO ₂ CH ₃
6-173	CO ₂ Me	CF ₃	SMe	SO ₂ CH ₃
6-174	CO ₂ Me	CF ₃	SEt	SO ₂ CH ₃
6-175	CO ₂ Me	CF ₃	S(O)Et	SO ₂ CH ₃
6-176	CO ₂ Me	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-177	CO ₂ Me	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-178	CO ₂ Me	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-179	CO ₂ Me	CF ₃	CH ₂ O-tetrahydrofuran-2-yl	SO ₂ Et
6-180	CO ₂ Me	SMe	SMe	F
6-181	CO ₂ Me	SMe	SEt	F
6-182	CO ₂ Me	SO ₂ CH ₃	F	Cl
6-183	CO ₂ Me	F	S(O)Me	CF ₃
6-184	CO ₂ Me	F	SMe	CF ₃
6-185	benzyl	NO ₂	H	SO ₂ Me
6-186	benzyl	Cl	H	SO ₂ Me

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No.	R	X	Y	Z
6-187	benzyl	SO ₂ Me	H	CF ₃
6-188	benzyl	NO ₂	H	OMe
6-189	benzyl	NO ₂	H	Br
6-190	benzyl	NO ₂	H	CF ₃
6-191	benzyl	NO ₂	H	NO ₂
6-192	benzyl	NO ₂	H	Cl
6-193	benzyl	NO ₂	H	Me
6-194	benzyl	NO ₂	H	F
6-195	benzyl	OMe	H	SO ₂ Me
6-196	benzyl	CF ₃	H	NO ₂
6-197	benzyl	CH ₂ SO ₂ Me	H	Br
6-198	benzyl	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-199	benzyl	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-200	benzyl	Cl	5-cyanomethyl- 4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-201	benzyl	Cl	4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-202	benzyl	Cl	CH ₂ OCH ₂ - tetrahydrofuran-2- yl	SO ₂ Me
6-203	benzyl	Cl	SMe	Cl
6-204	benzyl	Cl	SMe	SO ₂ Me
6-205	benzyl	Cl	Me	SO ₂ Et
6-206	benzyl	Cl	O(CH ₂) ₂ OMe	Cl
6-207	benzyl	Cl	OCH ₂ -cyclopropyl	Cl
6-208	benzyl	Cl	OMe	Cl
6-209	benzyl	Cl	NHAc	Cl
6-210	benzyl	Cl	OCH ₂ C(O)NMe ₂	Cl
6-211	benzyl	Cl	Cl	SO ₂ Me
6-212	benzyl	Cl	pyrazol-1-yl	SO ₂ Me
6-213	benzyl	Cl	4-methoxy- pyrazol-1-yl	SO ₂ Me
6-214	benzyl	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-215	benzyl	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-216	benzyl	Cl	F	SO ₂ Me
6-217	benzyl	Me	SO ₂ Me	SO ₂ Me
6-218	benzyl	Me	SO ₂ Me	CF ₃
6-219	benzyl	Me	NMe ₂	SO ₂ Me
6-220	benzyl	Me	S(O)Me	CF ₃
6-221	benzyl	Me	SMe	CF ₃
6-222	benzyl	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃

No.	R	X	Y	Z
6-223	benzyl	Me	pyrazol-1-yl	SO ₂ Me
6-224	benzyl	Me	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-225	benzyl	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-226	benzyl	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-227	benzyl	Me	Cl	SO ₂ Me
6-228	benzyl	Me	Me	SO ₂ Me
6-229	benzyl	Me	Me	SMe
6-230	benzyl	Me	SO ₂ Me	Cl
6-231	benzyl	Me	NMe ₂	SO ₂ Me
6-232	benzyl	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-233	benzyl	CF ₃	F	SO ₂ CH ₃
6-234	benzyl	CF ₃	SMe	SO ₂ CH ₃
6-235	benzyl	CF ₃	SEt	SO ₂ CH ₃
6-236	benzyl	CF ₃	S(O)Et	SO ₂ CH ₃
6-237	benzyl	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-238	benzyl	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-239	benzyl	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-240	benzyl	CF ₃	CH ₂ O-tetrahydrofuran-2-yl	SO ₂ Et
6-241	benzyl	SMe	SMe	F
6-242	benzyl	SMe	SEt	F
6-243	benzyl	SO ₂ CH ₃	F	Cl
6-244	benzyl	F	S(O)Me	CF ₃
6-245	benzyl	F	SMe	CF ₃
6-246	phenyl	NO ₂	H	SO ₂ Me
6-247	phenyl	Cl	H	SO ₂ Me
6-248	phenyl	SO ₂ Me	H	CF ₃
6-249	phenyl	NO ₂	H	OMe
6-250	phenyl	NO ₂	H	Br
6-251	phenyl	NO ₂	H	CF ₃
6-252	phenyl	NO ₂	H	NO ₂
6-253	phenyl	NO ₂	H	Cl
6-254	phenyl	NO ₂	H	Me
6-255	phenyl	NO ₂	H	F
6-256	phenyl	OMe	H	SO ₂ Me
6-257	phenyl	CF ₃	H	NO ₂
6-258	phenyl	CH ₂ SO ₂ Me	H	Br
6-259	phenyl	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-260	phenyl	Cl	CH ₂ OCH ₂ CF ₃	SMe

No.	R	X	Y	Z
6-261	phenyl	Cl	5-cyanomethyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
6-262	phenyl	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
6-263	phenyl	Cl	CH ₂ OCH ₂ -tetrahydrofuran-2-yl	SO ₂ Me
6-264	phenyl	Cl	SMe	Cl
6-265	phenyl	Cl	SMe	SO ₂ Me
6-266	phenyl	Cl	Me	SO ₂ Et
6-267	phenyl	Cl	O(CH ₂) ₂ OMe	Cl
6-268	phenyl	Cl	OCH ₂ -cyclopropyl	Cl
6-269	phenyl	Cl	OMe	Cl
6-270	phenyl	Cl	NHAc	Cl
6-271	phenyl	Cl	OCH ₂ C(O)NMe ₂	Cl
6-272	phenyl	Cl	Cl	SO ₂ Me
6-273	phenyl	Cl	pyrazol-1-yl	SO ₂ Me
6-274	phenyl	Cl	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-275	phenyl	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-276	phenyl	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-277	phenyl	Cl	F	SO ₂ Me
6-278	phenyl	Me	SO ₂ Me	SO ₂ Me
6-279	phenyl	Me	SO ₂ Me	CF ₃
6-280	phenyl	Me	NMe ₂	SO ₂ Me
6-281	phenyl	Me	S(O)Me	CF ₃
6-282	phenyl	Me	SMe	CF ₃
6-283	phenyl	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-284	phenyl	Me	pyrazol-1-yl	SO ₂ Me
6-285	phenyl	Me	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-286	phenyl	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-287	phenyl	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-288	phenyl	Me	Cl	SO ₂ Me
6-289	phenyl	Me	Me	SO ₂ Me
6-290	phenyl	Me	Me	SMe
6-291	phenyl	Me	SO ₂ Me	Cl
6-292	phenyl	Me	NMe ₂	SO ₂ Me
6-293	phenyl	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-294	phenyl	CF ₃	F	SO ₂ CH ₃
6-295	phenyl	CF ₃	SMe	SO ₂ CH ₃
6-296	phenyl	CF ₃	SEt	SO ₂ CH ₃

No.	R	X	Y	Z
6-297	phenyl	CF ₃	S(O)Et	SO ₂ CH ₃
6-298	phenyl	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-299	phenyl	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-300	phenyl	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-301	phenyl	CF ₃	CH ₂ O-tetrahydrofuran-2-yl	SO ₂ Et
6-302	phenyl	SMe	SMe	F
6-303	phenyl	SMe	SEt	F
6-304	phenyl	SO ₂ CH ₃	F	Cl
6-305	phenyl	F	S(O)Me	CF ₃
6-306	phenyl	F	SMe	CF ₃
6-307	pyrazin-2-yl	NO ₂	H	SO ₂ Me
6-308	pyrazin-2-yl	Cl	H	SO ₂ Me
6-309	pyrazin-2-yl	SO ₂ Me	H	CF ₃
6-310	pyrazin-2-yl	NO ₂	H	OMe
6-311	pyrazin-2-yl	NO ₂	H	Br
6-312	pyrazin-2-yl	NO ₂	H	CF ₃
6-313	pyrazin-2-yl	NO ₂	H	NO ₂
6-314	pyrazin-2-yl	NO ₂	H	Cl
6-315	pyrazin-2-yl	NO ₂	H	Me
6-316	pyrazin-2-yl	NO ₂	H	F
6-317	pyrazin-2-yl	OMe	H	SO ₂ Me
6-318	pyrazin-2-yl	CF ₃	H	NO ₂
6-319	pyrazin-2-yl	CH ₂ SO ₂ Me	H	Br
6-320	pyrazin-2-yl	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-321	pyrazin-2-yl	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-322	pyrazin-2-yl	Cl	5-cyanomethyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
6-323	pyrazin-2-yl	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et

No.	R	X	Y	Z
6-324	pyrazin-2-yl	Cl	CH ₂ OCH ₂ - tetrahydrofuran-2-yl	SO ₂ Me
6-325	pyrazin-2-yl	Cl	SMe	Cl
6-326	pyrazin-2-yl	Cl	SMe	SO ₂ Me
6-327	pyrazin-2-yl	Cl	Me	SO ₂ Et
6-328	pyrazin-2-yl	Cl	O(CH ₂) ₂ OMe	Cl
6-329	pyrazin-2-yl	Cl	OCH ₂ -cyclopropyl	Cl
6-330	pyrazin-2-yl	Cl	OMe	Cl
6-331	pyrazin-2-yl	Cl	NHAc	Cl
6-332	pyrazin-2-yl	Cl	OCH ₂ C(O)NMe ₂	Cl
6-333	pyrazin-2-yl	Cl	Cl	SO ₂ Me
6-334	pyrazin-2-yl	Cl	pyrazol-1-yl	SO ₂ Me
6-335	pyrazin-2-yl	Cl	4-methoxy- pyrazol-1-yl	SO ₂ Me
6-336	pyrazin-2-yl	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-337	pyrazin-2-yl	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-338	pyrazin-2-yl	Cl	F	SO ₂ Me
6-339	pyrazin-2-yl	Me	SO ₂ Me	SO ₂ Me
6-340	pyrazin-2-yl	Me	SO ₂ Me	CF ₃
6-341	pyrazin-2-yl	Me	NMe ₂	SO ₂ Me
6-342	pyrazin-2-yl	Me	S(O)Me	CF ₃
6-343	pyrazin-2-yl	Me	SMe	CF ₃
6-344	pyrazin-2-yl	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-345	pyrazin-2-yl	Me	pyrazol-1-yl	SO ₂ Me
6-346	pyrazin-2-yl	Me	4-methoxy- pyrazol-1-yl	SO ₂ Me

No.	R	X	Y	Z
6-347	pyrazin-2-yl	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-348	pyrazin-2-yl	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-349	pyrazin-2-yl	Me	Cl	SO ₂ Me
6-350	pyrazin-2-yl	Me	Me	SO ₂ Me
6-351	pyrazin-2-yl	Me	Me	SMe
6-352	pyrazin-2-yl	Me	SO ₂ Me	Cl
6-353	pyrazin-2-yl	Me	NMe ₂	SO ₂ Me
6-354	pyrazin-2-yl	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-355	pyrazin-2-yl	CF ₃	F	SO ₂ CH ₃
6-356	pyrazin-2-yl	CF ₃	SMe	SO ₂ CH ₃
6-357	pyrazin-2-yl	CF ₃	SEt	SO ₂ CH ₃
6-358	pyrazin-2-yl	CF ₃	S(O)Et	SO ₂ CH ₃
6-359	pyrazin-2-yl	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-360	pyrazin-2-yl	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-361	pyrazin-2-yl	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-362	pyrazin-2-yl	CF ₃	CH ₂ O-tetrahydrofuran-2-yl	SO ₂ Et
6-363	pyrazin-2-yl	SMe	SMe	F
6-364	pyrazin-2-yl	SMe	SEt	F
6-365	pyrazin-2-yl	SO ₂ CH ₃	F	Cl
6-366	pyrazin-2-yl	F	S(O)Me	CF ₃
6-367	pyrazin-2-yl	F	SMe	CF ₃
6-368	4-OMe-Ph	NO ₂	H	SO ₂ Me
6-369	4-OMe-Ph	Cl	H	SO ₂ Me
6-370	4-OMe-Ph	SO ₂ Me	H	CF ₃

No.	R	X	Y	Z
6-371	4-OMe-Ph	NO ₂	H	OMe
6-372	4-OMe-Ph	NO ₂	H	Br
6-373	4-OMe-Ph	NO ₂	H	CF ₃
6-374	4-OMe-Ph	NO ₂	H	NO ₂
6-375	4-OMe-Ph	NO ₂	H	Cl
6-376	4-OMe-Ph	NO ₂	H	Me
6-377	4-OMe-Ph	NO ₂	H	F
6-378	4-OMe-Ph	OMe	H	SO ₂ Me
6-379	4-OMe-Ph	CF ₃	H	NO ₂
6-380	4-OMe-Ph	CH ₂ SO ₂ Me	H	Br
6-381	4-OMe-Ph	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-382	4-OMe-Ph	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-383	4-OMe-Ph	Cl	5-cyanomethyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
6-384	4-OMe-Ph	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
6-385	4-OMe-Ph	Cl	CH ₂ OCH ₂ -tetrahydrofuran-2-yl	SO ₂ Me
6-386	4-OMe-Ph	Cl	SMe	Cl
6-387	4-OMe-Ph	Cl	SMe	SO ₂ Me
6-388	4-OMe-Ph	Cl	Me	SO ₂ Et
6-389	4-OMe-Ph	Cl	O(CH ₂) ₂ OMe	Cl
6-390	4-OMe-Ph	Cl	OCH ₂ -cyclopropyl	Cl
6-391	4-OMe-Ph	Cl	OMe	Cl
6-392	4-OMe-Ph	Cl	NHAc	Cl
6-393	4-OMe-Ph	Cl	OCH ₂ C(O)NMe ₂	Cl

No.	R	X	Y	Z
6-394	4-OMe-Ph	Cl	Cl	SO ₂ Me
6-395	4-OMe-Ph	Cl	pyrazol-1-yl	SO ₂ Me
6-396	4-OMe-Ph	Cl	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-397	4-OMe-Ph	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-398	4-OMe-Ph	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-399	4-OMe-Ph	Cl	F	SO ₂ Me
6-400	4-OMe-Ph	Me	SO ₂ Me	SO ₂ Me
6-401	4-OMe-Ph	Me	SO ₂ Me	CF ₃
6-402	4-OMe-Ph	Me	NMe ₂	SO ₂ Me
6-403	4-OMe-Ph	Me	S(O)Me	CF ₃
6-404	4-OMe-Ph	Me	SMe	CF ₃
6-405	4-OMe-Ph	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-406	4-OMe-Ph	Me	pyrazol-1-yl	SO ₂ Me
6-407	4-OMe-Ph	Me	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-408	4-OMe-Ph	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-409	4-OMe-Ph	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-410	4-OMe-Ph	Me	Cl	SO ₂ Me
6-411	4-OMe-Ph	Me	Me	SO ₂ Me
6-412	4-OMe-Ph	Me	Me	SMe
6-413	4-OMe-Ph	Me	SO ₂ Me	Cl
6-414	4-OMe-Ph	Me	NMe ₂	SO ₂ Me
6-415	4-OMe-Ph	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-416	4-OMe-Ph	CF ₃	F	SO ₂ CH ₃
6-417	4-OMe-Ph	CF ₃	SMe	SO ₂ CH ₃

No.	R	X	Y	Z
6-418	4-OMe-Ph	CF ₃	SEt	SO ₂ CH ₃
6-419	4-OMe-Ph	CF ₃	S(O)Et	SO ₂ CH ₃
6-420	4-OMe-Ph	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-421	4-OMe-Ph	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-422	4-OMe-Ph	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-423	4-OMe-Ph	CF ₃	CH ₂ O-tetrahydrofuran-2-yl	SO ₂ Et
6-424	4-OMe-Ph	SMe	SMe	F
6-425	4-OMe-Ph	SMe	SEt	F
6-426	4-OMe-Ph	SO ₂ CH ₃	F	Cl
6-427	4-OMe-Ph	F	S(O)Me	CF ₃
6-428	4-OMe-Ph	F	SMe	CF ₃
6-429	4-Cl-Ph	NO ₂	H	SO ₂ Me
6-430	4-Cl-Ph	Cl	H	SO ₂ Me
6-431	4-Cl-Ph	SO ₂ Me	H	CF ₃
6-432	4-Cl-Ph	NO ₂	H	OMe
6-433	4-Cl-Ph	NO ₂	H	Br
6-434	4-Cl-Ph	NO ₂	H	CF ₃
6-435	4-Cl-Ph	NO ₂	H	NO ₂
6-436	4-Cl-Ph	NO ₂	H	Cl
6-437	4-Cl-Ph	NO ₂	H	Me
6-438	4-Cl-Ph	NO ₂	H	F
6-439	4-Cl-Ph	OMe	H	SO ₂ Me
6-440	4-Cl-Ph	CF ₃	H	NO ₂
6-441	4-Cl-Ph	CH ₂ SO ₂ Me	H	Br
6-442	4-Cl-Ph	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-443	4-Cl-Ph	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-444	4-Cl-Ph	Cl	5-cyanomethyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
6-445	4-Cl-Ph	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
6-446	4-Cl-Ph	Cl	CH ₂ OCH ₂ -tetrahydrofuran-2-yl	SO ₂ Me

No.	R	X	Y	Z
6-447	4-Cl-Ph	Cl	SMe	Cl
6-448	4-Cl-Ph	Cl	SMe	SO ₂ Me
6-449	4-Cl-Ph	Cl	Me	SO ₂ Et
6-450	4-Cl-Ph	Cl	O(CH ₂) ₂ OMe	Cl
6-451	4-Cl-Ph	Cl	OCH ₂ -cyclopropyl	Cl
6-452	4-Cl-Ph	Cl	OMe	Cl
6-453	4-Cl-Ph	Cl	NHAc	Cl
6-454	4-Cl-Ph	Cl	OCH ₂ C(O)NMe ₂	Cl
6-455	4-Cl-Ph	Cl	Cl	SO ₂ Me
6-456	4-Cl-Ph	Cl	pyrazol-1-yl	SO ₂ Me
6-457	4-Cl-Ph	Cl	4-methoxy- pyrazol-1-yl	SO ₂ Me
6-458	4-Cl-Ph	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-459	4-Cl-Ph	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-460	4-Cl-Ph	Cl	F	SO ₂ Me
6-461	4-Cl-Ph	Me	SO ₂ Me	SO ₂ Me
6-462	4-Cl-Ph	Me	SO ₂ Me	CF ₃
6-463	4-Cl-Ph	Me	NMe ₂	SO ₂ Me
6-464	4-Cl-Ph	Me	S(O)Me	CF ₃
6-465	4-Cl-Ph	Me	SMe	CF ₃
6-466	4-Cl-Ph	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-467	4-Cl-Ph	Me	pyrazol-1-yl	SO ₂ Me
6-468	4-Cl-Ph	Me	4-methoxy- pyrazol-1-yl	SO ₂ Me
6-469	4-Cl-Ph	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-470	4-Cl-Ph	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-471	4-Cl-Ph	Me	Cl	SO ₂ Me
6-472	4-Cl-Ph	Me	Me	SO ₂ Me
6-473	4-Cl-Ph	Me	Me	SMe
6-474	4-Cl-Ph	Me	SO ₂ Me	Cl
6-475	4-Cl-Ph	Me	NMe ₂	SO ₂ Me
6-476	4-Cl-Ph	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-477	4-Cl-Ph	CF ₃	F	SO ₂ CH ₃
6-478	4-Cl-Ph	CF ₃	SMe	SO ₂ CH ₃
6-479	4-Cl-Ph	CF ₃	SEt	SO ₂ CH ₃
6-480	4-Cl-Ph	CF ₃	S(O)Et	SO ₂ CH ₃
6-481	4-Cl-Ph	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-482	4-Cl-Ph	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-483	4-Cl-Ph	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-484	4-Cl-Ph	CF ₃	CH ₂ O- tetrahydrofuran-2- yl	SO ₂ Et

No.	R	X	Y	Z
6-485	4-Cl-Ph	SMe	SMe	F
6-486	4-Cl-Ph	SMe	SEt	F
6-487	4-Cl-Ph	SO ₂ CH ₃	F	Cl
6-488	4-Cl-Ph	F	S(O)Me	CF ₃
6-489	4-Cl-Ph	F	SMe	CF ₃
6-490	tert-butyl	NO ₂	H	SO ₂ Me
6-491	tert-butyl	Cl	H	SO ₂ Me
6-492	tert-butyl	SO ₂ Me	H	CF ₃
6-493	tert-butyl	NO ₂	H	OMe
6-494	tert-butyl	NO ₂	H	Br
6-495	tert-butyl	NO ₂	H	CF ₃
6-496	tert-butyl	NO ₂	H	NO ₂
6-497	tert-butyl	NO ₂	H	Cl
6-498	tert-butyl	NO ₂	H	Me
6-499	tert-butyl	NO ₂	H	F
6-500	tert-butyl	OMe	H	SO ₂ Me
6-501	tert-butyl	CF ₃	H	NO ₂
6-502	tert-butyl	CH ₂ SO ₂ Me	H	Br
6-503	tert-butyl	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-504	tert-butyl	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-505	tert-butyl	Cl	5-cyanomethyl- 4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-506	tert-butyl	Cl	4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-507	tert-butyl	Cl	CH ₂ OCH ₂ - tetrahydrofuran-2- yl	SO ₂ Me
6-508	tert-butyl	Cl	SMe	Cl
6-509	tert-butyl	Cl	SMe	SO ₂ Me
6-510	tert-butyl	Cl	Me	SO ₂ Et
6-511	tert-butyl	Cl	O(CH ₂) ₂ OMe	Cl
6-512	tert-butyl	Cl	OCH ₂ -cyclopropyl	Cl
6-513	tert-butyl	Cl	OMe	Cl
6-514	tert-butyl	Cl	NHAc	Cl
6-515	tert-butyl	Cl	OCH ₂ C(O)NMe ₂	Cl
6-516	tert-butyl	Cl	Cl	SO ₂ Me
6-517	tert-butyl	Cl	pyrazol-1-yl	SO ₂ Me

No.	R	X	Y	Z
6-518	tert-butyl	Cl	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-519	tert-butyl	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-520	tert-butyl	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-521	tert-butyl	Cl	F	SO ₂ Me
6-522	tert-butyl	Me	SO ₂ Me	SO ₂ Me
6-523	tert-butyl	Me	SO ₂ Me	CF ₃
6-524	tert-butyl	Me	NMe ₂	SO ₂ Me
6-525	tert-butyl	Me	S(O)Me	CF ₃
6-526	tert-butyl	Me	SMe	CF ₃
6-527	tert-butyl	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-528	tert-butyl	Me	pyrazol-1-yl	SO ₂ Me
6-529	tert-butyl	Me	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-530	tert-butyl	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-531	tert-butyl	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-532	tert-butyl	Me	Cl	SO ₂ Me
6-533	tert-butyl	Me	Me	SO ₂ Me
6-534	tert-butyl	Me	Me	SMe
6-535	tert-butyl	Me	SO ₂ Me	Cl
6-536	tert-butyl	Me	NMe ₂	SO ₂ Me
6-537	tert-butyl	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-538	tert-butyl	CF ₃	F	SO ₂ CH ₃
6-539	tert-butyl	CF ₃	SMe	SO ₂ CH ₃
6-540	tert-butyl	CF ₃	SEt	SO ₂ CH ₃
6-541	tert-butyl	CF ₃	S(O)Et	SO ₂ CH ₃
6-542	tert-butyl	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-543	tert-butyl	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-544	tert-butyl	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-545	tert-butyl	CF ₃	CH ₂ O-tetrahydrofuran-2-yl	SO ₂ Et
6-546	tert-butyl	SMe	SMe	F
6-547	tert-butyl	SMe	SEt	F
6-548	tert-butyl	SO ₂ CH ₃	F	Cl
6-549	tert-butyl	F	S(O)Me	CF ₃
6-550	tert-butyl	F	SMe	CF ₃
6-551	furan-2-yl	NO ₂	H	SO ₂ Me
6-552	furan-2-yl	Cl	H	SO ₂ Me

No.	R	X	Y	Z
6-553	furan-2-yl	SO ₂ Me	H	CF ₃
6-554	furan-2-yl	NO ₂	H	OMe
6-555	furan-2-yl	NO ₂	H	Br
6-556	furan-2-yl	NO ₂	H	CF ₃
6-557	furan-2-yl	NO ₂	H	NO ₂
6-558	furan-2-yl	NO ₂	H	Cl
6-559	furan-2-yl	NO ₂	H	Me
6-560	furan-2-yl	NO ₂	H	F
6-561	furan-2-yl	OMe	H	SO ₂ Me
6-562	furan-2-yl	CF ₃	H	NO ₂
6-563	furan-2-yl	CH ₂ SO ₂ Me	H	Br
6-564	furan-2-yl	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-565	furan-2-yl	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-566	furan-2-yl	Cl	5-cyanomethyl- 4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-567	furan-2-yl	Cl	4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-568	furan-2-yl	Cl	CH ₂ OCH ₂ - tetrahydrofuran-2- yl	SO ₂ Me
6-569	furan-2-yl	Cl	SMe	Cl
6-570	furan-2-yl	Cl	SMe	SO ₂ Me
6-571	furan-2-yl	Cl	Me	SO ₂ Et
6-572	furan-2-yl	Cl	O(CH ₂) ₂ OMe	Cl
6-573	furan-2-yl	Cl	OCH ₂ -cyclopropyl	Cl
6-574	furan-2-yl	Cl	OMe	Cl
6-575	furan-2-yl	Cl	NHAc	Cl
6-576	furan-2-yl	Cl	OCH ₂ C(O)NMe ₂	Cl
6-577	furan-2-yl	Cl	Cl	SO ₂ Me
6-578	furan-2-yl	Cl	pyrazol-1-yl	SO ₂ Me
6-579	furan-2-yl	Cl	4-methoxy- pyrazol-1-yl	SO ₂ Me
6-580	furan-2-yl	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-581	furan-2-yl	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-582	furan-2-yl	Cl	F	SO ₂ Me
6-583	furan-2-yl	Me	SO ₂ Me	SO ₂ Me
6-584	furan-2-yl	Me	SO ₂ Me	CF ₃

No.	R	X	Y	Z
6-585	furan-2-yl	Me	NMe ₂	SO ₂ Me
6-586	furan-2-yl	Me	S(O)Me	CF ₃
6-587	furan-2-yl	Me	SMe	CF ₃
6-588	furan-2-yl	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-589	furan-2-yl	Me	pyrazol-1-yl	SO ₂ Me
6-590	furan-2-yl	Me	4-methoxy- pyrazol-1-yl	SO ₂ Me
6-591	furan-2-yl	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-592	furan-2-yl	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-593	furan-2-yl	Me	Cl	SO ₂ Me
6-594	furan-2-yl	Me	Me	SO ₂ Me
6-595	furan-2-yl	Me	Me	SMe
6-596	furan-2-yl	Me	SO ₂ Me	Cl
6-597	furan-2-yl	Me	NMe ₂	SO ₂ Me
6-598	furan-2-yl	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-599	furan-2-yl	CF ₃	F	SO ₂ CH ₃
6-600	furan-2-yl	CF ₃	SMe	SO ₂ CH ₃
6-601	furan-2-yl	CF ₃	SEt	SO ₂ CH ₃
6-602	furan-2-yl	CF ₃	S(O)Et	SO ₂ CH ₃
6-603	furan-2-yl	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-604	furan-2-yl	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-605	furan-2-yl	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-606	furan-2-yl	CF ₃	CH ₂ O- tetrahydrofuran- 2-yl	SO ₂ Et
6-607	furan-2-yl	SMe	SMe	F
6-608	furan-2-yl	SMe	SEt	F
6-609	furan-2-yl	SO ₂ CH ₃	F	Cl
6-610	furan-2-yl	F	S(O)Me	CF ₃
6-611	furan-2-yl	F	SMe	CF ₃
6-612	isopropyl	NO ₂	H	SO ₂ Me
6-613	isopropyl	Cl	H	SO ₂ Me
6-614	isopropyl	SO ₂ Me	H	CF ₃
6-615	isopropyl	NO ₂	H	OMe
6-616	isopropyl	NO ₂	H	Br
6-617	isopropyl	NO ₂	H	CF ₃
6-618	isopropyl	NO ₂	H	NO ₂
6-619	isopropyl	NO ₂	H	Cl
6-620	isopropyl	NO ₂	H	Me
6-621	isopropyl	NO ₂	H	F

No.	R	X	Y	Z
6-622	isopropyl	OMe	H	SO ₂ Me
6-623	isopropyl	CF ₃	H	NO ₂
6-624	isopropyl	CH ₂ SO ₂ Me	H	Br
6-625	isopropyl	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-626	isopropyl	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-627	isopropyl	Cl	5-cyanomethyl- 4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-628	isopropyl	Cl	4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-629	isopropyl	Cl	CH ₂ OCH ₂ - tetrahydrofuran-2- yl	SO ₂ Me
6-630	isopropyl	Cl	SMe	Cl
6-631	isopropyl	Cl	SMe	SO ₂ Me
6-632	isopropyl	Cl	Me	SO ₂ Et
6-633	isopropyl	Cl	O(CH ₂) ₂ OMe	Cl
6-634	isopropyl	Cl	OCH ₂ -cyclopropyl	Cl
6-635	isopropyl	Cl	OMe	Cl
6-636	isopropyl	Cl	NHAc	Cl
6-637	isopropyl	Cl	OCH ₂ C(O)NMe ₂	Cl
6-638	isopropyl	Cl	Cl	SO ₂ Me
6-639	isopropyl	Cl	pyrazol-1-yl	SO ₂ Me
6-640	isopropyl	Cl	4-methoxy- pyrazol-1-yl	SO ₂ Me
6-641	isopropyl	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-642	isopropyl	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-643	isopropyl	Cl	F	SO ₂ Me
6-644	isopropyl	Me	SO ₂ Me	SO ₂ Me
6-645	isopropyl	Me	SO ₂ Me	CF ₃
6-646	isopropyl	Me	NMe ₂	SO ₂ Me
6-647	isopropyl	Me	S(O)Me	CF ₃
6-648	isopropyl	Me	SMe	CF ₃
6-649	isopropyl	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-650	isopropyl	Me	pyrazol-1-yl	SO ₂ Me
6-651	isopropyl	Me	4-methoxy- pyrazol-1-yl	SO ₂ Me
6-652	isopropyl	Me	1,2,3-triazol-1-yl	SO ₂ Me

No.	R	X	Y	Z
6-653	isopropyl	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-654	isopropyl	Me	Cl	SO ₂ Me
6-655	isopropyl	Me	Me	SO ₂ Me
6-656	isopropyl	Me	F	Cl
6-657	isopropyl	Me	SO ₂ Me	Cl
6-658	isopropyl	Me	NMe ₂	SO ₂ Me
6-659	isopropyl	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-660	isopropyl	CF ₃	F	SO ₂ CH ₃
6-661	isopropyl	CF ₃	SMe	SO ₂ CH ₃
6-662	isopropyl	CF ₃	SEt	SO ₂ CH ₃
6-663	isopropyl	CF ₃	S(O)Et	SO ₂ CH ₃
6-664	isopropyl	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-665	isopropyl	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-666	isopropyl	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-667	isopropyl	CF ₃	CH ₂ O- tetrahydrofuran-2- yl	SO ₂ Et
6-668	isopropyl	SMe	SMe	F
6-669	isopropyl	SMe	SEt	F
6-670	isopropyl	SO ₂ CH ₃	F	Cl
6-671	isopropyl	F	S(O)Me	CF ₃
6-672	isopropyl	F	SMe	CF ₃
6-673	CH ₂ CH ₂ O Me	NO ₂	H	SO ₂ Me
6-674	CH ₂ CH ₂ O Me	Cl	H	SO ₂ Me
6-675	CH ₂ CH ₂ O Me	SO ₂ Me	H	CF ₃
6-676	CH ₂ CH ₂ O Me	NO ₂	H	OMe
6-677	CH ₂ CH ₂ O Me	NO ₂	H	Br
6-678	CH ₂ CH ₂ O Me	NO ₂	H	CF ₃
6-679	CH ₂ CH ₂ O Me	NO ₂	H	NO ₂
6-680	CH ₂ CH ₂ O Me	NO ₂	H	Cl
6-681	CH ₂ CH ₂ O Me	NO ₂	H	Me
6-682	CH ₂ CH ₂ O Me	NO ₂	H	F

No.	R	X	Y	Z
6-683	CH ₂ CH ₂ O Me	OMe	H	SO ₂ Me
6-684	CH ₂ CH ₂ O Me	CF ₃	H	NO ₂
6-685	CH ₂ CH ₂ O Me	CH ₂ SO ₂ Me	H	Br
6-686	CH ₂ CH ₂ O Me	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-687	CH ₂ CH ₂ O Me	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-688	CH ₂ CH ₂ O Me	Cl	5-cyanomethyl- 4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-689	CH ₂ CH ₂ O Me	Cl	4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-690	CH ₂ CH ₂ O Me	Cl	CH ₂ OCH ₂ - tetrahydrofuran-2- yl	SO ₂ Me
6-691	CH ₂ CH ₂ O Me	Cl	SMe	Cl
6-692	CH ₂ CH ₂ O Me	Cl	SMe	SO ₂ Me
6-693	CH ₂ CH ₂ O Me	Cl	Me	SO ₂ Et
6-694	CH ₂ CH ₂ O Me	Cl	O(CH ₂) ₂ OMe	Cl
6-695	CH ₂ CH ₂ O Me	Cl	OCH ₂ -cyclopropyl	Cl
6-696	CH ₂ CH ₂ O Me	Cl	OMe	Cl
6-697	CH ₂ CH ₂ O Me	Cl	NHAc	Cl
6-698	CH ₂ CH ₂ O Me	Cl	OCH ₂ C(O)NMe ₂	Cl
6-699	CH ₂ CH ₂ O Me	Cl	Cl	SO ₂ Me
6-700	CH ₂ CH ₂ O Me	Cl	pyrazol-1-yl	SO ₂ Me
6-701	CH ₂ CH ₂ O Me	Cl	4-methoxy- pyrazol-1-yl	SO ₂ Me
6-702	CH ₂ CH ₂ O Me	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-703	CH ₂ CH ₂ O Me	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-704	CH ₂ CH ₂ O Me	Cl	F	SO ₂ Me
6-705	CH ₂ CH ₂ O Me	Me	SO ₂ Me	SO ₂ Me

No.	R	X	Y	Z
6-706	CH ₂ CH ₂ O Me	Me	SO ₂ Me	CF ₃
6-707	CH ₂ CH ₂ O Me	Me	NMe ₂	SO ₂ Me
6-708	CH ₂ CH ₂ O Me	Me	S(O)Me	CF ₃
6-709	CH ₂ CH ₂ O Me	Me	SMe	CF ₃
6-710	CH ₂ CH ₂ O Me	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-711	CH ₂ CH ₂ O Me	Me	pyrazol-1-yl	SO ₂ Me
6-712	CH ₂ CH ₂ O Me	Me	4-methoxy- pyrazol-1-yl	SO ₂ Me
6-713	CH ₂ CH ₂ O Me	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-714	CH ₂ CH ₂ O Me	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-715	CH ₂ CH ₂ O Me	Me	Cl	SO ₂ Me
6-716	CH ₂ CH ₂ O Me	Me	Me	SO ₂ Me
6-717	CH ₂ CH ₂ O Me	Me	Me	SMe
6-718	CH ₂ CH ₂ O Me	Me	SO ₂ Me	Cl
6-719	CH ₂ CH ₂ O Me	Me	NMe ₂	SO ₂ Me
6-720	CH ₂ CH ₂ O Me	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-721	CH ₂ CH ₂ O Me	CF ₃	F	SO ₂ CH ₃
6-722	CH ₂ CH ₂ O Me	CF ₃	SMe	SO ₂ CH ₃
6-723	CH ₂ CH ₂ O Me	CF ₃	SEt	SO ₂ CH ₃
6-724	CH ₂ CH ₂ O Me	CF ₃	S(O)Et	SO ₂ CH ₃
6-725	CH ₂ CH ₂ O Me	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-726	CH ₂ CH ₂ O Me	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-727	CH ₂ CH ₂ O Me	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-728	CH ₂ CH ₂ O Me	CF ₃	CH ₂ O- tetrahydrofuran-2- yl	SO ₂ Et
6-729	CH ₂ CH ₂ O Me	SMe	SMe	F

No.	R	X	Y	Z
6-730	CH ₂ CH ₂ O Me	SMe	SEt	F
6-731	CH ₂ CH ₂ O Me	SO ₂ CH ₃	F	Cl
6-732	CH ₂ CH ₂ O Me	F	S(O)Me	CF ₃
6-733	CH ₂ CH ₂ O Me	F	SMe	CF ₃
6-734	CH ₂ CF ₃	NO ₂	H	SO ₂ Me
6-735	CH ₂ CF ₃	Cl	H	SO ₂ Me
6-736	CH ₂ CF ₃	SO ₂ Me	H	CF ₃
6-737	CH ₂ CF ₃	NO ₂	H	OMe
6-738	CH ₂ CF ₃	NO ₂	H	Br
6-739	CH ₂ CF ₃	NO ₂	H	CF ₃
6-740	CH ₂ CF ₃	NO ₂	H	NO ₂
6-741	CH ₂ CF ₃	NO ₂	H	Cl
6-742	CH ₂ CF ₃	NO ₂	H	Me
6-743	CH ₂ CF ₃	NO ₂	H	F
6-744	CH ₂ CF ₃	OMe	H	SO ₂ Me
6-745	CH ₂ CF ₃	CF ₃	H	NO ₂
6-746	CH ₂ CF ₃	CH ₂ SO ₂ Me	H	Br
6-747	CH ₂ CF ₃	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-748	CH ₂ CF ₃	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-749	CH ₂ CF ₃	Cl	5-cyanomethyl- 4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-750	CH ₂ CF ₃	Cl	4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-751	CH ₂ CF ₃	Cl	CH ₂ OCH ₂ - tetrahydrofuran-2- yl	SO ₂ Me
6-752	CH ₂ CF ₃	Cl	SMe	Cl
6-753	CH ₂ CF ₃	Cl	SMe	SO ₂ Me
6-754	CH ₂ CF ₃	Cl	Me	SO ₂ Et
6-755	CH ₂ CF ₃	Cl	O(CH ₂) ₂ OMe	Cl
6-756	CH ₂ CF ₃	Cl	OCH ₂ -cyclopropyl	Cl
6-757	CH ₂ CF ₃	Cl	OMe	Cl
6-758	CH ₂ CF ₃	Cl	NHAc	Cl
6-759	CH ₂ CF ₃	Cl	OCH ₂ C(O)NMe ₂	Cl
6-760	CH ₂ CF ₃	Cl	Cl	SO ₂ Me
6-761	CH ₂ CF ₃	Cl	pyrazol-1-yl	SO ₂ Me

No.	R	X	Y	Z
6-762	CH ₂ CF ₃	Cl	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-763	CH ₂ CF ₃	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-764	CH ₂ CF ₃	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-765	CH ₂ CF ₃	Cl	F	SO ₂ Me
6-766	CH ₂ CF ₃	Me	SO ₂ Me	SO ₂ Me
6-767	CH ₂ CF ₃	Me	SO ₂ Me	CF ₃
6-768	CH ₂ CF ₃	Me	NMe ₂	SO ₂ Me
6-769	CH ₂ CF ₃	Me	S(O)Me	CF ₃
6-770	CH ₂ CF ₃	Me	SMe	CF ₃
6-771	CH ₂ CF ₃	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-772	CH ₂ CF ₃	Me	pyrazol-1-yl	SO ₂ Me
6-773	CH ₂ CF ₃	Me	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-774	CH ₂ CF ₃	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-775	CH ₂ CF ₃	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-776	CH ₂ CF ₃	Me	Cl	SO ₂ Me
6-777	CH ₂ CF ₃	Me	Me	SO ₂ Me
6-778	CH ₂ CF ₃	Me	Me	SMe
6-779	CH ₂ CF ₃	Me	SO ₂ Me	Cl
6-780	CH ₂ CF ₃	Me	NMe ₂	SO ₂ Me
6-781	CH ₂ CF ₃	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-782	CH ₂ CF ₃	CF ₃	F	SO ₂ CH ₃
6-783	CH ₂ CF ₃	CF ₃	SMe	SO ₂ CH ₃
6-784	CH ₂ CF ₃	CF ₃	SEt	SO ₂ CH ₃
6-785	CH ₂ CF ₃	CF ₃	S(O)Et	SO ₂ CH ₃
6-786	CH ₂ CF ₃	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-787	CH ₂ CF ₃	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-788	CH ₂ CF ₃	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-789	CH ₂ CF ₃	CF ₃	CH ₂ O-tetrahydrofuran-2-yl	SO ₂ Et
6-790	CH ₂ CF ₃	SMe	SMe	F
6-791	CH ₂ CF ₃	SMe	SEt	F
6-792	CH ₂ CF ₃	SO ₂ CH ₃	F	Cl
6-793	CH ₂ CF ₃	F	S(O)Me	CF ₃
6-794	CH ₂ CF ₃	F	SMe	CF ₃
6-795	tetrahydrofuran-2-yl	NO ₂	H	SO ₂ Me

No.	R	X	Y	Z
6-796	tetra-hydro-furan-2-yl	Cl	H	SO ₂ Me
6-797	tetra-hydro-furan-2-yl	SO ₂ Me	H	CF ₃
6-798	tetra-hydro-furan-2-yl	NO ₂	H	OMe
6-799	tetra-hydro-furan-2-yl	NO ₂	H	Br
6-800	tetra-hydro-furan-2-yl	NO ₂	H	CF ₃
6-801	tetra-hydro-furan-2-yl	NO ₂	H	NO ₂
6-802	tetra-hydro-furan-2-yl	NO ₂	H	Cl
6-803	tetra-hydro-furan-2-yl	NO ₂	H	Me
6-804	tetra-hydro-furan-2-yl	NO ₂	H	F
6-805	tetra-hydro-furan-2-yl	OMe	H	SO ₂ Me
6-806	tetra-hydro-furan-2-yl	CF ₃	H	NO ₂
6-807	tetra-hydro-furan-2-yl	CH ₂ SO ₂ Me	H	Br
6-808	tetra-hydro-furan-2-yl	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-809	tetra-hydro-furan-2-yl	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-810	tetra-hydro-furan-2-yl	Cl	5-cyanomethyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
6-811	tetra-hydro-furan-2-yl	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
6-812	tetra-hydro-furan-2-yl	Cl	CH ₂ OCH ₂ -tetrahydrofuran-2-yl	SO ₂ Me

No.	R	X	Y	Z
6-813	tetra-hydro-furan-2-yl	Cl	SMe	Cl
6-814	tetra-hydro-furan-2-yl	Cl	SMe	SO ₂ Me
6-815	tetra-hydro-furan-2-yl	Cl	Me	SO ₂ Et
6-816	tetra-hydro-furan-2-yl	Cl	O(CH ₂) ₂ OMe	Cl
6-817	tetra-hydro-furan-2-yl	Cl	OCH ₂ -cyclopropyl	Cl
6-818	tetra-hydro-furan-2-yl	Cl	OMe	Cl
6-819	tetra-hydro-furan-2-yl	Cl	NHAc	Cl
6-820	tetra-hydro-furan-2-yl	Cl	OCH ₂ C(O)NMe ₂	Cl
6-821	tetra-hydro-furan-2-yl	Cl	Cl	SO ₂ Me
6-822	tetra-hydro-furan-2-yl	Cl	pyrazol-1-yl	SO ₂ Me
6-823	tetra-hydro-furan-2-yl	Cl	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-824	tetra-hydro-furan-2-yl	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-825	tetra-hydro-furan-2-yl	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-826	tetra-hydro-furan-2-yl	Cl	F	SO ₂ Me
6-827	tetra-hydro-furan-2-yl	Me	SO ₂ Me	SO ₂ Me
6-828	tetra-hydro-furan-2-yl	Me	SO ₂ Me	CF ₃
6-829	tetra-hydro-furan-2-yl	Me	NMe ₂	SO ₂ Me

No.	R	X	Y	Z
6-830	tetra-hydro-furan-2-yl	Me	S(O)Me	CF ₃
6-831	tetra-hydro-furan-2-yl	Me	SMe	CF ₃
6-832	tetra-hydro-furan-2-yl	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-833	tetra-hydro-furan-2-yl	Me	pyrazol-1-yl	SO ₂ Me
6-834	tetra-hydro-furan-2-yl	Me	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-835	tetra-hydro-furan-2-yl	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-836	tetra-hydro-furan-2-yl	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-837	tetra-hydro-furan-2-yl	Me	Cl	SO ₂ Me
6-838	tetra-hydro-furan-2-yl	Me	Me	SO ₂ Me
6-839	tetra-hydro-furan-2-yl	Me	Me	SMe
6-840	tetra-hydro-furan-2-yl	Me	SO ₂ Me	Cl
6-841	tetra-hydro-furan-2-yl	Me	NMe ₂	SO ₂ Me
6-842	tetra-hydro-furan-2-yl	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-843	tetra-hydro-furan-2-yl	CF ₃	F	SO ₂ CH ₃
6-844	tetra-hydro-furan-2-yl	CF ₃	SMe	SO ₂ CH ₃
6-845	tetra-hydro-furan-2-yl	CF ₃	SEt	SO ₂ CH ₃
6-846	tetra-hydro-furan-2-yl	CF ₃	S(O)Et	SO ₂ CH ₃

No.	R	X	Y	Z
6-847	tetrahydrofuran-2-yl	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-848	tetrahydrofuran-2-yl	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-849	tetrahydrofuran-2-yl	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-850	tetrahydrofuran-2-yl	CF ₃	CH ₂ O-tetrahydrofuran-2-yl	SO ₂ Et
6-851	tetrahydrofuran-2-yl	SMe	SMe	F
6-852	tetrahydrofuran-2-yl	SMe	SEt	F
6-853	tetrahydrofuran-2-yl	SO ₂ CH ₃	F	Cl
6-854	tetrahydrofuran-2-yl	F	S(O)Me	CF ₃
6-855	tetrahydrofuran-2-yl	F	SMe	CF ₃
6-856	n-Pr	NO ₂	H	SO ₂ Me
6-857	n-Pr	Cl	H	SO ₂ Me
6-858	n-Pr	SO ₂ Me	H	CF ₃
6-859	n-Pr	NO ₂	H	OMe
6-860	n-Pr	NO ₂	H	Br
6-861	n-Pr	NO ₂	H	Cl
6-862	n-Pr	NO ₂	H	CF ₃
6-863	n-Pr	NO ₂	H	NO ₂
6-864	n-Pr	NO ₂	H	Me
6-865	n-Pr	NO ₂	H	F
6-866	n-Pr	OMe	H	SO ₂ Me
6-867	n-Pr	CF ₃	H	NO ₂
6-868	n-Pr	CH ₂ SO ₂ Me	H	Br
6-869	n-Pr	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-870	n-Pr	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-871	n-Pr	Cl	5-cyanomethyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
6-872	n-Pr	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et

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No.	R	X	Y	Z
6-873	n-Pr	Cl	CH ₂ OCH ₂ - tetrahydrofuran-2- yl	SO ₂ Me
6-874	n-Pr	Cl	SMe	Cl
6-875	n-Pr	Cl	SMe	SO ₂ Me
6-876	n-Pr	Cl	Me	SO ₂ Et
6-877	n-Pr	Cl	O(CH ₂) ₂ OMe	Cl
6-878	n-Pr	Cl	OCH ₂ -cyclopropyl	Cl
6-879	n-Pr	Cl	OMe	Cl
6-880	n-Pr	Cl	NHAc	Cl
6-881	n-Pr	Cl	OCH ₂ C(O)NMe ₂	Cl
6-882	n-Pr	Cl	Cl	SO ₂ Me
6-883	n-Pr	Cl	pyrazol-1-yl	SO ₂ Me
6-884	n-Pr	Cl	4-methoxy- pyrazol-1-yl	SO ₂ Me
6-885	n-Pr	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-886	n-Pr	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-887	n-Pr	Cl	F	SO ₂ Me
6-888	n-Pr	Me	SO ₂ Me	SO ₂ Me
6-889	n-Pr	Me	SO ₂ Me	CF ₃
6-890	n-Pr	Me	NMe ₂	SO ₂ Me
6-891	n-Pr	Me	S(O)Me	CF ₃
6-892	n-Pr	Me	SMe	CF ₃
6-893	n-Pr	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-894	n-Pr	Me	pyrazol-1-yl	SO ₂ Me
6-895	n-Pr	Me	4-methoxy- pyrazol-1-yl	SO ₂ Me
6-896	n-Pr	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-897	n-Pr	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-898	n-Pr	Me	Cl	SO ₂ Me
6-899	n-Pr	Me	Me	SO ₂ Me
6-900	n-Pr	Me	Me	SMe
6-901	n-Pr	Me	SO ₂ Me	Cl
6-902	n-Pr	Me	NMe ₂	SO ₂ Me
6-903	n-Pr	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-904	n-Pr	CF ₃	F	SO ₂ CH ₃
6-905	n-Pr	CF ₃	SMe	SO ₂ CH ₃
6-906	n-Pr	CF ₃	SEt	SO ₂ CH ₃
6-907	n-Pr	CF ₃	S(O)Et	SO ₂ CH ₃
6-908	n-Pr	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃

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No.	R	X	Y	Z
6-909	n-Pr	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-910	n-Pr	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-911	n-Pr	CF ₃	CH ₂ O- tetrahydrofuran-2- yl	SO ₂ Et
6-912	n-Pr	SMe	SMe	F
6-913	n-Pr	SMe	SEt	F
6-914	n-Pr	SO ₂ CH ₃	F	Cl
6-915	n-Pr	F	S(O)Me	CF ₃
6-916	n-Pr	F	SMe	CF ₃
6-917	CH ₂ OEt	NO ₂	H	SO ₂ Me
6-918	CH ₂ OEt	Cl	H	SO ₂ Me
6-919	CH ₂ OEt	SO ₂ Me	H	CF ₃
6-920	CH ₂ OEt	NO ₂	H	OMe
6-921	CH ₂ OEt	NO ₂	H	Br
6-922	CH ₂ OEt	NO ₂	H	CF ₃
6-923	CH ₂ OEt	NO ₂	H	NO ₂
6-924	CH ₂ OEt	NO ₂	H	Cl
6-925	CH ₂ OEt	NO ₂	H	Me
6-926	CH ₂ OEt	NO ₂	H	F
6-927	CH ₂ OEt	OMe	H	SO ₂ Me
6-928	CH ₂ OEt	CF ₃	H	NO ₂
6-929	CH ₂ OEt	CH ₂ SO ₂ Me	H	Br
6-930	CH ₂ OEt	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-931	CH ₂ OEt	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-932	CH ₂ OEt	Cl	5-cyanomethyl- 4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-933	CH ₂ OEt	Cl	4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-934	CH ₂ OEt	Cl	CH ₂ OCH ₂ - tetrahydrofuran-2- yl	SO ₂ Me
6-935	CH ₂ OEt	Cl	SMe	Cl
6-936	CH ₂ OEt	Cl	SMe	SO ₂ Me
6-937	CH ₂ OEt	Cl	Me	SO ₂ Et
6-938	CH ₂ OEt	Cl	O(CH ₂) ₂ OMe	Cl
6-939	CH ₂ OEt	Cl	OCH ₂ -cyclopropyl	Cl
6-940	CH ₂ OEt	Cl	OMe	Cl
6-941	CH ₂ OEt	Cl	NHAc	Cl
6-942	CH ₂ OEt	Cl	OCH ₂ C(O)NMe ₂	Cl
6-943	CH ₂ OEt	Cl	Cl	SO ₂ Me
6-944	CH ₂ OEt	Cl	pyrazol-1-yl	SO ₂ Me

No.	R	X	Y	Z
6-945	CH ₂ OEt	Cl	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-946	CH ₂ OEt	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-947	CH ₂ OEt	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-948	CH ₂ OEt	Cl	F	SO ₂ Me
6-949	CH ₂ OEt	Me	SO ₂ Me	SO ₂ Me
6-950	CH ₂ OEt	Me	SO ₂ Me	CF ₃
6-951	CH ₂ OEt	Me	NMe ₂	SO ₂ Me
6-952	CH ₂ OEt	Me	S(O)Me	CF ₃
6-953	CH ₂ OEt	Me	SMe	CF ₃
6-954	CH ₂ OEt	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-955	CH ₂ OEt	Me	pyrazol-1-yl	SO ₂ Me
6-956	CH ₂ OEt	Me	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-957	CH ₂ OEt	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-958	CH ₂ OEt	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-959	CH ₂ OEt	Me	Cl	SO ₂ Me
6-960	CH ₂ OEt	Me	Me	SO ₂ Me
6-961	CH ₂ OEt	Me	Me	SMe
6-962	CH ₂ OEt	Me	SO ₂ Me	Cl
6-963	CH ₂ OEt	Me	NMe ₂	SO ₂ Me
6-964	CH ₂ OEt	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-965	CH ₂ OEt	CF ₃	F	SO ₂ CH ₃
6-966	CH ₂ OEt	CF ₃	SMe	SO ₂ CH ₃
6-967	CH ₂ OEt	CF ₃	SEt	SO ₂ CH ₃
6-968	CH ₂ OEt	CF ₃	S(O)Et	SO ₂ CH ₃
6-969	CH ₂ OEt	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-970	CH ₂ OEt	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-971	CH ₂ OEt	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-972	CH ₂ OEt	CF ₃	CH ₂ O-tetrahydrofuran-2-yl	SO ₂ Et
6-973	CH ₂ OEt	SMe	SMe	F
6-974	CH ₂ OEt	SMe	SEt	F
6-975	CH ₂ OEt	SO ₂ CH ₃	F	Cl
6-976	CH ₂ OEt	F	S(O)Me	CF ₃
6-977	CH ₂ OEt	F	SMe	CF ₃
6-978	cyclobutyl	NO ₂	H	SO ₂ Me
6-979	cyclobutyl	Cl	H	SO ₂ Me
6-980	cyclobutyl	SO ₂ Me	H	CF ₃
6-981	cyclobutyl	NO ₂	H	OMe
6-982	cyclobutyl	NO ₂	H	Br

No.	R	X	Y	Z
6-983	cyclobutyl	SMe	H	CF ₃
6-984	cyclobutyl	NO ₂	H	NO ₂
6-985	cyclobutyl	NO ₂	H	Cl
6-986	cyclobutyl	NO ₂	H	Me
6-987	cyclobutyl	NO ₂	H	F
6-988	cyclobutyl	OMe	H	SO ₂ Me
6-989	cyclobutyl	CF ₃	H	NO ₂
6-990	cyclobutyl	CH ₂ SO ₂ Me	H	Br
6-991	cyclobutyl	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-992	cyclobutyl	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-993	cyclobutyl	Cl	5-cyanomethyl- 4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-994	cyclobutyl	Cl	4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-995	cyclobutyl	Cl	CH ₂ OCH ₂ - tetrahydrofuran-2- yl	SO ₂ Me
6-996	cyclobutyl	Cl	SMe	Cl
6-997	cyclobutyl	Cl	SMe	SO ₂ Me
6-998	cyclobutyl	Cl	Me	SO ₂ Et
6-999	cyclobutyl	Cl	O(CH ₂) ₂ OMe	Cl
6-1000	cyclobutyl	Cl	OCH ₂ -cyclopropyl	Cl
6-1001	cyclobutyl	Cl	OMe	Cl
6-1002	cyclobutyl	Cl	NHAc	Cl
6-1003	cyclobutyl	Cl	OCH ₂ C(O)NMe ₂	Cl
6-1004	cyclobutyl	Cl	Cl	SO ₂ Me
6-1005	cyclobutyl	Cl	pyrazol-1-yl	SO ₂ Me
6-1006	cyclobutyl	Cl	4-methoxy- pyrazol-1-yl	SO ₂ Me
6-1007	cyclobutyl	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-1008	cyclobutyl	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-1009	cyclobutyl	Cl	F	SO ₂ Me
6-1010	cyclobutyl	Me	SO ₂ Me	SO ₂ Me
6-1011	cyclobutyl	Me	SO ₂ Me	CF ₃
6-1012	cyclobutyl	Me	NMe ₂	SO ₂ Me
6-1013	cyclobutyl	Me	S(O)Me	CF ₃
6-1014	cyclobutyl	Me	SMe	CF ₃
6-1015	cyclobutyl	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃

No.	R	X	Y	Z
6-1016	cyclobutyl	Me	pyrazol-1-yl	SO ₂ Me
6-1017	cyclobutyl	Me	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-1018	cyclobutyl	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-1019	cyclobutyl	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-1020	cyclobutyl	Me	Cl	SO ₂ Me
6-1021	cyclobutyl	Me	Me	SO ₂ Me
6-1022	cyclobutyl	Me	Me	SMe
6-1023	cyclobutyl	Me	SO ₂ Me	Cl
6-1024	cyclobutyl	Me	NMe ₂	SO ₂ Me
6-1025	cyclobutyl	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-1026	cyclobutyl	CF ₃	F	SO ₂ CH ₃
6-1027	cyclobutyl	CF ₃	SMe	SO ₂ CH ₃
6-1028	cyclobutyl	CF ₃	SEt	SO ₂ CH ₃
6-1029	cyclobutyl	CF ₃	S(O)Et	SO ₂ CH ₃
6-1030	cyclobutyl	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-1031	cyclobutyl	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-1032	cyclobutyl	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-1033	cyclobutyl	CF ₃	CH ₂ O-tetrahydrofuran-2-yl	SO ₂ Et
6-1034	cyclobutyl	SMe	SMe	F
6-1035	cyclobutyl	SMe	SEt	F
6-1036	cyclobutyl	SO ₂ CH ₃	F	Cl
6-1037	cyclobutyl	F	S(O)Me	CF ₃
6-1038	cyclobutyl	F	SMe	CF ₃
6-1039	cyclopentyl	NO ₂	H	SO ₂ Me
6-1040	cyclopentyl	Cl	H	SO ₂ Me
6-1041	cyclopentyl	SO ₂ Me	H	CF ₃
6-1042	cyclopentyl	NO ₂	H	OMe
6-1043	cyclopentyl	NO ₂	H	Br
6-1044	cyclopentyl	SMe	H	CF ₃
6-1045	cyclopentyl	NO ₂	H	NO ₂
6-1046	cyclopentyl	NO ₂	H	Cl

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No.	R	X	Y	Z
6-1047	cyclopentyl	NO ₂	H	Me
6-1048	cyclopentyl	NO ₂	H	F
6-1049	cyclopentyl	OMe	H	SO ₂ Me
6-1050	cyclopentyl	CF ₃	H	NO ₂
6-1051	cyclopentyl	CH ₂ SO ₂ Me	H	Br
6-1052	cyclopentyl	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-1053	cyclopentyl	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-1054	cyclopentyl	Cl	5-cyanomethyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
6-1055	cyclopentyl	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
6-1056	cyclopentyl	Cl	CH ₂ OCH ₂ -tetrahydrofuran-2-yl	SO ₂ Me
6-1057	cyclopentyl	Cl	SMe	Cl
6-1058	cyclopentyl	Cl	SMe	SO ₂ Me
6-1059	cyclopentyl	Cl	Me	SO ₂ Et
6-1060	cyclopentyl	Cl	O(CH ₂) ₂ OMe	Cl
6-1061	cyclopentyl	Cl	OCH ₂ -cyclopropyl	Cl
6-1062	cyclopentyl	Cl	OMe	Cl
6-1063	cyclopentyl	Cl	NHAc	Cl
6-1064	cyclopentyl	Cl	OCH ₂ C(O)NMe ₂	Cl
6-1065	cyclopentyl	Cl	Cl	SO ₂ Me
6-1066	cyclopentyl	Cl	pyrazol-1-yl	SO ₂ Me
6-1067	cyclopentyl	Cl	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-1068	cyclopentyl	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-1069	cyclopentyl	Cl	1,2,3-triazol-2-yl	SO ₂ Me

No.	R	X	Y	Z
6-1070	cyclopentyl	Cl	F	SO ₂ Me
6-1071	cyclopentyl	Me	SO ₂ Me	SO ₂ Me
6-1072	cyclopentyl	Me	SO ₂ Me	CF ₃
6-1073	cyclopentyl	Me	NMe ₂	SO ₂ Me
6-1074	cyclopentyl	Me	S(O)Me	CF ₃
6-1075	cyclopentyl	Me	SMe	CF ₃
6-1076	cyclopentyl	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-1077	cyclopentyl	Me	pyrazol-1-yl	SO ₂ Me
6-1078	cyclopentyl	Me	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-1079	cyclopentyl	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-1080	cyclopentyl	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-1081	cyclopentyl	Me	Cl	SO ₂ Me
6-1082	cyclopentyl	Me	Me	SO ₂ Me
6-1083	cyclopentyl	Me	Me	SMe
6-1084	cyclopentyl	Me	SO ₂ Me	Cl
6-1085	cyclopentyl	Me	NMe ₂	SO ₂ Me
6-1086	cyclopentyl	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-1087	cyclopentyl	CF ₃	F	SO ₂ CH ₃
6-1088	cyclopentyl	CF ₃	SMe	SO ₂ CH ₃
6-1089	cyclopentyl	CF ₃	SEt	SO ₂ CH ₃
6-1090	cyclopentyl	CF ₃	S(O)Et	SO ₂ CH ₃
6-1091	cyclopentyl	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-1092	cyclopentyl	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-1093	cyclopentyl	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me

No.	R	X	Y	Z
6-1094	cyclopentyl	CF ₃	CH ₂ O-tetrahydrofuran-2-yl	SO ₂ Et
6-1095	cyclopentyl	SMe	SMe	F
6-1096	cyclopentyl	SMe	SEt	F
6-1097	cyclopentyl	SO ₂ CH ₃	F	Cl
6-1098	cyclopentyl	F	S(O)Me	CF ₃
6-1099	cyclopentyl	F	SMe	CF ₃
6-1100	Me ₂ N	NO ₂	H	SO ₂ Me
6-1101	Me ₂ N	Cl	H	SO ₂ Me
6-1102	Me ₂ N	SO ₂ Me	H	CF ₃
6-1103	Me ₂ N	NO ₂	H	OMe
6-1104	Me ₂ N	NO ₂	H	Br
6-1105	Me ₂ N	NO ₂	H	CF ₃
6-1106	Me ₂ N	NO ₂	H	NO ₂
6-1107	Me ₂ N	NO ₂	H	Cl
6-1108	Me ₂ N	NO ₂	H	Me
6-1109	Me ₂ N	NO ₂	H	F
6-1110	Me ₂ N	OMe	H	SO ₂ Me
6-1111	Me ₂ N	CF ₃	H	NO ₂
6-1112	Me ₂ N	CH ₂ SO ₂ Me	H	Br
6-1113	Me ₂ N	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-1114	Me ₂ N	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-1115	Me ₂ N	Cl	5-cyanomethyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
6-1116	Me ₂ N	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
6-1117	Me ₂ N	Cl	CH ₂ OCH ₂ -tetrahydrofuran-2-yl	SO ₂ Me
6-1118	Me ₂ N	Cl	SMe	Cl
6-1119	Me ₂ N	Cl	SMe	SO ₂ Me
6-1120	Me ₂ N	Cl	Me	SO ₂ Et
6-1121	Me ₂ N	Cl	O(CH ₂) ₂ OMe	Cl
6-1122	Me ₂ N	Cl	OCH ₂ -cyclopropyl	Cl
6-1123	Me ₂ N	Cl	OMe	Cl
6-1124	Me ₂ N	Cl	NHAc	Cl
6-1125	Me ₂ N	Cl	OCH ₂ C(O)NMe ₂	Cl

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No.	R	X	Y	Z
6-1126	Me ₂ N	Cl	Cl	SO ₂ Me
6-1127	Me ₂ N	Cl	pyrazol-1-yl	SO ₂ Me
6-1128	Me ₂ N	Cl	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-1129	Me ₂ N	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-1130	Me ₂ N	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-1131	Me ₂ N	Cl	F	SO ₂ Me
6-1132	Me ₂ N	Me	SO ₂ Me	SO ₂ Me
6-1133	Me ₂ N	Me	SO ₂ Me	CF ₃
6-1134	Me ₂ N	Me	NMe ₂	SO ₂ Me
6-1135	Me ₂ N	Me	S(O)Me	CF ₃
6-1136	Me ₂ N	Me	SMe	CF ₃
6-1137	Me ₂ N	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-1138	Me ₂ N	Me	pyrazol-1-yl	SO ₂ Me
6-1139	Me ₂ N	Me	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-1140	Me ₂ N	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-1141	Me ₂ N	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-1142	Me ₂ N	Me	Cl	SO ₂ Me
6-1143	Me ₂ N	Me	Me	SO ₂ Me
6-1144	Me ₂ N	Me	Me	SMe
6-1145	Me ₂ N	Me	SO ₂ Me	Cl
6-1146	Me ₂ N	Me	NMe ₂	SO ₂ Me
6-1147	Me ₂ N	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-1148	Me ₂ N	CF ₃	F	SO ₂ CH ₃
6-1149	Me ₂ N	CF ₃	SMe	SO ₂ CH ₃
6-1150	Me ₂ N	CF ₃	SEt	SO ₂ CH ₃
6-1151	Me ₂ N	CF ₃	S(O)Et	SO ₂ CH ₃
6-1152	Me ₂ N	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-1153	Me ₂ N	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-1154	Me ₂ N	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-1155	Me ₂ N	CF ₃	CH ₂ O-tetrahydrofuran-2-yl	SO ₂ Et
6-1156	Me ₂ N	SMe	SMe	F
6-1157	Me ₂ N	SMe	SEt	F
6-1158	Me ₂ N	SO ₂ CH ₃	F	Cl
6-1159	Me ₂ N	F	S(O)Me	CF ₃
6-1160	Me ₂ N	F	SMe	CF ₃
6-1161	Ph-NH	NO ₂	H	SO ₂ Me

No.	R	X	Y	Z
6-1162	Ph-NH	Cl	H	SO ₂ Me
6-1163	Ph-NH	SO ₂ Me	H	CF ₃
6-1164	Ph-NH	NO ₂	H	OMe
6-1165	Ph-NH	NO ₂	H	Br
6-1166	Ph-NH	NO ₂	H	CF ₃
6-1167	Ph-NH	NO ₂	H	NO ₂
6-1168	Ph-NH	NO ₂	H	Cl
6-1169	Ph-NH	NO ₂	H	Me
6-1170	Ph-NH	NO ₂	H	F
6-1171	Ph-NH	OMe	H	SO ₂ Me
6-1172	Ph-NH	CF ₃	H	NO ₂
6-1173	Ph-NH	CH ₂ SO ₂ Me	H	Br
6-1174	Ph-NH	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-1175	Ph-NH	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-1176	Ph-NH	Cl	5-cyanomethyl- 4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-1177	Ph-NH	Cl	4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-1178	Ph-NH	Cl	CH ₂ OCH ₂ - tetrahydrofuran-2- yl	SO ₂ Me
6-1179	Ph-NH	Cl	SMe	Cl
6-1180	Ph-NH	Cl	SMe	SO ₂ Me
6-1181	Ph-NH	Cl	Me	SO ₂ Et
6-1182	Ph-NH	Cl	O(CH ₂) ₂ OMe	Cl
6-1183	Ph-NH	Cl	OCH ₂ -cyclopropyl	Cl
6-1184	Ph-NH	Cl	OMe	Cl
6-1185	Ph-NH	Cl	NHAc	Cl
6-1186	Ph-NH	Cl	OCH ₂ C(O)NMe ₂	Cl
6-1187	Ph-NH	Cl	Cl	SO ₂ Me
6-1188	Ph-NH	Cl	pyrazol-1-yl	SO ₂ Me
6-1189	Ph-NH	Cl	4-methoxy- pyrazol-1-yl	SO ₂ Me
6-1190	Ph-NH	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-1191	Ph-NH	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-1192	Ph-NH	Cl	F	SO ₂ Me
6-1193	Ph-NH	Me	SO ₂ Me	SO ₂ Me
6-1194	Ph-NH	Me	SO ₂ Me	CF ₃
6-1195	Ph-NH	Me	NMe ₂	SO ₂ Me
6-1196	Ph-NH	Me	S(O)Me	CF ₃
6-1197	Ph-NH	Me	SMe	CF ₃

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No.	R	X	Y	Z
6-1198	Ph-NH	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-1199	Ph-NH	Me	pyrazol-1-yl	SO ₂ Me
6-1200	Ph-NH	Me	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-1201	Ph-NH	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-1202	Ph-NH	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-1203	Ph-NH	Me	Cl	SO ₂ Me
6-1204	Ph-NH	Me	Me	SO ₂ Me
6-1205	Ph-NH	Me	Me	SMe
6-1206	Ph-NH	Me	SO ₂ Me	Cl
6-1207	Ph-NH	Me	NMe ₂	SO ₂ Me
6-1208	Ph-NH	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-1209	Ph-NH	CF ₃	F	SO ₂ CH ₃
6-1210	Ph-NH	CF ₃	SMe	SO ₂ CH ₃
6-1211	Ph-NH	CF ₃	SEt	SO ₂ CH ₃
6-1212	Ph-NH	CF ₃	S(O)Et	SO ₂ CH ₃
6-1213	Ph-NH	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-1214	Ph-NH	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-1215	Ph-NH	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-1216	Ph-NH	CF ₃	CH ₂ O-tetrahydrofuran-2-yl	SO ₂ Et
6-1217	Ph-NH	SMe	SMe	F
6-1218	Ph-NH	SMe	SEt	F
6-1219	Ph-NH	SO ₂ CH ₃	F	Cl
6-1220	Ph-NH	F	S(O)Me	CF ₃
6-1221	Ph-NH	F	SMe	CF ₃
6-1222	morpholin-1-yl	NO ₂	H	SO ₂ Me
6-1223	morpholin-1-yl	Cl	H	SO ₂ Me
6-1224	morpholin-1-yl	SO ₂ Me	H	CF ₃
6-1225	morpholin-1-yl	NO ₂	H	OMe
6-1226	morpholin-1-yl	NO ₂	H	Br
6-1227	morpholin-1-yl	NO ₂	H	CF ₃
6-1228	morpholin-1-yl	NO ₂	H	NO ₂
6-1229	morpholin-1-yl	NO ₂	H	Cl
6-1230	morpholin-1-yl	NO ₂	H	Me

No.	R	X	Y	Z
6-1231	morpholin -1-yl	NO ₂	H	F
6-1232	morpholin -1-yl	OMe	H	SO ₂ Me
6-1233	morpholin -1-yl	CF ₃	H	NO ₂
6-1234	morpholin -1-yl	CH ₂ SO ₂ Me	H	Br
6-1235	morpholin -1-yl	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-1236	morpholin -1-yl	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-1237	morpholin -1-yl	Cl	5-cyanomethyl- 4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-1238	morpholin -1-yl	Cl	4,5-dihydro-1,2- oxazol-3-yl	SO ₂ Et
6-1239	morpholin -1-yl	Cl	CH ₂ OCH ₂ - tetrahydrofuran-2- yl	SO ₂ Me
6-1240	morpholin -1-yl	Cl	SMe	Cl
6-1241	morpholin -1-yl	Cl	SMe	SO ₂ Me
6-1242	morpholin -1-yl	Cl	Me	SO ₂ Et
6-1243	morpholin -1-yl	Cl	O(CH ₂) ₂ OMe	Cl
6-1244	morpholin -1-yl	Cl	OCH ₂ -cyclopropyl	Cl
6-1245	morpholin -1-yl	Cl	OMe	Cl
6-1246	morpholin -1-yl	Cl	NHAc	Cl
6-1247	morpholin -1-yl	Cl	OCH ₂ C(O)NMe ₂	Cl
6-1248	morpholin -1-yl	Cl	Cl	SO ₂ Me
6-1249	morpholin -1-yl	Cl	pyrazol-1-yl	SO ₂ Me
6-1250	morpholin -1-yl	Cl	4-methoxy- pyrazol-1-yl	SO ₂ Me
6-1251	morpholin -1-yl	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-1252	morpholin -1-yl	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-1253	morpholin -1-yl	Cl	F	SO ₂ Me

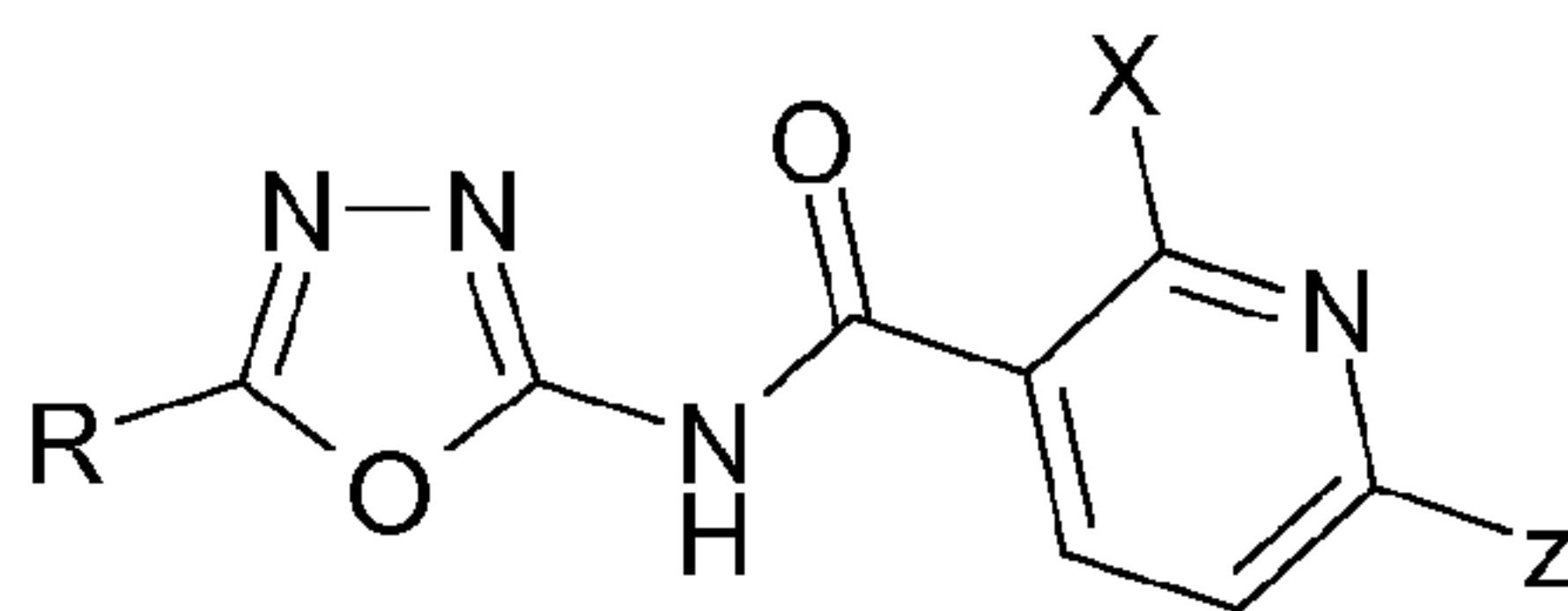
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No.	R	X	Y	Z
6-1254	morpholin -1-yl	Me	SO ₂ Me	SO ₂ Me
6-1255	morpholin -1-yl	Me	SO ₂ Me	CF ₃
6-1256	morpholin -1-yl	Me	NMe ₂	SO ₂ Me
6-1257	morpholin -1-yl	Me	S(O)Me	CF ₃
6-1258	morpholin -1-yl	Me	SMe	CF ₃
6-1259	morpholin -1-yl	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-1260	morpholin -1-yl	Me	pyrazol-1-yl	SO ₂ Me
6-1261	morpholin -1-yl	Me	4-methoxy- pyrazol-1-yl	SO ₂ Me
6-1262	morpholin -1-yl	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-1263	morpholin -1-yl	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-1264	morpholin -1-yl	Me	Cl	SO ₂ Me
6-1265	morpholin -1-yl	Me	Me	SO ₂ Me
6-1266	morpholin -1-yl	Me	Me	SMe
6-1267	morpholin -1-yl	Me	SO ₂ Me	Cl
6-1268	morpholin -1-yl	Me	NMe ₂	SO ₂ Me
6-1269	morpholin -1-yl	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-1270	morpholin -1-yl	CF ₃	F	SO ₂ CH ₃
6-1271	morpholin -1-yl	CF ₃	SMe	SO ₂ CH ₃
6-1272	morpholin -1-yl	CF ₃	SEt	SO ₂ CH ₃
6-1273	morpholin -1-yl	CF ₃	S(O)Et	SO ₂ CH ₃
6-1274	morpholin -1-yl	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-1275	morpholin -1-yl	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-1276	morpholin -1-yl	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-1277	morpholin -1-yl	CF ₃	CH ₂ O- tetrahydrofuran-2- yl	SO ₂ Et

No.	R	X	Y	Z
6-1278	morpholin-1-yl	SMe	SMe	F
6-1279	morpholin-1-yl	SMe	SEt	F
6-1280	morpholin-1-yl	SO ₂ CH ₃	F	Cl
6-1281	morpholin-1-yl	F	S(O)Me	CF ₃
6-1282	morpholin-1-yl	F	SMe	CF ₃
6-1283	sec-Bu	NO ₂	H	SO ₂ Me
6-1284	sec-Bu	Cl	H	SO ₂ Me
6-1285	sec-Bu	SO ₂ Me	H	CF ₃
6-1286	sec-Bu	NO ₂	H	OMe
6-1287	sec-Bu	NO ₂	H	Br
6-1288	sec-Bu	NO ₂	H	CF ₃
6-1289	sec-Bu	NO ₂	H	NO ₂
6-1290	sec-Bu	NO ₂	H	Cl
6-1291	sec-Bu	NO ₂	H	Me
6-1292	sec-Bu	NO ₂	H	F
6-1293	sec-Bu	OMe	H	SO ₂ Me
6-1294	sec-Bu	CF ₃	H	NO ₂
6-1295	sec-Bu	CH ₂ SO ₂ Me	H	Br
6-1296	sec-Bu	Cl	CH ₂ OCH ₂ CF ₃	SO ₂ Me
6-1297	sec-Bu	Cl	CH ₂ OCH ₂ CF ₃	SMe
6-1298	sec-Bu	Cl	5-cyanomethyl-4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
6-1299	sec-Bu	Cl	4,5-dihydro-1,2-oxazol-3-yl	SO ₂ Et
6-1300	sec-Bu	Cl	CH ₂ OCH ₂ -tetrahydrofuran-2-yl	SO ₂ Me
6-1301	sec-Bu	Cl	SMe	Cl
6-1302	sec-Bu	Cl	SMe	SO ₂ Me
6-1303	sec-Bu	Cl	Me	SO ₂ Et
6-1304	sec-Bu	Cl	O(CH ₂) ₂ OMe	Cl
6-1305	sec-Bu	Cl	OCH ₂ -cyclopropyl	Cl
6-1306	sec-Bu	Cl	OMe	Cl
6-1307	sec-Bu	Cl	NHAc	Cl
6-1308	sec-Bu	Cl	OCH ₂ C(O)NMe ₂	Cl
6-1309	sec-Bu	Cl	Cl	SO ₂ Me
6-1310	sec-Bu	Cl	pyrazol-1-yl	SO ₂ Me

No.	R	X	Y	Z
6-1311	sec-Bu	Cl	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-1312	sec-Bu	Cl	1,2,3-triazol-1-yl	SO ₂ Me
6-1313	sec-Bu	Cl	1,2,3-triazol-2-yl	SO ₂ Me
6-1314	sec-Bu	Cl	F	SO ₂ Me
6-1315	sec-Bu	Me	SO ₂ Me	SO ₂ Me
6-1316	sec-Bu	Me	SO ₂ Me	CF ₃
6-1317	sec-Bu	Me	NMe ₂	SO ₂ Me
6-1318	sec-Bu	Me	S(O)Me	CF ₃
6-1319	sec-Bu	Me	SMe	CF ₃
6-1320	sec-Bu	Me	SO ₂ CH ₂ CH ₂ OMe	CF ₃
6-1321	sec-Bu	Me	pyrazol-1-yl	SO ₂ Me
6-1322	sec-Bu	Me	4-methoxy-pyrazol-1-yl	SO ₂ Me
6-1323	sec-Bu	Me	1,2,3-triazol-1-yl	SO ₂ Me
6-1324	sec-Bu	Me	1,2,3-triazol-2-yl	SO ₂ Me
6-1325	sec-Bu	Me	Cl	SO ₂ Me
6-1326	sec-Bu	Me	Me	SO ₂ Me
6-1327	sec-Bu	Me	Me	SMe
6-1328	sec-Bu	Me	SO ₂ Me	Cl
6-1329	sec-Bu	Me	NMe ₂	SO ₂ Me
6-1330	sec-Bu	Me	NH(CH ₂) ₂ OMe	SO ₂ Me
6-1331	sec-Bu	CF ₃	F	SO ₂ CH ₃
6-1332	sec-Bu	CF ₃	SMe	SO ₂ CH ₃
6-1333	sec-Bu	CF ₃	SEt	SO ₂ CH ₃
6-1334	sec-Bu	CF ₃	S(O)Et	SO ₂ CH ₃
6-1335	sec-Bu	CF ₃	SO ₂ CH ₃	SO ₂ CH ₃
6-1336	sec-Bu	CF ₃	OCH ₂ CH ₂ OMe	SO ₂ CH ₃
6-1337	sec-Bu	CF ₃	OCH ₂ (CO)NMe ₂	SO ₂ Me
6-1338	sec-Bu	CF ₃	CH ₂ O-tetrahydrofuran-2-yl	SO ₂ Et
6-1339	sec-Bu	SMe	SMe	F
6-1340	sec-Bu	SMe	SEt	F
6-1341	sec-Bu	SO ₂ CH ₃	F	Cl
6-1342	sec-Bu	F	S(O)Me	CF ₃
6-1343	sec-Bu	F	SMe	CF ₃

Table 7: Compounds of the general formula (I) in which A is nitrogen, and R, X, and Z are as defined below.



No.	R	X	Z
7-1	H	Cl	CF ₃
7-2	Me	Cl	CF ₃
7-3	Et	Cl	CF ₃
7-4	CF ₃	Cl	CF ₃
7-5	CH ₂ OMe	Cl	CF ₃
7-6	c-Pr	Cl	CF ₃
7-7	CO ₂ Et	Cl	CF ₃
7-8	CO ₂ Me	Cl	CF ₃
7-9	benzyl	Cl	CF ₃
7-10	phenyl	Cl	CF ₃
7-11	pyrazin-2-yl	Cl	CF ₃
7-12	4-OMe-Ph	Cl	CF ₃
7-13	4-Cl-Ph	Cl	CF ₃
7-14	t-Bu	Cl	CF ₃
7-15	furan-2-yl	Cl	CF ₃
7-16	i-Pr	Cl	CF ₃
7-17	CH ₂ CH ₂ OMe	Cl	CF ₃
7-18	CH ₂ CF ₃	Cl	CF ₃
7-19	tetrahydrofuran -2-yl	Cl	CF ₃
7-20	n-Pr	Cl	CF ₃
7-21	CH ₂ OEt	Cl	CF ₃
7-22	cyclobutyl	Cl	CF ₃
7-23	cyclopentyl	Cl	CF ₃
7-24	Me ₂ N	Cl	CF ₃
7-25	Ph-NH	Cl	CF ₃
7-26	morpholin-1-yl	Cl	CF ₃
7-27	H	Cl	Cl
7-28	Me	Cl	Cl
7-29	Et	Cl	Cl
7-30	CF ₃	Cl	Cl
7-31	CH ₂ OMe	Cl	Cl
7-32	c-Pr	Cl	Cl

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No.	R	X	Z
7-33	CO ₂ Et	Cl	Cl
7-34	CO ₂ Me	Cl	Cl
7-35	benzyl	Cl	Cl
7-36	phenyl	Cl	Cl
7-37	pyrazin-2-yl	Cl	Cl
7-38	4-OMe-Ph	Cl	Cl
7-39	4-Cl-Ph	Cl	Cl
7-40	t-Bu	Cl	Cl
7-41	furan-2-yl	Cl	Cl
7-42	i-Pr	Cl	Cl
7-43	CH ₂ CH ₂ OMe	Cl	Cl
7-44	CH ₂ CF ₃	Cl	Cl
7-45	tetrahydrofuran -2-yl	Cl	Cl
7-46	n-Pr	Cl	Cl
7-47	CH ₂ OEt	Cl	Cl
7-48	cyclobutyl	Cl	Cl
7-49	cyclopentyl	Cl	Cl
7-50	Me ₂ N	Cl	Cl
7-51	Ph-NH	Cl	Cl
7-52	morpholin-1-yl	Cl	Cl
7-53	H	Me	Cl
7-54	Me	Me	Cl
7-55	Et	Me	Cl
7-56	CF ₃	Me	Cl
7-57	CH ₂ OMe	Me	Cl
7-58	c-Pr	Me	Cl
7-59	CO ₂ Et	Me	Cl
7-60	CO ₂ Me	Me	Cl
7-61	benzyl	Me	Cl
7-62	phenyl	Me	Cl
7-63	pyrazin-2-yl	Me	Cl
7-64	4-OMe-Ph	Me	Cl
7-65	4-Cl-Ph	Me	Cl
7-66	t-Bu	Me	Cl
7-67	furan-2-yl	Me	Cl
7-68	i-Pr	Me	Cl
7-69	CH ₂ CH ₂ OMe	Me	Cl
7-70	CH ₂ CF ₃	Me	Cl
7-71	tetrahydrofuran -2-yl	Me	Cl

No.	R	X	Z
7-72	n-Pr	Me	Cl
7-73	CH ₂ OEt	Me	Cl
7-74	cyclobutyl	Me	Cl
7-75	cyclopentyl	Me	Cl
7-76	Me ₂ N	Me	Cl
7-77	Ph-NH	Me	Cl
7-78	morpholin-1-yl	Me	Cl
7-79	H	Cl	SMe
7-80	Me	Cl	SMe
7-81	Et	Cl	SMe
7-82	CF ₃	Cl	SMe
7-83	CH ₂ OMe	Cl	SMe
7-84	c-Pr	Cl	SMe
7-85	CO ₂ Et	Cl	SMe
7-86	CO ₂ Me	Cl	SMe
7-87	benzyl	Cl	SMe
7-88	phenyl	Cl	SMe
7-89	pyrazin-2-yl	Cl	SMe
7-90	4-OMe-Ph	Cl	SMe
7-91	4-Cl-Ph	Cl	SMe
7-92	t-Bu	Cl	SMe
7-93	furan-2-yl	Cl	SMe
7-94	i-Pr	Cl	SMe
7-95	CH ₂ CH ₂ OMe	Cl	SMe
7-96	CH ₂ CF ₃	Cl	SMe
7-97	tetrahydrofuran -2-yl	Cl	SMe
7-98	n-Pr	Cl	SMe
7-99	CH ₂ OEt	Cl	SMe
7-100	cyclobutyl	Cl	SMe
7-101	cyclopentyl	Cl	SMe
7-102	Me ₂ N	Cl	SMe
7-103	Ph-NH	Cl	SMe
7-104	morpholin-1-yl	Cl	SMe
7-105	H	Cl	SO ₂ Me
7-106	Me	Cl	SO ₂ Me
7-107	Et	Cl	SO ₂ Me
7-108	CF ₃	Cl	SO ₂ Me
7-109	CH ₂ OMe	Cl	SO ₂ Me
7-110	c-Pr	Cl	SO ₂ Me
7-111	CO ₂ Et	Cl	SO ₂ Me

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No.	R	X	Z
7-112	CO ₂ Me	Cl	SO ₂ Me
7-113	benzyl	Cl	SO ₂ Me
7-114	phenyl	Cl	SO ₂ Me
7-115	pyrazin-2-yl	Cl	SO ₂ Me
7-116	4-OMe-Ph	Cl	SO ₂ Me
7-117	4-Cl-Ph	Cl	SO ₂ Me
7-118	t-Bu	Cl	SO ₂ Me
7-119	furan-2-yl	Cl	SO ₂ Me
7-120	i-Pr	Cl	SO ₂ Me
7-121	CH ₂ CH ₂ OMe	Cl	SO ₂ Me
7-122	CH ₂ CF ₃	Cl	SO ₂ Me
7-123	tetrahydrofuran -2-yl	Cl	SO ₂ Me
7-124	n-Pr	Cl	SO ₂ Me
7-125	CH ₂ OEt	Cl	SO ₂ Me
7-126	cyclobutyl	Cl	SO ₂ Me
7-127	cyclopentyl	Cl	SO ₂ Me
7-128	Me ₂ N	Cl	SO ₂ Me
7-129	Ph-NH	Cl	SO ₂ Me
7-130	morpholin-1-yl	Cl	SO ₂ Me
7-131	H	Me	CF ₃
7-132	Me	Me	CF ₃
7-133	Et	Me	CF ₃
7-134	CF ₃	Me	CF ₃
7-135	CH ₂ OMe	Me	CF ₃
7-136	c-Pr	Me	CF ₃
7-137	CO ₂ Et	Me	CF ₃
7-138	CO ₂ Me	Me	CF ₃
7-139	benzyl	Me	CF ₃
7-140	phenyl	Me	CF ₃
7-141	pyrazin-2-yl	Me	CF ₃
7-142	4-OMe-Ph	Me	CF ₃
7-143	4-Cl-Ph	Me	CF ₃
7-144	t-Bu	Me	CF ₃
7-145	furan-2-yl	Me	CF ₃
7-146	i-Pr	Me	CF ₃
7-147	CH ₂ CH ₂ OMe	Me	CF ₃
7-148	CH ₂ CF ₃	Me	CF ₃
7-149	tetrahydrofuran -2-yl	Me	CF ₃
7-150	n-Pr	Me	CF ₃

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No.	R	X	Z
7-151	CH ₂ OEt	Me	CF ₃
7-152	cyclobutyl	Me	CF ₃
7-153	cyclopentyl	Me	CF ₃
7-154	Me ₂ N	Me	CF ₃
7-155	Ph-NH	Me	CF ₃
7-156	morpholin-1-yl	Me	CF ₃
7-157	H	CH ₂ OMe	CF ₃
7-158	Me	CH ₂ OMe	CF ₃
7-159	Et	CH ₂ OMe	CF ₃
7-160	CF ₃	CH ₂ OMe	CF ₃
7-161	CH ₂ OMe	CH ₂ OMe	CF ₃
7-162	c-Pr	CH ₂ OMe	CF ₃
7-163	CO ₂ Et	CH ₂ OMe	CF ₃
7-164	CO ₂ Me	CH ₂ OMe	CF ₃
7-165	benzyl	CH ₂ OMe	CF ₃
7-166	phenyl	CH ₂ OMe	CF ₃
7-167	pyrazin-2-yl	CH ₂ OMe	CF ₃
7-168	4-OMe-Ph	CH ₂ OMe	CF ₃
7-169	4-Cl-Ph	CH ₂ OMe	CF ₃
7-170	t-Bu	CH ₂ OMe	CF ₃
7-171	furan-2-yl	CH ₂ OMe	CF ₃
7-172	i-Pr	CH ₂ OMe	CF ₃
7-173	CH ₂ CH ₂ OMe	CH ₂ OMe	CF ₃
7-174	CH ₂ CF ₃	CH ₂ OMe	CF ₃
7-175	tetrahydrofuran -2-yl	CH ₂ OMe	CF ₃
7-176	n-Pr	CH ₂ OMe	CF ₃
7-177	CH ₂ OEt	CH ₂ OMe	CF ₃
7-178	cyclobutyl	CH ₂ OMe	CF ₃
7-179	cyclopentyl	CH ₂ OMe	CF ₃
7-180	Me ₂ N	CH ₂ OMe	CF ₃
7-181	Ph-NH	CH ₂ OMe	CF ₃
7-182	morpholin-1-yl	CH ₂ OMe	CF ₃
7-183	H	CH ₂ SMe	CF ₃
7-184	Me	CH ₂ SMe	CF ₃
7-185	Et	CH ₂ SMe	CF ₃
7-186	CF ₃	CH ₂ SMe	CF ₃
7-187	CH ₂ OMe	CH ₂ SMe	CF ₃
7-188	c-Pr	CH ₂ SMe	CF ₃
7-189	CO ₂ Et	CH ₂ SMe	CF ₃
7-190	CO ₂ Me	CH ₂ SMe	CF ₃

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No.	R	X	Z
7-191	benzyl	CH ₂ SMe	CF ₃
7-192	phenyl	CH ₂ SMe	CF ₃
7-193	pyrazin-2-yl	CH ₂ SMe	CF ₃
7-194	4-OMe-Ph	CH ₂ SMe	CF ₃
7-195	4-Cl-Ph	CH ₂ SMe	CF ₃
7-196	t-Bu	CH ₂ SMe	CF ₃
7-197	furan-2-yl	CH ₂ SMe	CF ₃
7-198	i-Pr	CH ₂ SMe	CF ₃
7-199	CH ₂ CH ₂ OMe	CH ₂ SMe	CF ₃
7-200	CH ₂ CF ₃	CH ₂ SMe	CF ₃
7-201	tetrahydrofuran -2-yl	CH ₂ SMe	CF ₃
7-202	n-Pr	CH ₂ SMe	CF ₃
7-203	CH ₂ OEt	CH ₂ SMe	CF ₃
7-204	cyclobutyl	CH ₂ SMe	CF ₃
7-205	cyclopentyl	CH ₂ SMe	CF ₃
7-206	Me ₂ N	CH ₂ SMe	CF ₃
7-207	Ph-NH	CH ₂ SMe	CF ₃
7-208	morpholin-1-yl	CH ₂ SMe	CF ₃
7-209	H	CH ₂ SO ₂ Me	CF ₃
7-210	Me	CH ₂ SO ₂ Me	CF ₃
7-211	Et	CH ₂ SO ₂ Me	CF ₃
7-212	CF ₃	CH ₂ SO ₂ Me	CF ₃
7-213	CH ₂ OMe	CH ₂ SO ₂ Me	CF ₃
7-214	c-Pr	CH ₂ SO ₂ Me	CF ₃
7-215	CO ₂ Et	CH ₂ SO ₂ Me	CF ₃
7-216	CO ₂ Me	CH ₂ SO ₂ Me	CF ₃
7-217	benzyl	CH ₂ SO ₂ Me	CF ₃
7-218	phenyl	CH ₂ SO ₂ Me	CF ₃
7-219	pyrazin-2-yl	CH ₂ SO ₂ Me	CF ₃
7-220	4-OMe-Ph	CH ₂ SO ₂ Me	CF ₃
7-221	4-Cl-Ph	CH ₂ SO ₂ Me	CF ₃
7-222	t-Bu	CH ₂ SO ₂ Me	CF ₃
7-223	furan-2-yl	CH ₂ SO ₂ Me	CF ₃
7-224	i-Pr	CH ₂ SO ₂ Me	CF ₃
7-225	CH ₂ CH ₂ OMe	CH ₂ SO ₂ Me	CF ₃
7-226	CH ₂ CF ₃	CH ₂ SO ₂ Me	CF ₃
7-227	tetrahydro- furan-2-yl	CH ₂ SO ₂ Me	CF ₃
7-228	n-Pr	CH ₂ SO ₂ Me	CF ₃
7-229	CH ₂ OEt	CH ₂ SO ₂ Me	CF ₃

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No.	R	X	Z
7-230	cyclobutyl	CH ₂ SO ₂ Me	CF ₃
7-231	cyclopentyl	CH ₂ SO ₂ Me	CF ₃
7-232	Me ₂ N	CH ₂ SO ₂ Me	CF ₃
7-233	Ph-NH	CH ₂ SO ₂ Me	CF ₃
7-234	morpholin-1-yl	CH ₂ SO ₂ Me	CF ₃
7-235	H	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-236	Me	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-237	Et	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-238	CF ₃	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-239	CH ₂ OMe	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-240	c-Pr	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-241	CO ₂ Et	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-242	CO ₂ Me	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-243	benzyl	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-244	phenyl	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-245	pyrazin-2-yl	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-246	4-OMe-Ph	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-247	4-Cl-Ph	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-248	t-Bu	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-249	furan-2-yl	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-250	i-Pr	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-251	CH ₂ CH ₂ OMe	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-252	CH ₂ CF ₃	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-253	tetrahydro- furan-2-yl	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-254	n-Pr	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-255	CH ₂ OEt	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-256	cyclobutyl	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-257	cyclopentyl	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-258	Me ₂ N	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-259	Ph-NH	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-260	morpholin-1-yl	CH ₂ OC ₂ H ₄ OMe	CF ₃
7-261	H	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-262	Me	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-263	Et	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-264	CF ₃	OCH ₂ - tetrahydro-	CF ₃

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No.	R	X	Z
		furan-2-yl	
7-265	CH ₂ OMe	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-266	c-Pr	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-267	CO ₂ Et	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-268	CO ₂ Me	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-269	benzyl	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-270	phenyl	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-271	pyrazin-2-yl	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-272	4-OMe-Ph	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-273	4-Cl-Ph	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-274	t-Bu	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-275	furan-2-yl	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-276	i-Pr	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-277	CH ₂ CH ₂ OMe	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-278	CH ₂ CF ₃	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-279	tetrahydro- furan-2-yl	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-280	n-Pr	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-281	CH ₂ OEt	OCH ₂ - tetrahydro- furan-2-yl	CF ₃

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No.	R	X	Z
7-282	cyclobutyl	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-283	cyclopentyl	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-284	Me ₂ N	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-285	Ph-NH	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-286	morpholin-1-yl	OCH ₂ - tetrahydro- furan-2-yl	CF ₃
7-287	H	(1,1-dioxido-1,2- thiadiazolidin-1- yl)methyl	CF ₃
7-288	Me	(1,1-dioxido-1,2- thiadiazolidin-1- yl)methyl	CF ₃
7-289	Et	(1,1-dioxido-1,2- thiadiazolidin-1- yl)methyl	CF ₃
7-290	CF ₃	(1,1-dioxido-1,2- thiadiazolidin-1- yl)methyl	CF ₃
7-291	CH ₂ OMe	(1,1-dioxido-1,2- thiadiazolidin-1- yl)methyl	CF ₃
7-292	c-Pr	(1,1-dioxido-1,2- thiadiazolidin-1- yl)methyl	CF ₃
7-293	CO ₂ Et	(1,1-dioxido-1,2- thiadiazolidin-1- yl)methyl	CF ₃
7-294	CO ₂ Me	(1,1-dioxido-1,2- thiadiazolidin-1- yl)methyl	CF ₃
7-295	benzyl	(1,1-dioxido-1,2- thiadiazolidin-1- yl)methyl	CF ₃
7-296	phenyl	(1,1-dioxido-1,2- thiadiazolidin-1- yl)methyl	CF ₃
7-297	pyrazin-2-yl	(1,1-dioxido-1,2- thiadiazolidin-1- yl)methyl	CF ₃
7-298	4-OMe-Ph	(1,1-dioxido-1,2- thiadiazolidin-1- yl)methyl	CF ₃

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No.	R	X	Z
7-299	4-Cl-Ph	(1,1-dioxido-1,2-thiadiazolidin-1-yl)methyl	CF ₃
7-300	t-Bu	(1,1-dioxido-1,2-thiadiazolidin-1-yl)methyl	CF ₃
7-301	furan-2-yl	(1,1-dioxido-1,2-thiadiazolidin-1-yl)methyl	CF ₃
7-302	i-Pr	(1,1-dioxido-1,2-thiadiazolidin-1-yl)methyl	CF ₃
7-303	CH ₂ CH ₂ OMe	(1,1-dioxido-1,2-thiadiazolidin-1-yl)methyl	CF ₃
7-304	CH ₂ CF ₃	(1,1-dioxido-1,2-thiadiazolidin-1-yl)methyl	CF ₃
7-305	tetrahydrofuran-2-yl	(1,1-dioxido-1,2-thiadiazolidin-1-yl)methyl	CF ₃
7-306	n-Pr	(1,1-dioxido-1,2-thiadiazolidin-1-yl)methyl	CF ₃
7-307	CH ₂ OEt	(1,1-dioxido-1,2-thiadiazolidin-1-yl)methyl	CF ₃
7-308	cyclobutyl	(1,1-dioxido-1,2-thiadiazolidin-1-yl)methyl	CF ₃
7-309	cyclopentyl	(1,1-dioxido-1,2-thiadiazolidin-1-yl)methyl	CF ₃
7-310	Me ₂ N	(1,1-dioxido-1,2-thiadiazolidin-1-yl)methyl	CF ₃
7-311	Ph-NH	(1,1-dioxido-1,2-thiadiazolidin-1-yl)methyl	CF ₃
7-312	morpholin-1-yl	(1,1-dioxido-1,2-thiadiazolidin-1-yl)methyl	CF ₃
7-313	H	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-314	Me	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-315	Et	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃

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No.	R	X	Z
7-316	CF ₃	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-317	CH ₂ OMe	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-318	c-Pr	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-319	CO ₂ Et	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-320	CO ₂ Me	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-321	benzyl	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-322	phenyl	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-323	pyrazin-2-yl	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-324	4-OMe-Ph	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-325	4-Cl-Ph	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-326	t-Bu	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-327	furan-2-yl	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-328	i-Pr	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-329	CH ₂ CH ₂ OMe	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-330	CH ₂ CF ₃	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-331	tetrahydro-furan-2-yl	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-332	n-Pr	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃

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No.	R	X	Z
7-333	CH ₂ OEt	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-334	cyclobutyl	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-335	cyclopentyl	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-336	Me ₂ N	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-337	Ph-NH	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-338	morpholin-1-yl	(3-methyl-2-oxoimidazolidin-1-yl)methyl	CF ₃
7-339	H	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-340	Me	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-341	Et	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-342	CF ₃	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-343	CH ₂ OMe	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-344	c-Pr	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃

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No.	R	X	Z
7-345	CO ₂ Et	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-346	CO ₂ Me	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-347	benzyl	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-348	phenyl	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-349	pyrazin-2-yl	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-350	4-OMe-Ph	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-351	4-Cl-Ph	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-352	t-Bu	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-353	furan-2-yl	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-354	i-Pr	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃

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No.	R	X	Z
7-355	CH ₂ CH ₂ OMe	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-356	CH ₂ CF ₃	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-357	tetrahydro-furan-2-yl	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-358	n-Pr	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-359	CH ₂ OEt	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-360	cyclobutyl	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-361	cyclopentyl	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-362	Me ₂ N	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-363	Ph-NH	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-364	morpholin-1-yl	(3-methoxy-4-methyl-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)methyl	CF ₃
7-365	i-Pr	Cl	Me

As already disclosed in WO2012/126932, the compounds of the formula (I) and/or their salts to be used according to the invention, herein below also referred to together as “compounds according to the invention”, have excellent herbicidal efficacy against a broad spectrum of economically important monocotyledonous and dicotyledonous annual
5 harmful plants. The active compounds act efficiently even on perennial weeds which produce shoots from rhizomes, rootstocks and other perennial organs and which are difficult to control.

The present invention therefore relates to a method for controlling unwanted plants in
10 areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides by containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b)
15 *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA
20 sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 ,
25 (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms,
30 preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize

(Zea mays) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present

application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), comprising the application of one or more N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above to the plants (for example harmful plants such as monocotyledonous or dicotyledonous weeds or undesired crop plants), to the seed (for example grains, seeds or vegetative propagules such as tubers or shoot parts with buds) or to the area on which the plants grow (for example the area under cultivation). Specific examples may be mentioned of some representatives of the monocotyledonous and dicotyledonous weed flora which can be controlled by the compounds according to the invention, without the enumeration being restricted to certain species.

Monocotyledonous harmful plants of the genera: *Aegilops*, *Agropyron*, *Agrostis*, *Alopecurus*, *Apera*, *Avena*, *Brachiaria*, *Bromus*, *Cenchrus*, *Commelina*, *Cynodon*, *Cyperus*, *Dactyloctenium*, *Digitaria*, *Echinochloa*, *Eleocharis*, *Eleusine*, *Eragrostis*, *Eriochloa*, *Festuca*, *Fimbristylis*, *Heteranthera*, *Imperata*, *Ischaemum*, *Leptochloa*, *Lolium*, *Monochoria*, *Panicum*, *Paspalum*, *Phalaris*, *Phleum*, *Poa*, *Rottboellia*, *Sagittaria*, *Scirpus*, *Setaria*, *Sorghum*.

Dicotyledonous weeds of the genera: *Abutilon*, *Amaranthus*, *Ambrosia*, *Anoda*, *Anthemis*, *Aphanes*, *Artemisia*, *Atriplex*, *Bellis*, *Bidens*, *Capsella*, *Carduus*, *Cassia*, *Centaurea*, *Chenopodium*, *Cirsium*, *Convolvulus*, *Datura*, *Desmodium*, *Emex*, *Erysimum*, *Euphorbia*, *Galeopsis*, *Galinsoga*, *Galium*, *Hibiscus*, *Ipomoea*, *Kochia*, *Lamium*, *Lepidium*, *Lindernia*, *Matricaria*, *Mentha*, *Mercurialis*, *Mullugo*, *Myosotis*, *Papaver*, *Pharbitis*, *Plantago*, *Polygonum*, *Portulaca*, *Ranunculus*, *Raphanus*, *Rorippa*, *Rotala*, *Rumex*, *Salsola*,

Senecio, Sesbania, Sida, Sinapis, Solanum, Sonchus, Sphenoclea, Stellaria, Taraxacum, Thlaspi, Trifolium, Urtica, Veronica, Viola, Xanthium.

Transgenic crop plants of economically important crops to which the N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above might be applied are, for example dicotyledonous crops of the genera Arachis, Beta, Brassica, Cucumis, Cucurbita, Helianthus, Daucus, Glycine, Gossypium, Ipomoea, Lactuca, Linum, Lycopersicon, Nicotiana, Phaseolus, Pisum, Solanum, Vicia, or monocotyledonous crops of the genera Allium, Ananas, Asparagus, Avena, Hordeum, Oryza, Panicum, Saccharum, Secale, Sorghum, Triticale, Triticum, Zea, in particular Zea and Triticum.

This is why the present invention preferably relates to the method for controlling unwanted plants in areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides by containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No. 12 encoding HPPD defined by SEQ ID No. 13, (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially

one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A

(Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated

5 sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E

10 (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), comprising the application of one or more N-

15 (1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above to the plants (for example harmful plants such as monocotyledonous or dicotyledonous weeds or undesired crop plants), to the seed (for example grains, seeds or vegetative propagules such as tubers or shoot parts with buds) or to the area on which the plants grow (for example the area under cultivation) in dicotyledonous crops of the genera *Arachis*, *Beta*, *Brassica*, *Cucumis*,

20 *Cucurbita*, *Helianthus*, *Daucus*, *Glycine*, *Gossypium*, *Ipomoea*, *Lactuca*, *Linum*, *Lycopersicon*, *Nicotiana*, *Phaseolus*, *Pisum*, *Solanum*, *Vicia*, or monocotyledonous crops of the genera *Allium*, *Ananas*, *Asparagus*, *Avena*, *Hordeum*, *Oryza*, *Panicum*, *Saccharum*, *Secale*, *Sorghum*, *Triticale*, *Triticum*, *Zea*, in particular *Zea* and *Triticum*.

25 It is preferred to use the N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts in economically important transgenic crops of useful plants and ornamentals, for example of cereals such as wheat, barley, rye, oats, sorghum/millet, rice, cassava and maize or else crops of sugar beet, sugar cane, cotton, soybean, oilseed rape, potato, tomato, peas and other vegetables, which crops contain one or more chimeric gene(s) (I)

30 comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD

defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID

5 No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably

10 comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968,

15 WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in

20 PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at

25 position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and

30 an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement

at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

The invention also relates to the use, in a method for transforming plants, of a nucleic acid which encodes an HPPD as a marker gene or as a coding sequence which makes it

possible to confer to the plant tolerance to herbicides which are HPPD inhibitors, and the use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts on plants containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of

5 organisms consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA

10 sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ

15 ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical

20 to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially

25 one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp)

30 replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being

disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in

5 PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356

10 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named

15 Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser)

20 replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A

25 (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro)

30 replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position

336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

5

In the commercial production of crops, it is desirable to eliminate under reliable pesticidal management unwanted plants (i.e., "weeds") from a field of crop plants. An ideal treatment would be one which could be applied to an entire field but which would eliminate only the unwanted plants while leaving the crop plants unaffected. One such treatment system

10 would involve the use of crop plants which are tolerant to an herbicide so that when the herbicide is sprayed on a field of herbicide-tolerant crop plants, the crop plants would continue to thrive while non-herbicide-tolerant weeds are killed or severely damaged. Ideally, such treatment systems would take advantage of varying herbicide properties so that weed control could provide the best possible combination of flexibility and economy.

15 For example, individual herbicides have different longevities in the field, and some herbicides persist and are effective for a relatively long time after they are applied to a field while other herbicides are quickly broken down into other and/or non-active compounds. An ideal treatment system would allow the use of different herbicides so that growers could tailor the choice of herbicides for a particular situation.

20

While a number of herbicide-tolerant crop plants are presently commercially available, one issue that has arisen for many commercial herbicides and herbicide/crop combinations is that individual herbicides typically have incomplete spectrum of activity against common weed species. For most individual herbicides which have been in use for some time,

25 populations of herbicide resistant weed species and biotypes have become more prevalent (see, e.g., Tranel and Wright (2002) *Weed Science* 50: 700-712; Owen and Zelaya (2005) *Pest Manag. Sci.* 61: 301-311). Transgenic plants which are resistant to more than one herbicide have been described (see, e.g., W02005/012515). However, improvements in every aspect of crop production, weed control options, extension of residual weed control,

30 and improvement in crop yield are continuously in demand.

The above defined chimeric gene(s) encoding one or more HPPD protein(s) or mutants thereof being functional in transgenic plants in order to perform tolerance to HPPD inhibitor herbicides belonging to the class of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined

above or their salts is/are advantageously combined in plants with other genes which encode proteins or RNAs that confer useful agronomic properties to such plants. Among the genes which encode proteins or RNAs that confer useful agronomic properties on the transformed plants, mention can be made of the DNA sequences encoding proteins which
5 confer tolerance to one or more herbicides that, according to their chemical structure, differ from HPPD inhibitor herbicides, and others which confer tolerance to certain insects, those which confer tolerance to certain diseases and or biotic and abiotic stresses, DNAs that encodes RNAs that provide nematode or insect control, etc..

Such genes are in particular described in published PCT Patent Applications WO
10 91/02071 and WO95/06128.

Among the DNA sequences encoding proteins which confer tolerance to certain herbicides on the transformed plant cells and plants, mention can be made of a bar or PAT gene or the *Streptomyces coelicolor* gene described in WO2009/152359 which confers tolerance
15 to glufosinate herbicides, a gene encoding a suitable EPSPS which confers tolerance to herbicides having EPSPS as a target, such as glyphosate and its salts (US 4,535,060, US 4,769,061, US 5,094,945, US 4,940,835, US 5,188,642, US 4,971,908, US 5,145,783, US 5,310,667, US 5,312,910, US 5,627,061, US 5,633,435), or a gene encoding glyphosate oxydoreductase (US 5,463,175).

Among the DNA sequences encoding a suitable EPSPS which confer tolerance to the herbicides which have EPSPS as a target, mention will more particularly be made of the gene which encodes a plant EPSPS, in particular maize EPSPS, particularly a maize EPSPS which comprises two mutations, particularly a mutation at amino acid position 102
25 and a mutation at amino acid position 106 (WO 2004/074443), and which is described in Patent Application US 6566587, hereinafter named double mutant maize EPSPS or 2mEPSPS, or the gene which encodes an EPSPS isolated from *Agrobacterium* and which is described by SEQ ID No. 2 and SEQ ID No. 3 of US Patent 5,633,435, also named CP4.

Among the DNA sequences encoding a suitable EPSPS which confer tolerance to the herbicides which have EPSPS as a target, mention will more particularly be made of the gene which encodes an EPSPS GRG23 from *Arthrobacter globiformis*, but also the mutants GRG23 ACE1, GRG23 ACE2, or GRG23 ACE3, particularly the mutants or

variants of GRG23 as described in WO2008/100353, such as GRG23(ace3)R173K of SEQ ID No. 29 in WO2008/100353.

5 In the case of the DNA sequences encoding EPSPS, and more particularly encoding the above genes, the sequence encoding these enzymes is advantageously preceded by a sequence encoding a transit peptide, in particular the “optimized transit peptide” described in US Patent 5,510,471 or 5,633,448.

10 In WO 2007/024782, plants being tolerant to glyphosate and at least one ALS (acetolactate synthase) inhibitor are disclosed. More specifically plants containing genes encoding a GAT (Glyphosate-N-Acetyltransferase) polypeptide and a polypeptide conferring resistance to ALS inhibitors are disclosed.

In US 6855533, transgenic tobacco plants containing mutated Arabidopsis ALS/AHAS genes were disclosed.

15 In US 6,153,401, plants containing genes encoding 2,4-D-monooxygenases conferring tolerance to 2,4-D (2,4-dichlorophenoxyacetic acid) by metabolism are disclosed.

20 In US 2008/0119361 and US 2008/0120739, plants containing genes encoding Dicamba monooxygenases conferring tolerance to dicamba (3,6-dichloro-2-methoxybenzoic acid) by metabolism are disclosed.

25 In WO2011/028833 and WO2011/028832 plants containing genes encoding mutagenized or recombinant Acetyl-coenzyme-A carboxylase (ACCase) conferring tolerance to at least one herbicide is selected from the group consisting of alloxydim, butroxydim, clethodim, cloproxydim, cycloxydim, sethoxydim, tepraloxym, tralkoxydim, chlorazifop, clodinafop, clofop, diclofop, fenoxaprop, fenoxaprop-P, fenthiaprop, fluazifop, fluazifop-P, haloxyfop, haloxyfop-P, isoxapyrifop, propaquizafop, quizalofop, quizalofop-P, trifop, and pinoxaden or agronomically acceptable salts or esters of any of these herbicides are disclosed.

30 All the above mentioned herbicide tolerance traits can be combined with those performing HPPD tolerance in plants concerning N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts by containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more

preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No. 12 encoding HPPD defined by SEQ ID No. 13, (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present

application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas* (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

Among the DNA sequences encoding proteins concerning properties of tolerance to insects, mention will more particularly be made of the Bt proteins widely described in the literature and well known to those skilled in the art. Mention will also be made of proteins extracted from bacteria such as *Photorhabdus* (WO 97/17432 & WO 98/08932).

5 Among such DNA sequences encoding proteins of interest which confer novel properties of tolerance to insects, mention will more particularly be made of the Bt Cry or VIP proteins widely described in the literature and well known to those skilled in the art. These include the Cry1F protein or hybrids derived from a Cry1F protein (e.g., the hybrid Cry1A-Cry1F proteins described in US 6,326,169; US 6,281,016; US 6,218,188, or toxic fragments
10 thereof), the Cry1A-type proteins or toxic fragments thereof, preferably the Cry1Ac protein or hybrids derived from the Cry1Ac protein (e.g., the hybrid Cry1Ab-Cry1Ac protein described in US 5,880,275) or the Cry1Ab or Bt2 protein or insecticidal fragments thereof as described in EP451878, the Cry2Ae, Cry2Af or Cry2Ag proteins as described in WO02/057664 or toxic fragments thereof, the Cry1A.105 protein described in WO
15 2007/140256 (SEQ ID No. 7) or a toxic fragment thereof, the VIP3Aa19 protein of NCBI accession ABG20428, the VIP3Aa20 protein of NCBI accession ABG20429 (SEQ ID No. 2 in WO 2007/142840), the VIP3A proteins produced in the COT202 or COT203 cotton events (WO 2005/054479 and WO 2005/054480, respectively), the Cry proteins as described in WO01/47952, the VIP3Aa protein or a toxic fragment thereof as described in
20 Estruch et al. (1996), Proc Natl Acad Sci U S A. 28;93(11):5389-94 and US 6,291,156, the insecticidal proteins from *Xenorhabdus* (as described in WO98/50427), *Serratia* (particularly from *S. entomophila*) or *Photorhabdus* species strains, such as Tc-proteins from *Photorhabdus* as described in WO98/08932 (e.g., Waterfield et al., 2001, Appl Environ Microbiol. 67(11):5017-24; Ffrench-Constant and Bowen, 2000, Cell Mol Life Sci.;
25 57(5):828-33). Also any variants or mutants of any one of these proteins differing in some (1-10, preferably 1-5) amino acids from any of the above sequences, particularly the sequence of their toxic fragment, or which are fused to a transit peptide, such as a plastid transit peptide, or another protein or peptide, is included herein.

30 The present invention also relates to the use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts in transgenic plants comprising a chimeric gene (or expression cassette) which comprises a coding sequence as well as heterologous regulatory elements, at the 5' and/or 3' position, at least at the 5' position, which are able

to function in a host organism, in particular plant cells or plants, with the coding sequence containing at least one nucleic acid sequence which encodes an HPPD

(I) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1

5 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3

encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably

Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No.

6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma*

10 *japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8

encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp.

(strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to

SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain

RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID

15 No.12 encoding HPPD defined by SEQ ID No. 13, (f) *Picrophilaceae*, preferably

Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No.

14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more

preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD

defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of

20 HPPD encoding genes of the before defined organisms, preferably mutants as described

in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877,

WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO

2012/021785, according to the latter, comprising more especially one or more mutated

DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean

25 (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III)

comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically

a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E

(Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at

position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in

30 PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii)

comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser)

replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named

PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being

disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P

(Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or

5 (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in

10 PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and

15 being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named

20 Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being

25 disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A

30 (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln)

replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

- 5 In another particular embodiment, the present invention relates to the use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts in transgenic plant comprising a chimeric gene as previously described, wherein the chimeric gene contains in the 5' position of the nucleic acid sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) (I) derived from a member of a group of organisms, consisting of (a)
- 10 Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No.
- 15 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain
- 20 RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD
- 25 defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO
- 30 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), especially preferable HPPD encoding genes from maize (Zea mays) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at

position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named

5 PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in

10 PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356

15 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named

20 Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser)

25 replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A

30 (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro)

replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A
 (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being
 disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present
 application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E
 5 (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position
 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln)
 replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ
 ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD
 protein sequence under SEQ ID No 37), a nucleic acid sequence which encodes a plant
 10 transit peptide, with this sequence being arranged between the promoter region and the
 nucleic acid sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) (I) derived
 from a member of a group of organisms, consisting of (a) Avena, preferably Avena sativa,
 more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD
 defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more
 15 preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined
 by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably
 comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ
 ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably
 comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID
 20 No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more
 preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD
 defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more
 preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined
 by SEQ ID No. 13, (f) Picrophilaceae, preferably Picrophilus torridus, more preferably
 25 comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ
 ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA
 sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II)
 comprising one or more mutated DNA sequences of HPPD encoding genes of the before
 defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968,
 30 WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892,
 WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising
 more especially one or more mutated DNA sequences of HPPD encoding genes obtained
 from maize (Zea mays) or soybean (Glycine max), especially preferable HPPD encoding
 genes from maize (Zea mays) or (III) comprising a mutated DNA sequence described in

PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a

mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), so as to permit expression of a transit peptide/HPPD fusion protein.

In a further particular embodiment, the present invention relates to the use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts on plants, plant parts, or plant seeds containing one or more chimeric gene(s) (I) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No. 12 encoding HPPD defined by SEQ ID No. 13, (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079,

WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (Zea mays) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No

40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), or to the use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts on soil where such plants, plant parts or seeds are to be grown or sown, either alone or in combination with one or more other known herbicides acting in a different manner to HPPD inhibitors.

In a further particular embodiment, the N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts herbicide can applied in combination either in mixture, simultaneously or successively with HPPD inhibitor herbicides selected from the group consisting of triketones (named triketone HPPD inhibitor), such as tembotrione, sulcotrione mesotrione, bicyclopyrone, tefuryltrione, particularly tembotrione, of the class diketone such as diketonitrile of the class of isoxazoles such as isoxaflutole or of the class of pyrazolates (named pyrazolate HPPD inhibitor), such as pyrasulfotole, pyrazolate, topramezone, benzofenap, even more specifically present invention relates to the application of tembotrione, mesotrione, diketonitrile, bicyclopyrone, tefuryltrione, benzofenap, pyrasulfotole, pyrazolate and sulcotrione to such HPPD inhibitor tolerant plants, plant parts or plant seeds containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined

by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ

5 ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more

10 preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13, (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II)

15 comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained

20 from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and

25 being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No.

30 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described

in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas* (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID

5 No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and

10 being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named

15 Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being

20 disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A

25 (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln)

30 replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

As a regulatory sequence which functions as a promoter in plant cells and plants, use may be made of any promoter sequence of a gene which is naturally expressed in plants, in particular a promoter which is expressed especially in the leaves of plants, such as for example “constitutive” promoters of bacterial, viral or plant origin, or “light-dependent” promoters, such as that of a plant ribulose-biscarboxylase/oxygenase (RuBisCO) small subunit gene, or any suitable known promoter-expressible which may be used. Among the promoters of plant origin, mention will be made of the histone promoters as described in EP 0 507 698 A1, the rice actin promoter (US 5,641,876), or a plant ubiquitin promoter (US 5,510,474). Among the promoters of a plant virus gene, mention will be made of that of the cauliflower mosaic virus (CaMV 19S or 35S, Sanders et al. (1987), Nucleic Acids Res. 15(4):1543-58.), the circovirus (AU 689 311) or the Cassava vein mosaic virus (CsVMV, US 7,053,205).

In a further particular embodiment, present invention relates to the use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts on plants, plant parts, or plant seeds comprising a promoter sequence specific for particular regions or tissues of plants can be used to express one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No. 12 encoding HPPD defined by SEQ ID No. 13, (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or

more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially

5 one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp)

10 replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being

15 disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or

20 (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in

25 PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and

30 being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named

Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), such as promoters specific for seeds (Datla, R. et al., 1997, *Biotechnology Ann. Rev.* 3, 269-296), especially the napin promoter (EP 255 378 A1), the phaseolin promoter, the glutenin promoter, the helianthinin promoter (WO 92/17580), the albumin promoter (WO 98/45460), the oleosin promoter (WO 98/45461), the SAT1 promoter or the SAT3 promoter (PCT/US98/06978).

Use may also be made of an inducible promoter advantageously chosen from the phenylalanine ammonia lyase (PAL), HMG-CoA reductase (HMG), chitinase, glucanase, proteinase inhibitor (PI), PR1 family gene, nopaline synthase (nos) and vspB promoters (US 5 670 349, Table 3), the HMG2 promoter (US 5 670 349), the apple beta-galactosidase (ABG1) promoter and the apple aminocyclopropane carboxylate synthase (ACC synthase) promoter (WO 98/45445).

The genes encoding hydroxyphenylpyruvate dioxygenase (HPPD) (I) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more

preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably

5 comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined

10 by SEQ ID No. 13 , (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before

15 defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding

20 genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present

25 application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W

30 (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas*

(=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD

5 protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No

10 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and

15 being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present

20 application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being

25 disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ

30 ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37) may also be used in combination with the promoter, of other regulatory sequences, which are located between the promoter and the coding sequence, such as transcription activators ("enhancers"), for instance the translation activator of the tobacco mosaic virus (TMV) described in Application WO

87/07644, or of the tobacco etch virus (TEV) described by Carrington & Freed 1990, J. Virol. 64: 1590-1597, for example, or introns such as the adh1 intron of maize or intron 1 of rice actin in order to perform a sufficient tolerance to N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts.

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In a further particular embodiment, the present invention relates to the use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts on plants, plant parts, or plant seeds containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No. 12 encoding HPPD defined by SEQ ID No. 13, (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp)

replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named

5 PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in

10 PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356

15 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named

20 Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser)

25 replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A

30 (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro)

replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37) and also containing a CYP450 Maize monooxygenase (nsf1 gene) gene being under the control of an identical or different plant expressible promoter in order to confer tolerance to N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts.

As a regulatory terminator or polyadenylation sequence, use may be made of any corresponding sequence of bacterial origin, such as for example the nos terminator of *Agrobacterium tumefaciens*, of viral origin, such as for example the CaMV 35S terminator, or of plant origin, such as for example a histone terminator as described in published Patent Application EP 0 633 317 A1.

It is to be understood that in order to obtain an optimized expression by a host adapted codon usage of the respective chimeric gene(s), one could adopt non-planta genes to the codon usage of the respective plant organism in which such chimeric genes will be inserted. Accordingly, in all of the described chimeric genes expressing HPPD of non-planta origin, the respective HPPD encoding DNA sequence can be replaced by an amended DNA sequence encoding the identical amino acid sequence, i.e. SEQ ID No. 3 can be replaced by SEQ ID No. 5., SEQ ID No. 6 can be replaced by SEQ ID No. 18, SEQ ID No. 8 can be replaced by SEQ ID No. 19, SEQ ID No. 10 can be replaced by SEQ ID No. 20, SEQ ID No. 12 can be replaced by SEQ ID No. 21, SEQ ID No. 14 can be replaced by SEQ ID No. 22, SEQ ID No. 16 can be replaced by SEQ ID No. 23.

The term "gene", as used herein refers to a DNA coding region flanked by 5' and/or 3' regulatory sequences allowing RNA to be transcribed which can be translated to a protein, typically comprising at least a promoter region. A "chimeric gene", when referring to an

HPPD encoding DNA, refers to an HPPD encoding DNA sequence having 5' and/or 3' regulatory sequences different from the naturally occurring bacterial 5' and/or 3' regulatory sequences which drive the expression of the HPPD protein in its native host cell (also referred to as "heterologous promoter" or "heterologous regulatory sequences").

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The terms "DNA/protein comprising the sequence X" and "DNA/protein with the sequence comprising sequence X", as used herein, refer to a DNA or protein including or containing at least the sequence X in their nucleotide or amino acid sequence, so that other nucleotide or amino acid sequences can be included at the 5' (or N-terminal) and/or 3' (or C-terminal) end, e.g., a N-terminal transit or signal peptide. The term "comprising", as used herein, is open-ended language in the meaning of "including", meaning that other elements than those specifically recited can also be present. The term "consisting of", as used herein, is closed-ended language, i.e., only those elements specifically recited are present. The term "DNA encoding a protein comprising sequence X", as used herein, refers to a DNA comprising a coding sequence which after transcription and translation results in a protein containing at least amino acid sequence X. A DNA encoding a protein need not be a naturally occurring DNA, and can be a semi-synthetic, fully synthetic or artificial DNA and can include introns and 5' and/or 3' flanking regions. The term "nucleotide sequence", as used herein, refers to the sequence of a DNA or RNA molecule, which can be in single- or double-stranded form.

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HPPD proteins according to the invention may be equipped with a signal peptide according to procedures known in the art, see, e.g., published PCT patent application WO 96/10083, or they can be replaced by another peptide such as a chloroplast transit peptide (e.g., Van Den Broeck et al., 1985, Nature 313, 358, or a modified chloroplast transit peptide of US patent 5, 510,471) causing transport of the protein to the chloroplasts, by a secretory signal peptide or a peptide targeting the protein to other plastids, mitochondria, the ER, or another organelle, or it can be replaced by a methionine amino acid or by a methionine-alanine dipeptide. Signal sequences for targeting to intracellular organelles or for secretion outside the plant cell or to the cell wall are found in naturally targeted or secreted proteins, preferably those described by Klösgen et al. (1989, Mol. Gen. Genet. 217, 155-161), Klösgen and Weil (1991, Mol. Gen. Genet. 225, 297-304), Neuhaus & Rogers (1998, Plant Mol. Biol. 38, 127-144), Bih et al. (1999, J. Biol. Chem. 274, 22884-22894), Morris et al. (1999, Biochem. Biophys. Res. Commun. 255, 328-333), Hesse et al.

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(1989, EMBO J. 8 2453-2461), Tavladoraki et al. (1998, FEBS Lett. 426, 62-66), Terashima et al. (1999, Appl. Microbiol. Biotechnol. 52, 516-523), Park et al. (1997, J. Biol. Chem. 272, 6876-6881), Shcherban et al. (1995, Proc. Natl. Acad. Sci USA 92, 9245-9249), all of which are incorporated herein by reference, particularly the signal peptide sequences from targeted or secreted proteins of corn, cotton, soybean, or rice. A DNA sequence encoding such a plant signal peptide can be inserted in the chimeric gene encoding the HPPD protein for expression in plants.

The invention also encompasses variant HPPD enzymes which are amino acid sequences similar to the HPPD amino acid sequence of SEQ ID No. 2, SEQ ID No. 4, SEQ ID No. 7, SEQ ID No. 9, SEQ ID No. 11, SEQ ID No. 13, SEQ ID No. 15, and SEQ ID No. 17 wherein in each of the before one or more amino acids have been inserted, deleted or substituted. In the present context, variants of an amino acid sequence refer to those polypeptides, enzymes or proteins which have a similar catalytic activity as the amino acid sequences described herein, notwithstanding any amino acid substitutions, additions or deletions thereto. Preferably the variant amino acid sequence has a sequence identity of at least about 80%, or 85 or 90%, 95%, 97%, 98% or 99% with the amino acid sequence of SEQ ID No. 2, SEQ ID No. 4, SEQ ID No. 7, SEQ ID No. 9, SEQ ID No. 11, SEQ ID No. 13, SEQ ID No. 15, and SEQ ID No. 17, respectively. Also preferably, a polypeptide comprising the variant amino acid sequence has HPPD enzymatic activity. Methods to determine HPPD enzymatic activity are well known in the art and include assays as extensively described in WO 2009/144079 or in WO 2002/046387, or in PCT/EP2010/070561.

Substitutions encompass amino acid alterations in which an amino acid is replaced with a different naturally-occurring or a non-conventional amino acid residue. Such substitutions may be classified as "conservative", in which an amino acid residue contained in an HPPD protein of this invention is replaced with another naturally-occurring amino acid of similar character, for example Gly↔Ala, Val↔Ile↔Leu, Asp↔Glu, Lys↔Arg, Asn↔Gln or Phe↔Trp↔Tyr. Substitutions encompassed by the present invention may also be "non-conservative", in which an amino acid residue which is present in an HPPD protein of the invention is substituted with an amino acid with different properties, such as a naturally-occurring amino acid from a different group (e.g. substituting a charged or hydrophobic amino acid with alanine. Amino acid substitutions are typically of single residues, but may

be of multiple residues, either clustered or dispersed. Amino acid deletions will usually be of the order of about 1-10 amino acid residues, while insertions may be of any length. Deletions and insertions may be made to the N-terminus, the C-terminus or be internal deletions or insertions. Generally, insertions within the amino acid sequence will be smaller than amino- or carboxy-terminal fusions and of the order of 1 to 4 amino acid residues. "Similar amino acids", as used herein, refers to amino acids that have similar amino acid side chains, i.e. amino acids that have polar, non-polar or practically neutral side chains. "Non-similar amino acids", as used herein, refers to amino acids that have different amino acid side chains, for example an amino acid with a polar side chain is non-similar to an amino acid with a non-polar side chain. Polar side chains usually tend to be present on the surface of a protein where they can interact with the aqueous environment found in cells ("hydrophilic" amino acids). On the other hand, "non-polar" amino acids tend to reside within the center of the protein where they can interact with similar non-polar neighbors ("hydrophobic" amino acids"). Examples of amino acids that have polar side chains are arginine, asparagine, aspartate, cysteine, glutamine, glutamate, histidine, lysine, serine, and threonine (all hydrophilic, except for cysteine which is hydrophobic). Examples of amino acids that have non-polar side chains are alanine, glycine, isoleucine, leucine, methionine, phenylalanine, proline, and tryptophan (all hydrophobic, except for glycine which is neutral).

Unless otherwise stated in the examples, all procedures for making and manipulating recombinant DNA are carried out by the standard procedures described in Sambrook et al., *Molecular Cloning - A Laboratory Manual*, Second Ed., Cold Spring Harbor Laboratory Press, NY (1989), and in Volumes 1 and 2 of Ausubel et al. (1994) *Current Protocols in Molecular Biology*, Current Protocols, USA. Standard materials and methods for plant molecular biology work are described in *Plant Molecular Biology Labfax* (1993) by R.R.D. Croy, jointly published by BIOS Scientific Publications Ltd (UK) and Blackwell Scientific Publications (UK). Procedures for PCR technology can be found in "PCR protocols: a guide to methods and applications", Edited by M.A. Innis, D.H. Gelfand, J.J. Sninsky and T.J. White (Academic Press, Inc., 1990).

The terms "tolerance", "tolerant" or "less sensitive" are interchangeable used and mean the relative levels of inherent tolerance of the HPPD screened according to a visible indicator phenotype of the strain or plant transformed with a nucleic acid comprising the gene

coding for the respective HPPD protein in the presence of different concentrations of the various HPPD inhibitor herbicides. Dose responses and relative shifts in dose responses associated with these indicator phenotypes (formation of brown color, growth inhibition, bleaching, 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 increases in inherent tolerance of the expressed HPPD, 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

5 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 HPPD. Herbicides can suitably be applied pre-emergence or post emergence.

Likewise, tolerance level is screened via transgenesis, regeneration, breeding and spray

15 testing of a test plant such as tobacco, or a crop plant such as soybean or cotton and according to these results, such plants are at least 2-4x more tolerant to HPPD inhibitor herbicides, like N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts than plants that do not contain any exogenous gene encoding an HPPD protein, "Host organism" or "host" is understood as being any unicellular or multicellular

20 heterologous organism into which the nucleic acid or chimeric gene according to the invention can be introduced for the purpose of producing HPPD. These organisms are, in particular, bacteria, for example *E. coli*, yeast, in particular of the genera *Saccharomyces* or *Kluyveromyces*, *Pichia*, fungi, in particular *Aspergillus*, a baculovirus or, preferably, plant cells and plants.

25 "Plant cell" is understood, according to the invention, as being any cell which is derived from or found in a plant and which is able to form or is part of undifferentiated tissues, such as calli, differentiated tissues such as embryos, parts of plants, plants or seeds. This includes protoplasts and pollen, cultivated plants cells or protoplasts grown in vitro, and

30 plant cells that can regenerate into a complete plant.

"Plant" is understood, according to the invention, as being any differentiated multicellular organism which is capable of photosynthesis, in particular a monocotyledonous or dicotyledonous organism, more especially cultivated plants which are or are not intended

for animal or human nutrition, such as maize or corn, wheat, *Brassica spp.* plants such as *Brassica napus* or *Brassica juncea*, soya spp, rice, sugarcane, beetroot, tobacco, cotton, vegetable plants such as cucumber, leek, carrot, tomato, lettuce, peppers, melon, watermelon, etc. Transgenic plants, as used herein, refer to plants comprising one or more
5 foreign or heterologous gene(s) stably inserted in their genome.

In order perform tolerance to N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts, any promoter sequence of a gene which is expressed naturally in plants, or any hybrid or combination of promoter elements of genes expressed naturally in plants,
10 including *Agrobacterium* or plant virus promoters, or any promoter which is suitable for controlling the transcription of a herbicide tolerance gene in plants, can be used as the promoter sequence in the plants of the invention (named "plant-expressible promoter" herein). Examples of such suitable plant-expressible promoters are described above. In one embodiment of this invention, such plant-expressible promoters are operably-linked to
15 a (I) DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) that is derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined
20 by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus sp.*, more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus sp.* (strain RHA1), isolate ro03041 more
25 preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus sp.* (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ
30 ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892,

WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in

5 PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at

10 position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and

15 an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement

20 at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala)

25 replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD

30 protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp)

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replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a
5 mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present
10 application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD
15 protein sequence under SEQ ID No 37).

According to the invention, it is also possible to use, in combination with the promoter regulatory sequence, other regulatory sequences which are located between the promoter and the coding sequence, such as intron sequences, or transcription activators
20 (enhancers) in order to perform tolerance to N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts. Examples of such suitable regulatory sequences are described above.

Any corresponding sequence of bacterial or viral origin, such as the nos terminator from
25 *Agrobacterium tumefaciens*, or of plant origin, such as a histone terminator as described in application EP 0 633 317 A1, may be used as transcription termination (and polyadenylation) regulatory sequence.

In a further particular embodiment, the present invention relates to the use of N-(1,3,4-
30 Oxadiazol-2-yl)arylcarboxamides as defined above or their salts on plants, plant parts, or plant seeds containing a nucleic acid sequence which encodes a transit peptide is employed 5' (upstream) of the nucleic acid sequence encoding the exogenous chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) *Avena*,

preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably

5 *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to

10 SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No. 12 encoding HPPD defined by SEQ ID No. 13, (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more

15 preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO

20 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E

25 (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named

30 PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in

PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas* (=Comamonas) *testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37) and also containing with this transit peptide

sequence being arranged between the promoter region and the sequence encoding the exogenous HPPD so as to permit expression of a transit peptide-HPPD fusion protein. The transit peptide makes it possible to direct the HPPD into the plastids, more especially the chloroplasts, with the fusion protein being cleaved between the transit peptide and the

5 HPPD protein when the latter enters the plastid. The transit peptide may be a single peptide, such as an EPSPS transit peptide (described in US patent 5,188,642) or a transit peptide of the plant ribulose biphosphate carboxylase/ oxygenase small subunit (RuBisCO ssu), where appropriate, including a few amino acids of the N-terminal part of the mature RuBisCO ssu (EP 189 707 A1), or else may be a fusion of several transit

10 peptides such as a transit peptide which comprises a first plant transit peptide which is fused to a part of the N-terminal sequence of a mature protein having a plastid location, with this part in turn being fused to a second plant transit peptide as described in patent EP 508 909 A1, and, more especially, the optimized transit peptide which comprises a transit peptide of the sunflower RuBisCO ssu fused to 22 amino acids of the

15 N-terminal end of the maize RuBisCO ssu, in turn fused to the transit peptide of the maize RuBisCO ssu, as described, with its coding sequence, in patent EP 508 909 A1.

The present invention also relates to the transit peptide HPPD fusion protein and a nucleic acid or plant-expressible chimeric gene encoding such fusion protein, wherein the two

20 elements of this fusion protein are as defined above.

In a further particular embodiment, the present invention relates to the use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts on plants, plant parts, or plant seeds obtained by cloning, transformation with an expression vector, which

25 expression vector contains at least one chimeric gene encoding the hydroxyphenylpyruvate dioxygenase (HPPD) (I) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA

30 sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e)

Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 ,

5 (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms,

10 preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), especially preferable HPPD encoding genes from maize

15 (Zea mays) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No.

20 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K

25 (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD

30 protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at

position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No

5 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and

10 being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present

15 application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being

20 disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ

25 ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37). In addition to the above chimeric gene, this vector can contain an origin of replication. This vector can be a plasmid or plasmid portion, a cosmid, or a bacteriophage or a virus which has been transformed by introducing the chimeric gene according to the invention. Transformation vectors are well known to the

30 skilled person and widely described in the literature. The transformation vector which can be used, in particular, for transforming plant cells or plants may be a virus, which can be employed for transforming plant cells or plants and which additionally contains its own replication and expression elements. The vector for transforming plant cells or plants is preferably a plasmid, such as a disarmed *Agrobacterium* Ti plasmid.

In a further particular embodiment, the present invention relates to the use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts on plants, plant parts, or plant seeds containing a chimeric gene which comprises a sequence encoding the

5 hydroxyphenylpyruvate dioxygenase (HPPD) (I) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c)

10 *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably

15 comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No. 12 encoding HPPD defined by SEQ ID No. 13, (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g)

20 *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885,

25 WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i)

30 comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named

PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at

5 position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S

10 (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala)

15 replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD

20 protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp)

25 replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated

30 sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E

(Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), and the use of the plants or seeds in a field to grow a crop and harvest a plant product, e.g., soya spp, rice, wheat, barley or corn grains or cotton bolls, where in one embodiment said use involves the application of an N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts to such plants to control weeds.

In another particular embodiment, the present invention relates to the use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts on plants, plant parts, or plant seeds characterized in that it contains one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13, (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising

more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A

(Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated

5 sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E

10 (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37) and in addition further contains a chimeric gene

15 comprising a plant-expressible promoter as described above, operably-linked to a nucleic acid sequence encoding a PDH (prephenate dehydrogenase) enzyme (US 2005/0257283) in order to confer tolerance to N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts. A plant comprising such two transgenes can be obtained by transforming a plant with one transgene, and then re-transforming this transgenic plant with the second

20 transgene, or by transforming a plant with the two transgenes simultaneously (in the same or in 2 different transforming DNAs or vectors), or by crossing a plant comprising the first transgene with a plant comprising the second transgene, as is well known in the art.

One transformation method in order to obtain plants, plant parts or seeds being tolerant to

25 N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts by containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b)

30 *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA

sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising

5 a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or

10 more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea*

15 *mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID

20 No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P

25 (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or

(IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more

30 specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein

sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and

5 being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named

10 Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being

15 disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A

20 (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln)

25 replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37) comprises bombarding cells, protoplasts or tissues with solid or liquid particles to which DNA is attached, or containing DNA. Another transformation method comprises using, as mean for transfer into the plant, a chimeric

30 gene which is inserted into an *Agrobacterium tumefaciens* Ti plasmid or an *Agrobacterium rhizogenes* Ri plasmid. Other methods may be used, such as microinjection or electroporation or otherwise direct gene transfer using PEG. The skilled person can select any appropriate method for transforming the host organism of choice, in particular the plant cell or the plant. As examples, the technology for soybean transformation has been

extensively described in the examples 1 to 3 disclosed in EP 1186666 A1, incorporated herein by reference. For rice, *Agrobacterium*-mediated transformation (Hiei et al., 1994 Plant J 6:271-282, and Hiei et al., 1997 Plant Mol Biol. 35:205-21, incorporated herein by reference), electroporation (US 5,641,664 and US 5,679,558, incorporated herein by reference), or bombardment (Christou et al., 1991, Biotechnology 9:957 incorporated herein by reference) could be performed. A suitable technology for transformation of monocotyledonous plants, and particularly rice, is described in WO 92/09696, incorporated herein by reference. For cotton, *Agrobacterium*-mediated transformation (Gould J.H. and Magallanes-Cedeno M., 1998 Plant Molecular Biology reporter, 16:1-10 and Zapata C., 1999, Theoretical Applied Genetics, 98(2):1432-2242 incorporated herein by reference), polybrene and/or treatment-mediated transformation (Sawahel W.A., 2001, - Plant Molecular Biology reporter, 19:377a-377f, incorporated herein by reference) have been described.

Alternatively, N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts may be used on plants, plant parts, or plant seeds containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No. 12 encoding HPPD defined by SEQ ID No. 13, (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of

HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated

5 DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at

10 position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being

15 disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or

20 (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in

25 PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and

30 being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named

Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37) which HPPD is expressed directly in the plastids, such as the chloroplasts, using transformation of the plastid, such as the chloroplast genome. A suitable method comprises the bombardment of plant cells or tissue by solid particles coated with the DNA or liquid particles comprising the DNA, and integration of the introduced gene by homologous recombination. Suitable vectors and selection systems are known to the person skilled in the art. An example of means and methods which can be used for such integration into the chloroplast genome of tobacco plants is given in WO 06/108830, the content of which is hereby incorporated by reference

The present invention also relates to a method for obtaining a plant tolerant to N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts, characterized in that the plant is transformed with one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c)

Synechococcoideae, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e)

5 Rhodococcus, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably *Picrophilus torridus*, more preferably comprising a DNA

10 sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079,

15 WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598,

20 more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at

25 position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S

30

(Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

Therefore, the present invention also relates to a method for obtaining a plant tolerant to N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts by containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding

hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA

5 sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e)

10 *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No. 12 encoding HPPD defined by SEQ ID No. 13 ,

(f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA

15 sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079,

20 WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598,

25 more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No.

30 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at

position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD

protein sequence under SEQ ID No 37), which comprises a coding sequence as well as a heterologous regulatory element in the 5' and optionally in the 3' positions, which are able to function in a host organism, characterized in that the coding sequence comprises at least a nucleic acid sequence defining a gene encoding an HPPD of the invention as
5 previously described in order to perform a sufficiently high level of tolerance to N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts.

In one embodiment of this invention, the HPPD inhibitor in the above method is a N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts either alone or in
10 combination with one or more HPPD inhibitor herbicides selected from the group consisting of triketone or pyrazolate herbicide, preferably tembotrione, mesotrione, bicyclopyrone, tefuryltrione pyrasulfotole, pyrazolate, diketonitrile, benzofenap, or sulcotrione, particularly tembotrione.

15 The invention also relates to a method for selectively removing weeds or preventing the germination of weeds in a field to be planted with plants or to be sown with seeds, or in a plant crop, by application of a N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts to such field or plant crop, which method is characterized in that this N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts is applied to plants which
20 have been transformed in accordance with one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more
25 preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID
30 No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picophilaceae, preferably Picophilus torridus, more preferably

comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, 5 WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding 10 genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present 15 application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W 20 (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas* 25 (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement 30 at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more

specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and
 5 being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present
 10 application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being
 15 disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ
 20 ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), either before sowing the crop (hereinafter named pre-planting application), before emergence of the crop (hereinafter named pre-emergence application), or after emergence of the crop (hereinafter named post-emergence application).

25
 The invention also relates to a method for controlling in an area or a field which contains transformed seeds as previously described in the present invention, which method comprises applying, to the said area of the field, a dose of an N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts which is toxic for the said weeds,
 30 without significantly affecting the seeds or plants containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*,

more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13, (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas*

(=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD

5 protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No

10 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and

15 being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present

20 application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being

25 disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ

30 ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

The present invention also relates to a method for cultivating the plants which have been transformed with one or more chimeric gene(s) (I) comprising a DNA sequence encoding

hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA

5 sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e)

10 *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No. 12 encoding HPPD defined by SEQ ID No. 13 ,

(f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA

15 sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079,

20 WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598,

25 more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No.

30 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at

position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas* (=Comamonas) *testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD

protein sequence under SEQ ID No 37). which method comprises planting seeds comprising a chimeric gene of before, in an area of a field which is appropriate for cultivating the said plants, and in applying, if weeds are present, a dose, which is toxic for the weeds, of one or more N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or
5 their salts to the said area of the said field, without significantly affecting the said transformed seeds or the said transformed plants, and in then harvesting the cultivated plants or plant parts when they reach the desired stage of maturity and, where appropriate, in separating the seeds from the harvested plants.

- 10 In the above methods, the N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts can be applied in accordance with the invention, either before sowing the crop, before the crop emerges or after the crop emerges.

Within the meaning of the present invention, "herbicide" is understood as being a
15 herbicidally active substance on its own or such a substance which is combined with an additive which alters its efficacy, such as, for example, an agent which increases its activity (a synergistic agent) or which limits its activity (a safener). It is of course to be understood that, for their application in practice, the above herbicides are combined, in a manner which is known per se, with the formulation adjuvants which are customarily
20 employed in agricultural chemistry.

Thus, transgenic plants can be obtained which - in addition to the one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) *Avena*,
25 preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No.
30 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain

RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named

Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).- have modified properties as the result of overexpression, suppression or inhibition of homologous (= natural) genes or gene sequences or expression of heterologous (= foreign) genes or gene sequences.

On the plants, plant cells or seeds containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably

comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13, (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu)

replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), it is preferred to employ one or more of the N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts in combination with one or more further HPPD inhibitor herbicides belonging to the class of triketones, such as tembotrione, sulcotrione and mesotrione, or of the class of pyrazolinates, such as pyrasulfotole and topramezone, particularly selected from tembotrione, sulcotrione, topramezone, bicyclopyrone, tefuryltrione and mesotrione, more particularly tembotrione in

transgenic crops which are also resistant to growth regulators such as, for example, 2,4-D or dicamba, or against herbicides which inhibit essential plant enzymes, for example acetolactate synthases (ALS), EPSP synthases, glutamine synthases (GS), Acetyl-coenzyme A carboxylase (ACCase), or against herbicides from the group of the

5 sulfonyleureas, imidazolinones, glyphosate, glufosinate, ACCase inhibitors and analogous active substances.

The invention therefore also relates to the use of herbicides applied to HPPD tolerant plants containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding

10 hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c)

15 *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably

20 comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No. 12 encoding HPPD defined by SEQ ID No. 13 , (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g)

25 *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885,

30 WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i)

comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated

sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37) for controlling harmful plants (i.e. weeds) which also extends to transgenic crop plants comprising a second or more herbicide resistance(s) beside the resistance against one or more N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts.

N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts can be formulated in various ways, depending on the prevailing biological and/or physico-chemical parameters. Examples of possible formulations are: wettable powders (WP), water-soluble powders (SP), water-soluble concentrates, emulsifiable concentrates (EC), emulsions (EW), such as oil-in-water and water-in-oil emulsions, sprayable solutions, suspension concentrates (SC), oil- or water-based dispersions, oil-miscible solutions, capsule suspensions (CS), dusts (DP), seed-dressing products, granules for application by broadcasting and on the soil, granules (GR) in the form of micro granules, spray granules, coated granules and adsorption granules, water-dispersible granules (WG), water-soluble granules (SG), ULV formulations, microcapsules and waxes.

These individual types of formulation are known in principle and are described, for example, in: Winnacker-Küchler, "Chemische Technologie" [Chemical technology], volume 7, C. Hanser Verlag Munich, 4th Ed. 1986; Wade van Valkenburg, "Pesticide Formulations", Marcel Dekker, N.Y., 1973; K. Martens, "Spray Drying" Handbook, 3rd Ed. 1979, G. Goodwin Ltd. London.

The formulation auxiliaries required, such as inert materials, surfactants, solvents and further additives, are also known and are described, for example, in: Watkins, "Handbook of Insecticide Dust Diluents and Carriers", 2nd Ed., Darland Books, Caldwell N.J., H.v.

Olphen, "Introduction to Clay Colloid Chemistry"; 2nd Ed., J. Wiley & Sons, N.Y.; C. Marsden, "Solvents Guide"; 2nd Ed., Interscience, N.Y. 1963; McCutcheon's "Detergents and Emulsifiers Annual", MC Publ. Corp., Ridgewood N.J.; Sisley and Wood, "Encyclopedia of Surface Active Agents", Chem. Publ. Co. Inc., N.Y. 1964; Schönfeldt, 5 "Grenzflächenaktive Äthylenoxidaddukte" [Interface-active ethylene oxide adducts], Wiss. Verlagsgesell., Stuttgart 1976; Winnacker-Küchler, "Chemische Technologie" [Chemical technology], volume 7, C. Hanser Verlag Munich, 4th Ed. 1986.

Based on these formulations, it is also possible to prepare combinations with other 10 pesticidally active substances such as, for example, insecticides, acaricides, herbicides, fungicides, and with safeners, fertilizers and/or growth regulators, for example in the form of a ready mix or a tank mix.

Wettable powders are preparations which are uniformly dispersible in water and which, 15 besides the active substance, also comprise ionic and/or nonionic surfactants (wettters, dispersers), for example polyoxyethylated alkylphenols, polyoxyethylated fatty alcohols, polyoxyethylated fatty amines, fatty alcohol polyglycol ether sulfates, alkanesulfonates, alkylbenzenesulfonates, sodium lignosulfonate, sodium 2,2'-dinaphthylmethane-6,6'-disulfonate, sodium dibutyl-naphthalenesulfonate or else 20 sodium oleoylmethyltaurate, besides a diluent or inert substance. To prepare the wettable powders, the herbicidally active substances are ground finely, for example in customary apparatuses such as hammer mills, blower mills and air-jet mills, and mixed with the formulation auxiliaries, either simultaneously or subsequently.

25 Emulsifiable concentrates are prepared by dissolving the active substance in an organic solvent, for example butanol, cyclohexanone, dimethylformamide, xylene or else higher-boiling aromatics or hydrocarbons or mixtures of the organic solvents with addition of one or more ionic and/or nonionic surfactants (emulsifiers). Examples of emulsifiers which may be used are: calcium alkylarylsulfonates such as calcium dodecylbenzenesulfonate, or 30 nonionic emulsifiers such as fatty acid polyglycol esters, alkylaryl polyglycol ethers, fatty alcohol polyglycol ethers, propylene oxide/ethylene oxide condensates, alkyl polyethers, sorbitan esters such as, for example, sorbitan fatty acid esters or polyoxyethylene sorbitan esters such as, for example, polyoxyethylene sorbitan fatty acid esters.

Dusts are obtained by grinding the active substance with finely divided solid materials such as, for example, talcum, natural clays such as kaolin, bentonite and pyrophyllite, or diatomaceous earth.

- 5 Suspension concentrates can be water- or oil-based. They can be prepared for example by wet-grinding by means of commercially available bead mills, if appropriate with addition of surfactants as already listed above for example in the case of the other formulation types.
- 10 Emulsions, for example oil-in-water emulsions (EW), can be prepared for example by means of stirrers, colloid mills and/or static mixers using aqueous organic solvents and, if appropriate, surfactants, as have already been mentioned for example above for the other formulation types.
- 15 Granules can be prepared either by spraying the active substance onto adsorptive, granulated inert material, or by applying active substance concentrates to the surface of carriers such as sand, kaolinites or granulated inert material with the aid of stickers, for example polyvinyl alcohol, sodium polyacrylate or else mineral oils. Suitable active substances can also be granulated in the manner which is customary for the production of
- 20 fertilizer granules, if desired as a mixture with fertilizers.

Water-dispersible granules are generally prepared by customary methods such as spray drying, fluidized-bed granulation, disk granulation, mixing with high-speed stirrers, and extrusion without solid inert material.

- 25 To prepare disk granules, fluidized-bed granules, extruder granules and spray granules, see, for example, methods in "Spray-Drying Handbook" 3rd ed. 1979, G. Goodwin Ltd., London; J.E. Browning, "Agglomeration", Chemical and Engineering 1967, pages 147 et seq.; "Perry's Chemical Engineer's Handbook", 5th Ed., McGraw-Hill, New York 1973,
- 30 p. 8-57.

For further details of the formulation of crop protection products see, for example, G.C. Klingman, "Weed Control as a Science", John Wiley and Sons, Inc., New York, 1961,

pages 81-96 and J.D. Freyer, S.A. Evans, "Weed Control Handbook", 5th Ed., Blackwell Scientific Publications, Oxford, 1968, pages 101-103.

As a rule, the agrochemical preparations comprise from 0.1 to 99% by weight, in particular
5 from 0.1 to 95% by weight, of compounds according to the invention.

In wettable powders, the active substance concentration is, for example, approximately 10 to 90% by weight, the remainder to 100% by weight being composed of customary formulation constituents. In the case of emulsifiable concentrates, the active substance concentration can amount to approximately 1 to 90, preferably 5 to 80% by weight.

10 Formulations in the form of dusts comprise from 1 to 30% by weight of active substance, preferably in most cases from 5 to 20% by weight of active substance, and sprayable solutions comprise approximately from 0.05 to 80, preferably from 2 to 50% by weight of active substance. In the case of water-dispersible granules, the active substance content depends partly on whether the active compound is in liquid or solid form, and on the
15 granulation auxiliaries, fillers and the like which are being used. In the case of the water-dispersible granules, for example, the active substance content is between 1 and 95% by weight, preferably between 10 and 80% by weight.

In addition, the active substance formulations mentioned comprise, if appropriate, the
20 auxiliaries which are conventional in each case, such as stickers, wetters, dispersants, emulsifiers, penetrations, preservatives, antifreeze agents, solvents, fillers, carriers, colorants, antifoams, evaporation inhibitors, and pH and viscosity regulators.

Based on these formulations, it is also possible to prepare combinations of an HPPD
25 inhibitor herbicide of the class of triketones, such as tembotrione, sulcotrione and mesotrione, or of the class of pyrazolines, such as pyrasulfotole and topramezone, particularly selected from tembotrione, sulcotrione, topramezone, bicyclopyrone, tefuryltrione and mesotrione, more particularly tembotrione with other pesticidally active substances such as, for example, insecticides, acaricides, herbicides, fungicides, and with
30 safeners, fertilizers and/or growth regulators, for example in the form of a ready mix or a tank mix to be applied to HPPD tolerant plants according to the invention.

Formulation examples

- a) A dust is obtained by mixing 10 parts by weight of a compound of the formula (I) and/or a salt thereof and 90 parts by weight of talc as inert substance and comminuting the mixture in a hammer mill.
- 5 b) A wettable powder which is readily dispersible in water is obtained by mixing 25 parts by weight of a compound of the formula (I) and/or a salt thereof, 64 parts by weight of kaolin-containing quartz as inert substance, 10 parts by weight of potassium lignosulfonate and 1 part by weight of sodium oleoylmethyltaurinate as wetting agent and dispersant, and grinding the mixture in a pinned-disk mill.
- 10 c) A readily water-dispersible dispersion concentrate is obtained by mixing 20 parts by weight of a compound of the formula (I) and/or a salt thereof with 6 parts by weight of alkylphenol polyglycol ether (®Triton X 207), 3 parts by weight of isotridecanol polyglycol ether (8 EO) and 71 parts by weight of paraffinic mineral oil (boiling range
- 15 for example about 255 to above 277°C) and grinding the mixture in a ball mill to a fineness of below 5 microns.
- d) An emulsifiable concentrate is obtained from 15 parts by weight of a compound of the formula (I) and/or a salt thereof, 75 parts by weight of cyclohexanone as solvent
- 20 and 10 parts by weight of oxethylated nonylphenol as emulsifier.
- e) Water-dispersible granules are obtained by mixing
- 25 75 parts by weight of a compound of the formula (I) and/or a salt thereof, 10 parts by weight of calcium lignosulfonate, 5 parts by weight of sodium lauryl sulfate, 3 parts by weight of polyvinyl alcohol and 7 parts by weight of kaolin, grinding the mixture in a pinned-disk mill, and granulating the powder in a fluidized bed by spraying on water as granulating liquid.
- 30 f) Water-dispersible granules are also obtained by homogenizing and precomminuting, in a colloid mill, 25 parts by weight of a compound of the formula (I) and/or a salt thereof, 5 parts by weight of sodium 2,2'-dinaphthylmethane-6,6'-disulfonate,

2 parts by weight of sodium oleoylmethyltaurate,

1 part by weight of polyvinyl alcohol,

17 parts by weight of calcium carbonate and

50 parts by weight of water,

5 subsequently grinding the mixture in a bead mill and atomizing and drying the resulting suspension in a spray tower by means of a single-substance nozzle.

A further aspect of present invention is the use of one or more N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts to HPPD tolerant plants containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No. 12 encoding HPPD defined by SEQ ID No. 13, (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize

(Zea mays) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present

application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37) in combination with further HPPD inhibitor herbicide belonging to the class of triketones, such as tembotrione, sulcotrione and mesotrione, or belonging to the class of pyrazolinates, such as pyrasulfotole and topramezone, particularly selected from tembotrione, sulcotrione, topramezone, bicyclopyrone, tefuryltrione and mesotrione, more particularly tembotrione in mixed formulations or in the tank mix, and/or with further known active substances which are based on the inhibition of, for example, acetolactate synthase, acetyl-CoA carboxylase, cellulose synthase, enolpyruvylshikimate-3-phosphate synthase, glutamine synthetase, p-hydroxyphenylpyruvate dioxygenase, phytoene desaturase, photosystem I, photosystem II, protoporphyrinogen oxidase, as are described in, for example, Weed Research 26 (1986) 441-445 or "The Pesticide Manual", 14th edition, The British Crop Protection Council and the Royal Soc. of Chemistry, 2003 and the literature cited therein. Known herbicides or plant growth regulators which can be combined with the compounds according to the invention are, for example, the following active substances (the compounds are either designated by the common name according to the International Organization for Standardization (ISO) or by a chemical name, if appropriate together with the code number) and always comprise all use forms such as acids, salts, esters and isomers such as stereoisomers and optical isomers. In this context, one and in some cases also several use forms are mentioned by way of example:

acetochlor, acibenzolar, acibenzolar-S-methyl, acifluorfen, acifluorfen-sodium, aclonifen, alachlor, allidochlor, alloxydim, alloxydim-sodium, ametryne, amicarbazone, amidochlor, amidosulfuron, aminocyclopyrachlor, aminopyralid, amitrole, ammonium sulfamate,

ancymidol, anilofos, asulam, atrazine, azafenidin, azimsulfuron, aziprotryne, BAH-043, BAS-140H, BAS-693H, BAS-714H, BAS-762H, BAS-776H, BAS-800H, beflubutamid, benazolin, benazolin-ethyl, bencarbazon, benfluralin, benfuresate, bensulide, bensulfuron-methyl, bentazone, benzfendizone, benzobicyclon, benzofenap, benzofluor, benzoylprop, bifenox, bilanafos, bilanafos-sodium, bispyribac, bispyribac-sodium, bromacil, bromobutide, bromofenoxim, bromoxynil, bromuron, buminafos, busoxinone, butachlor, butafenacil, butamifos, butenachlor, butralin, butroxydim, butylate, cafenstrole, carbetamide, carfentrazone, carfentrazone-ethyl, chlomethoxyfen, chloramben, chlorazifop, chlorazifop-butyl, chlorbromuron, chlorbufam, chlorfenac, chlorfenac-sodium, chlorfenprop, chlorflurenol, chlorflurenol-methyl, chloridazon, chlorimuron, chlorimuron-ethyl, chlormequat-chloride, chlornitrofen, chlorophthalim, chlorthal-dimethyl, chlorotoluron, chlorsulfuron, cinidon, cinidon-ethyl, cinmethylin, cinosulfuron, clethodim, clodinafop clodinafop-propargyl, clofencet, clomazone, clomeprop, cloprop, clopyralid, cloransulam, cloransulam-methyl, cumyluron, cyanamide, cyanazine, cyclanilide, cycloate, cyclosulfamuron, cycloxydim, cycluron, cyhalofop, cyhalofop-butyl, cyperquat, cyprazine, cyprazole, 2,4-D, 2,4-DB, daimuron/dymron, dalapon, daminozide, dazomet, n-decanol, desmedipham, desmetryn, detosyl-pyrazolate (DTP), di-allate, dicamba, dichlobenil, dichlorprop, dichlorprop-P, diclofop, diclofop-methyl, diclofop-P-methyl, diclosulam, diethatyl, diethatyl-ethyl, difenoxuron, difenzoquat, diflufenican, diflufenzopyr, diflufenzopyr-sodium, dimefuron, dikegulac-sodium, dimefuron, dimepiperate, dimethachlor, dimethametryn, dimethenamid, dimethenamid-P, dimethipin, dimetrasulfuron, dinitramine, dinoseb, dinoterb, diphenamid, dipropetryn, diquat, diquat-dibromide, dithiopyr, diuron, DNOC, eglinazine-ethyl, endothal, EPTC, esprocarb, ethalfluralin, ethametsulfuron-methyl, ethephon, ethidimuron, ethiozin, ethofumesate, ethoxyfen, ethoxyfen-ethyl, ethoxysulfuron, etobenzanid, F-5331, i.e. N-[2-chloro-4-fluoro-5-[4-(3-fluoro-propyl)-4,5-dihydro-5-oxo-1H-tetrazol-1-yl]-phenyl]ethanesulfonamide, fenoprop, fenoxaprop, fenoxaprop-P, fenoxaprop-ethyl, fenoxaprop-P-ethyl, fentrazamide, fenuron, flamprop, flamprop-M-isopropyl, flamprop-M-methyl, flazasulfuron, florasulam, fluazifop, fluazifop-P, fluazifop-butyl, fluazifop-P-butyl, fluazolate, flucarbazone, flucarbazone-sodium, flucetosulfuron, fluchloralin, flufenacet (thiafluamide), flufenpyr, flufenpyr-ethyl, flumetralin, flumetsulam, flumiclorac, flumiclorac-pentyl, flumioxazin, flumipropyn, fluometuron, fluorodifen, fluoroglycofen, fluoroglycofen-ethyl, flupoxam, flupropacil, flupropanate, flupyrsulfuron, flupyrsulfuron-methyl-sodium, flurenol, flurenol-butyl, fluridone, flurochloridone, fluroxypyr, fluroxypyr-meptyl, flurprimidol, flurtamone,

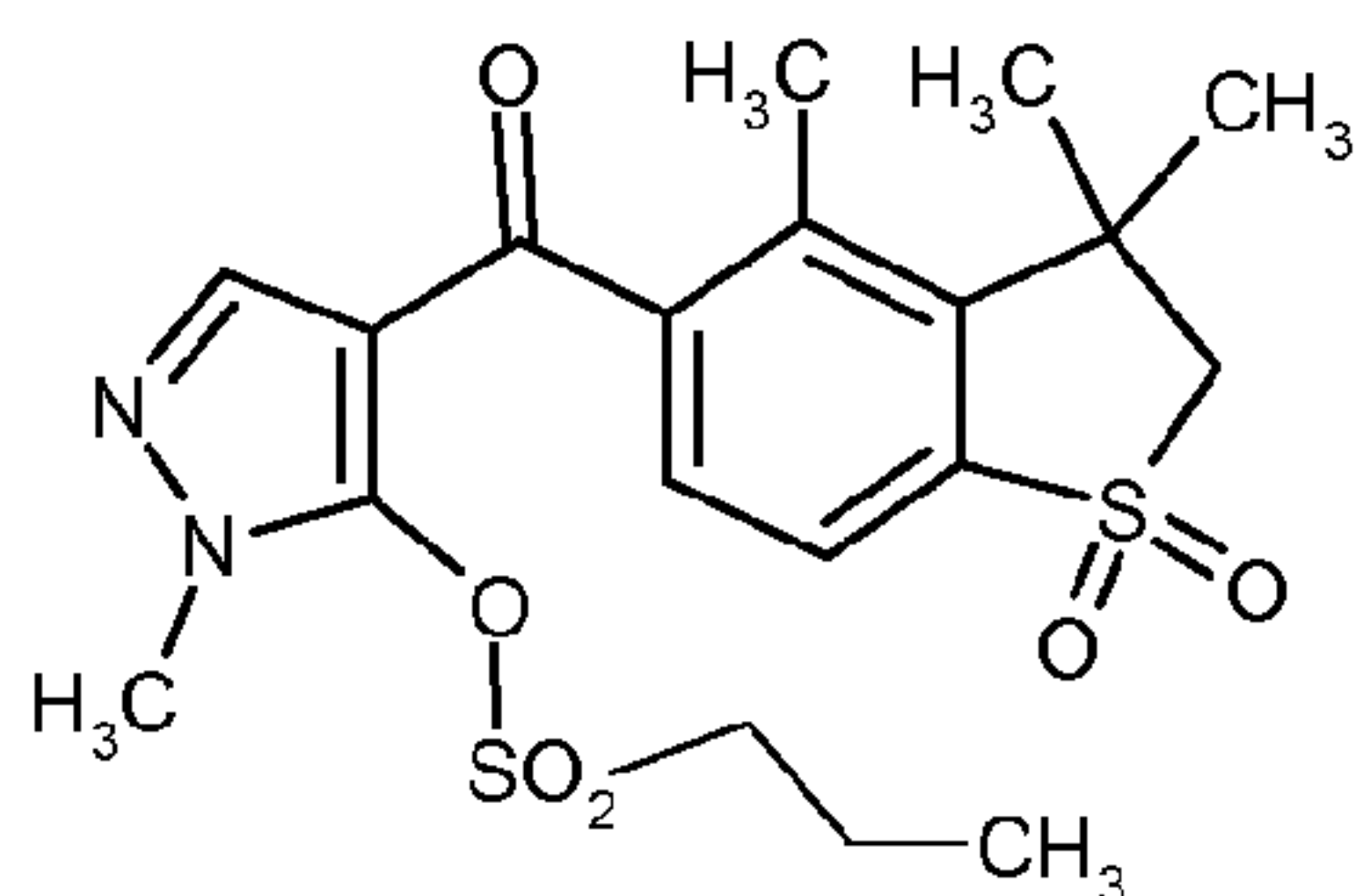
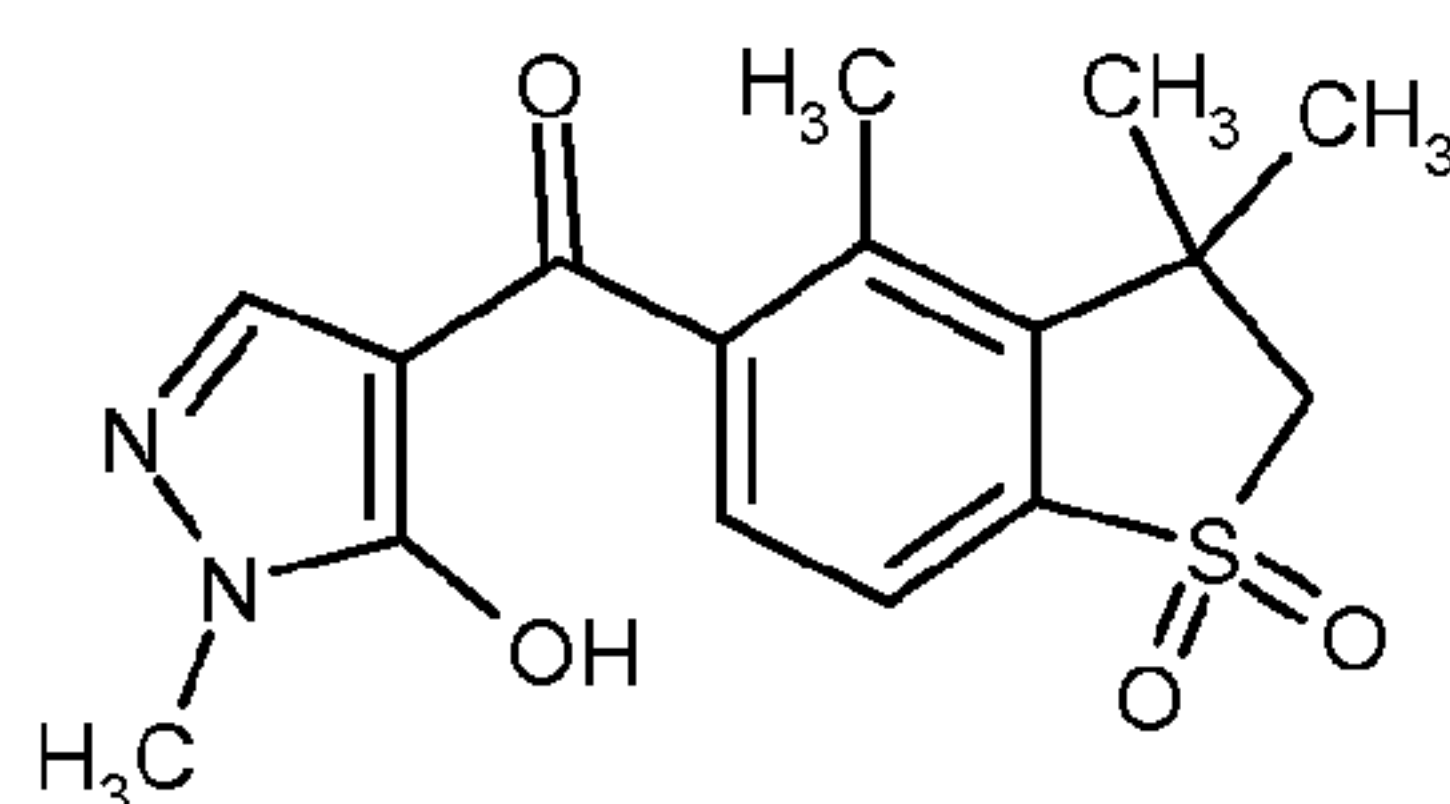
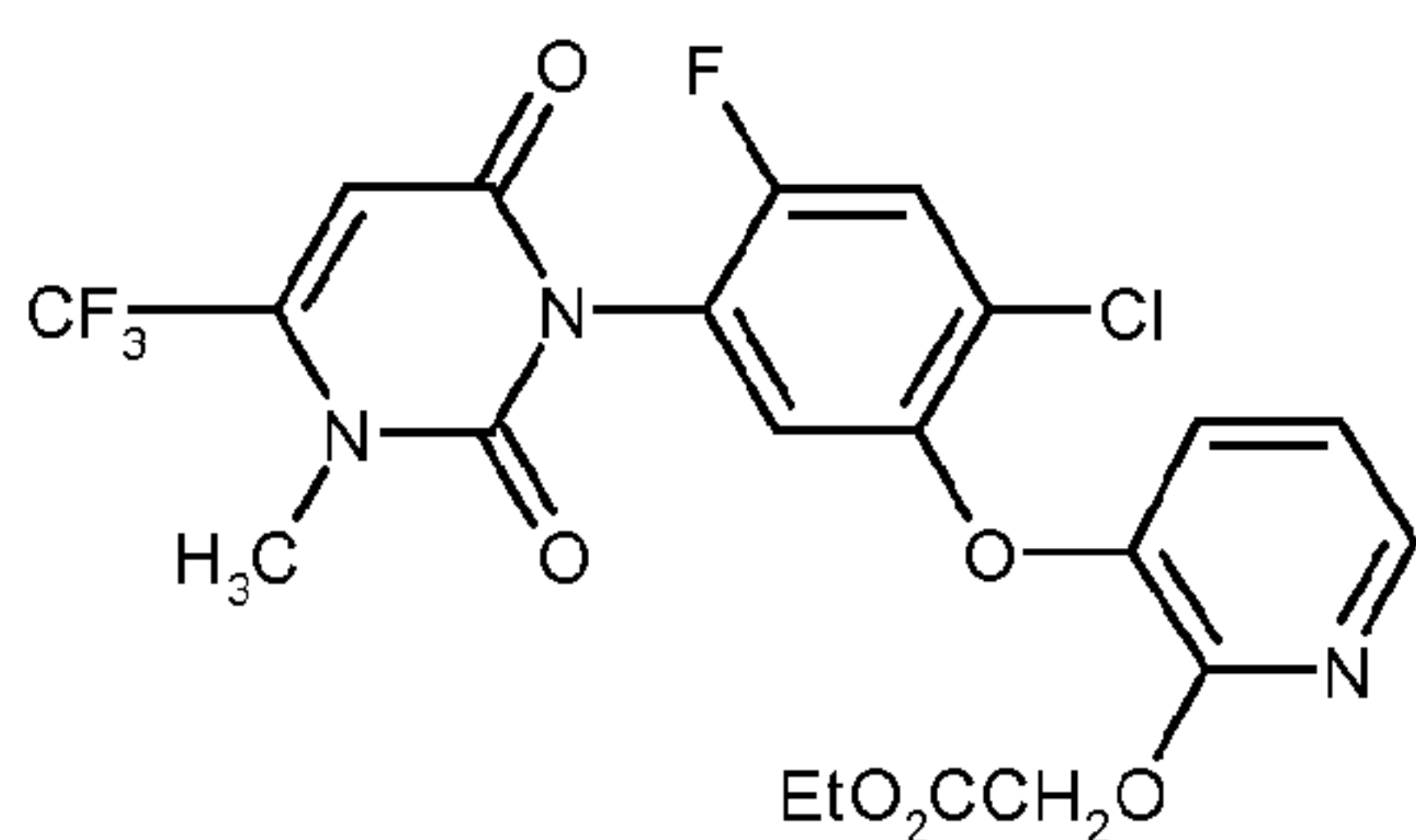
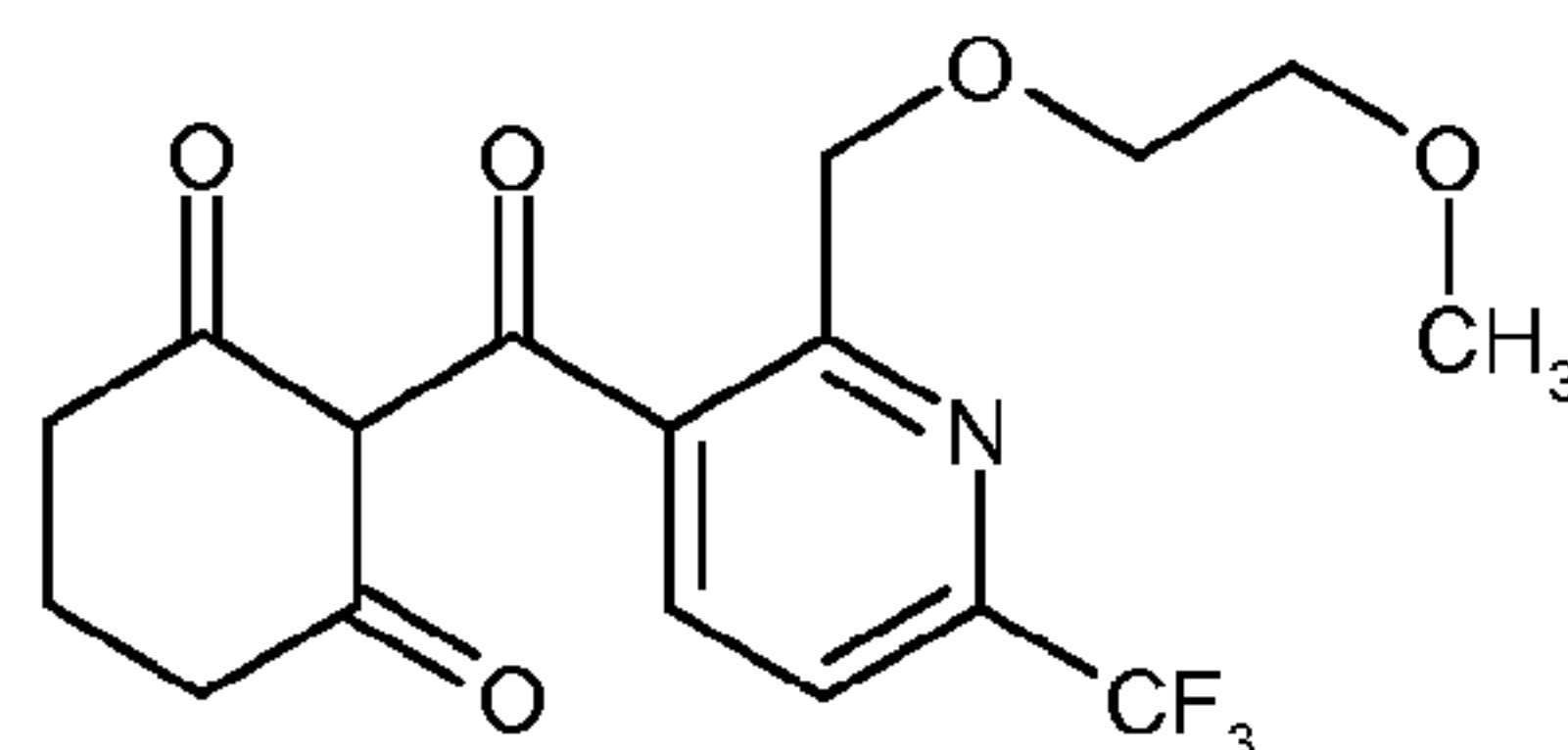
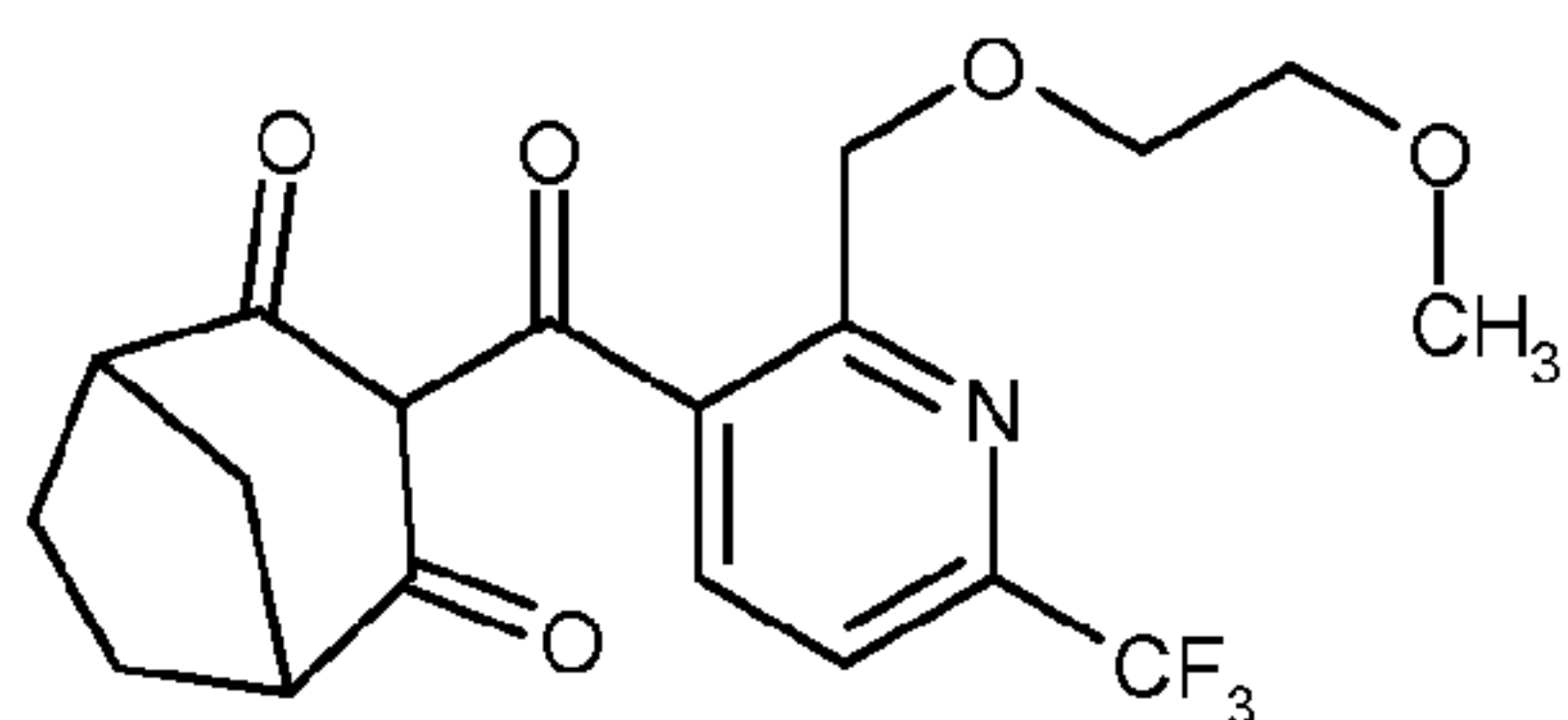
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 glufosinate-ammonium, glyphosate, glyphosate-isopropylammonium, H-9201, halosafen,
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 5 haloxyfop-P-ethoxyethyl, haloxyfop-methyl, haloxyfop-P-methyl, hexazinone, HNPC-9908,
 HOK-201, HW-02, imazamethabenz, imazamethabenz-methyl, imazamox, imazapic,
 imazapyr, imazaquin, imazethapyr, imazosulfuron, inabenfide, indanofan, indoleacetic acid
 (IAA), 4-indol-3-ylbutyric acid (IBA), iodosulfuron, iodosulfuron-methyl-sodium, ioxynil,
 isocarbamid, isopropalin, isoproturon, isouron, isoxaben, isoxachlortole, isoxaflutole,
 10 isoxapyrifop, KUH-043, KUH-071, karbutilate, ketospiradox, lactofen, lenacil, linuron,
 maleic hydrazide, MCPA, MCPB, MCPB-methyl, -ethyl and -sodium, mecoprop,
 mecoprop-sodium, mecoprop-butotyl, mecoprop-P-butotyl, mecoprop-P-
 dimethylammonium, mecoprop-P-2-ethylhexyl, mecoprop-P-potassium, mefenacet,
 mefluidide, mepiquat-chloride, mesosulfuron, mesosulfuron-methyl, methabenzthiazuron,
 15 metam, metamifop, metamitron, metazachlor, methazole, methoxyphenone,
 methyldymron, 1-methylcyclopropene, methyl isothiocyanate, metobenzuron,
 metobenzuron, metobromuron, metolachlor, S-metolachlor, metosulam, metoxuron,
 metribuzin, metsulfuron, metsulfuron-methyl, molinate, monalide, monocarbamide,
 monocarbamide dihydrogen sulfate, monolinuron, monosulfuron, monuron, MT 128, MT-
 20 5950, i.e. N-[3-chloro-4-(1-methylethyl)-phenyl]-2-methylpentanamide, NGGC-011,
 naproanilide, napropamide, naptalam, NC-310, i.e. 4-(2,4-dichlorobenzoyl)-1-methyl-5-
 benzyloxypyrazole, neburon, nicosulfuron, nipyraclufen, nitralin, nitrofen, nitrophenolat-
 sodium (isomer mixture), nitrofluorfen, nonanoic acid, norflurazon, orbencarb,
 orthosulfamuron, oryzalin, oxadiargyl, oxadiazon, oxasulfuron, oxaziclomefone,
 25 oxyfluorfen, paclobutrazole, paraquat, paraquat dichloride, pelargonic acid (nonanoic
 acid), pendimethalin, pendralin, penoxsulam, pentanochlor, pentoxazone, perfluidone,
 pethoxamid, phenisopham, phenmedipham, phenmedipham-ethyl, picloram, picolinafen,
 pinoxaden, piperophos, pirifenop, pirifenop-butyl, pretilachlor, primisulfuron, primisulfuron-
 methyl, probenazole, profluazol, procyazine, prodiamine, prifluraline, profoxydim,
 30 prohexadione, prohexadione-calcium, prohydrojasnone, prometon, prometryn, propachlor,
 propanil, propaquizafop, propazine, propham, propisochlor, propoxycarbazone,
 propoxycarbazone-sodium, propyzamide, prosulfalin, prosulfocarb, prosulfuron,
 prynachlor, pyraclonil, pyraflufen, pyraflufen-ethyl, pyrazolynate (pyrazolate),
 pyrazosulfuron-ethyl, pyrazoxyfen, pyribambenz, pyribambenz-isopropyl, pyribenzoxim,

pyributicarb, pyridafol, pyridate, pyriftalid, pyriminobac, pyriminobac-methyl, pyrimisulfan, pyrihiobac, pyrihiobac-sodium, pyroxasulfone, pyroxsulam, quinclorac, quinmerac, quinoelamine, quizalofop, quizalofop-ethyl, quizalofop-P, quizalofop-P-ethyl, quizalofop-P-tefuryl, rimsulfuron, saflufenacil, secbumeton, sethoxydim, siduron, simazine, simetryn,

5 SN-106279, sulf-allate (CDEC), sulfentrazone, sulfometuron, sulfometuron-methyl, sulfosate (glyphosate-trimesium), sulfosulfuron, SYN-523, SYP-249, SYP-298, SYP-300, tebutam, tebuthiuron, tecnazene, tepraloxym, terbacil, terbucarb, terbuchlor, terbumeton, terbuthylazine, terbutryne, TH-547, thenylchlor, thiafluamide, thiazafluron, thiazopyr,

10 thidiazimin, thidiazuron, thiencarbazon, thiencarbazon-methyl, thifensulfuron, thifensulfuron-methyl, thiobencarb, tiocarbamil, tralkoxydim, tri-allate, triasulfuron, triaziflam, triazofenamide, tribenuron, tribenuron-methyl, trichloroacetic acid (TCA), triclopyr, tridiphane, trietazine, trifloxysulfuron, trifloxysulfuron-sodium, trifluralin, triflusulfuron, triflusulfuron-methyl, trimeturon, trinexapac, trinexapac-ethyl, tritosulfuron, tsitodef, uniconazole, uniconazole-P, vernolate, ZJ-0166, ZJ-0270, ZJ-0543, ZJ-0862 and

15 the following compounds



The application rate required of an N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts to be applied to areas where HPPD tolerant plants containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a)

5 Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No.

10 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain

15 RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD

20 defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated

25 DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), especially preferable HPPD encoding genes from maize (Zea mays) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at

30 position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being

disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in

5 PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356

10 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named

15 Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser)

20 replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A

25 (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro)

30 replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position

336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37) are growing varies as a function of the external conditions such as temperature, humidity, the nature of the herbicide used and the like. It can vary within wide limits, for example between 0.001 and 1.0 kg/ha and more of active substance, but it is preferably between 0.005 and 750 g/ha.

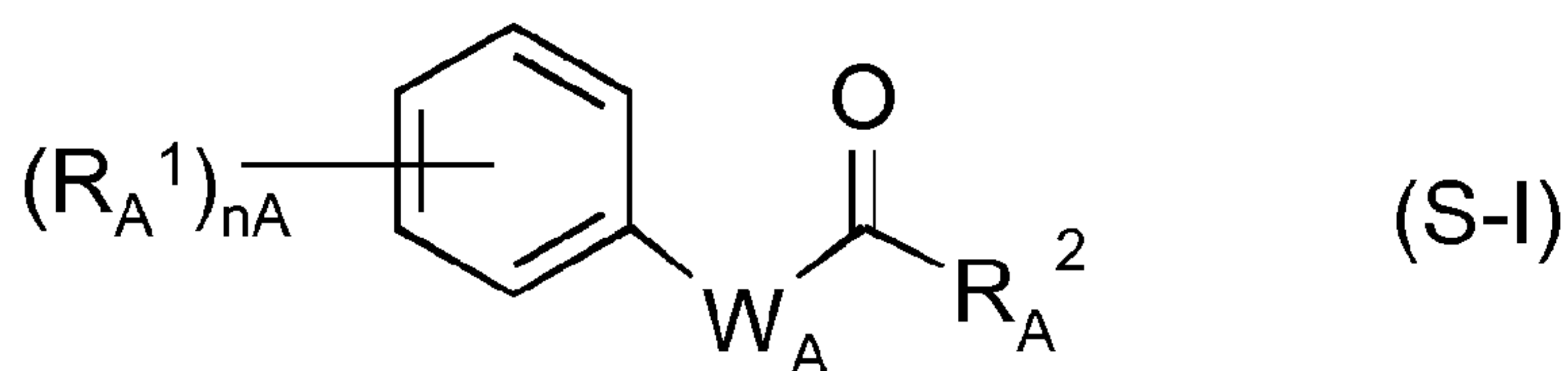
In case of combined applications of N-(tetrazol-4-yl)- or N-(triazol-3-yl)arylcarboxamides as defined above or their salts herbicides that differ from N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts to the HPPD tolerant plants containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No. 12 encoding HPPD defined by SEQ ID No. 13, (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea*

mays) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being

disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), these mixtures may cause crop injury, based on the presence herbicides different to N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts. In order to reduce/eliminate such crop injuries, appropriate safeners may be added. These safeners, which are employed in antidotically active amounts, reduce the phytotoxic side effects of herbicides/pesticides used, for example in economically important crops, such as cereals (wheat, barley, rye, corn, rice, millet), alfalfa, sugar beet, sugarcane, oilseed rape, cotton and soya spp., preferably corn, cotton, sugar beet, or soya spp.

The safeners are preferably selected from the group consisting of:

A) compounds of the formula (S-I)



where the symbols and indices have the following meanings:

n_A is a natural number from 0 to 5, preferably from 0 to 3;

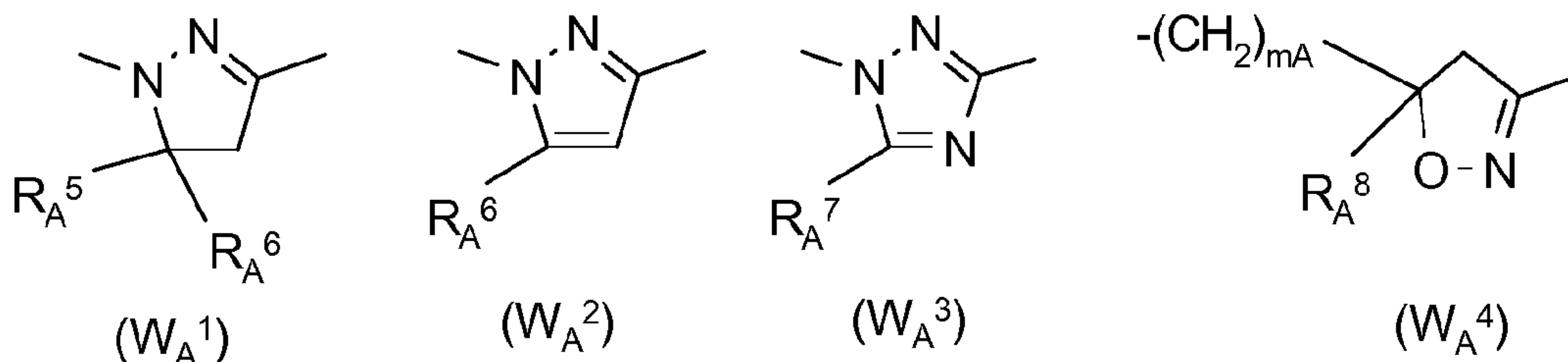
R_A^1 is halogen, (C₁-C₄)-alkyl, (C₁-C₄)-alkoxy, nitro or (C₁-C₄)-haloalkyl;

W_A is an unsubstituted or substituted divalent heterocyclic radical from the group

consisting of partially unsaturated or aromatic five-membered heterocycles having 1 to 3 hetero ring atoms of the type N or O, where at least one nitrogen atom and at

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most one oxygen atom is present in the ring, preferably a radical from the group consisting of (W_A^1) to (W_A^4) ,



m_A is 0 or 1;

5 R_A^2 is OR_A^3 , SR_A^3 or $NR_A^3R_A^4$ or a saturated

or unsaturated 3- to 7-membered heterocycle having at least one nitrogen atom and up to 3 heteroatoms, preferably from the group consisting of O and S, which is attached via the nitrogen atom to the carbonyl group in (S-I) and which is unsubstituted or substituted by radicals from the group consisting of (C_1-C_4) -alkyl, (C_1-C_4) -alkoxy and optionally substituted phenyl, preferably a radical of the formula OR_A^3 , NHR_A^4 or $N(CH_3)_2$, in particular of the formula OR_A^3 ;

R_A^3 is hydrogen or an unsubstituted or substituted aliphatic hydrocarbon radical having preferably a total of 1 to 18 carbon atoms;

R_A^4 is hydrogen, (C_1-C_6) -alkyl, (C_1-C_6) -alkoxy or substituted or unsubstituted phenyl;

15 R_A^5 is H, (C_1-C_8) -alkyl, (C_1-C_8) -haloalkyl, (C_1-C_4) -alkoxy- (C_1-C_8) -alkyl, cyano or $COOR_A^9$ where R_A^9 is hydrogen, (C_1-C_8) -alkyl, (C_1-C_8) -haloalkyl, (C_1-C_4) -alkoxy- (C_1-C_4) -alkyl, (C_1-C_6) -hydroxyalkyl, (C_3-C_{12}) -cycloalkyl or tri- (C_1-C_4) -alkylsilyl;

R_A^6 , R_A^7 , R_A^8 are identical or different and are hydrogen, (C_1-C_8) -alkyl, (C_1-C_8) -haloalkyl, (C_3-C_{12}) -cycloalkyl or substituted or unsubstituted phenyl;

20

preferably:

a) compounds of the type of the dichlorophenylpyrazoline-3-carboxylic acid, preferably compounds such as ethyl 1-(2,4-dichlorophenyl)-5-(ethoxycarbonyl)-5-methyl-2-pyrazoline-3-carboxylate (S1-1) ("mefenpyr-diethyl", see Pestic. Man.), and related compounds, as

25 described in WO 91/07874;

b) derivatives of dichlorophenylpyrazolecarboxylic acid, preferably compounds such as ethyl 1-(2,4-dichlorophenyl)-5-methylpyrazole-3-carboxylate (S1-2), ethyl 1-(2,4-dichlorophenyl)-5-isopropylpyrazole-3-carboxylate (S1-3), ethyl 1-(2,4-dichlorophenyl)-5-(1,1-dimethylethyl)pyrazole-3-carboxylate (S1-4), ethyl

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1-(2,4-dichlorophenyl)-5-phenylpyrazole-3-carboxylate (S1-5) and related compounds, as described in EP-A-333 131 and EP-A-269 806;

c) compounds of the type of the triazolecarboxylic acids, preferably compounds such as fenchlorazole(-ethyl ester), i.e. ethyl 1-(2,4-dichlorophenyl)-5-trichloro-

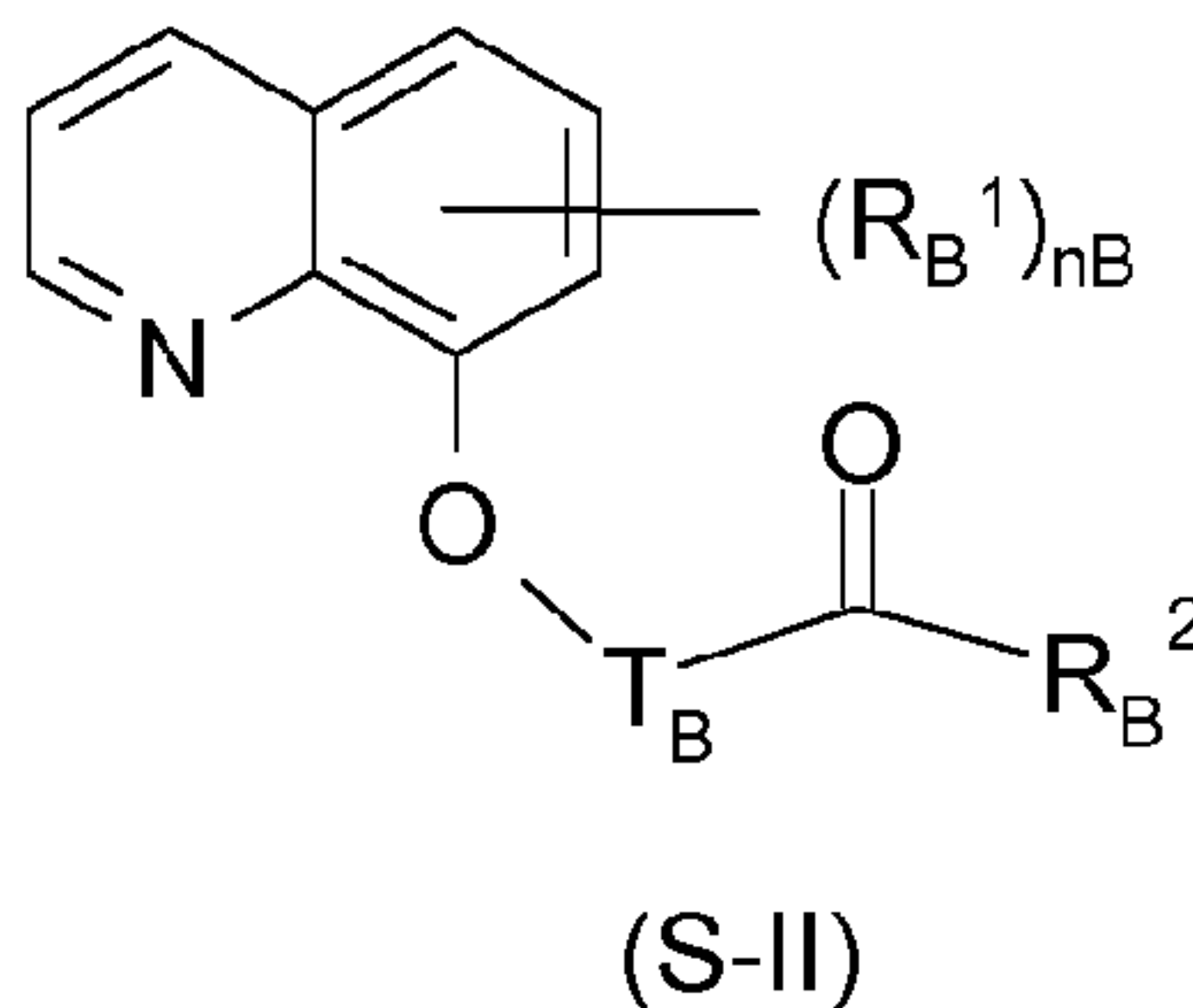
5 methyl-(1H)-1,2,4-triazole-3-carboxylate (S1-6), and related compounds, as described in EP-A-174 562 and EP-A-346 620;

d) compounds of the type of the 5-benzyl- or 5-phenyl-2-isoxazoline-3-carboxylic acid or the 5,5-diphenyl-2-isoxazoline-3-carboxylic acid, preferably compounds such as ethyl 5-(2,4-dichlorobenzyl)-2-isoxazoline-3-carboxylate (S1-7) or ethyl

10 5-phenyl-2-isoxazoline-3-carboxylate (S1-8) and related compounds, as described in WO 91/08202, or ethyl 5,5-diphenyl-2-isoxazolinecarboxylate (S1-9) ("isoxadifen-ethyl") or n-propyl 5,5-diphenyl-2-isoxazolinecarboxylate (S1-10) or ethyl 5-(4-fluorophenyl)-5-phenyl-2-isoxazoline-3-carboxylate (S1-11), as described in the patent application WO-A-95/07897.

15

B) Quinoline derivatives of the formula (S-II)



where the symbols and indices have the following meanings:

R_B^1 is halogen, (C₁-C₄)-alkyl, (C₁-C₄)-alkoxy, nitro or (C₁-C₄)-haloalkyl;

20 n_B is a natural number from 0 to 5, preferably from 0 to 3;

R_B^2 OR_B^3 , SR_B^3 or $NR_B^3R_B^4$ or a saturated

or unsaturated 3- to 7-membered heterocycle having at least one nitrogen atom and up to 3 heteroatoms, preferably from the group consisting of O and S, which is attached via the nitrogen atom to the carbonyl group in (S-II) and is unsubstituted or substituted by radicals

25 from the group consisting of (C₁-C₄)-alkyl, (C₁-C₄)-alkoxy or optionally substituted phenyl, preferably a radical of the formula OR_B^3 , NHR_B^4 or $N(CH_3)_2$, in particular of the formula OR_B^3 ;

R_B^3 is hydrogen or an unsubstituted or substituted aliphatic hydrocarbon radical having preferably a total of 1 to 18 carbon atoms;

R_B^4 is hydrogen, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy or substituted or unsubstituted phenyl;

T_B is a (C₁- or C₂)-alkanediyl chain which is unsubstituted or substituted by one or two (C₁-C₄)-alkyl radicals or by [(C₁-C₃)-alkoxy]carbonyl;

5 preferably:

a) compounds of the type of the 8-quinolinoxyacetic acid (S2), preferably 1-methylhexyl (5-chloro-8-quinolinoxy)acetate (common name "cloquintocet-mexyl" (S2-1) (see Pestic. Man.),

1,3-dimethylbut-1-yl (5-chloro-8-quinolinoxy)acetate (S2-2),

10 4-allyloxybutyl (5-chloro-8-quinolinoxy)acetate (S2-3),

1-allyloxyprop-2-yl (5-chloro-8-quinolinoxy)acetate- (S2-4),

ethyl (5-chloro-8-quinolinoxy)acetate (S2-5),

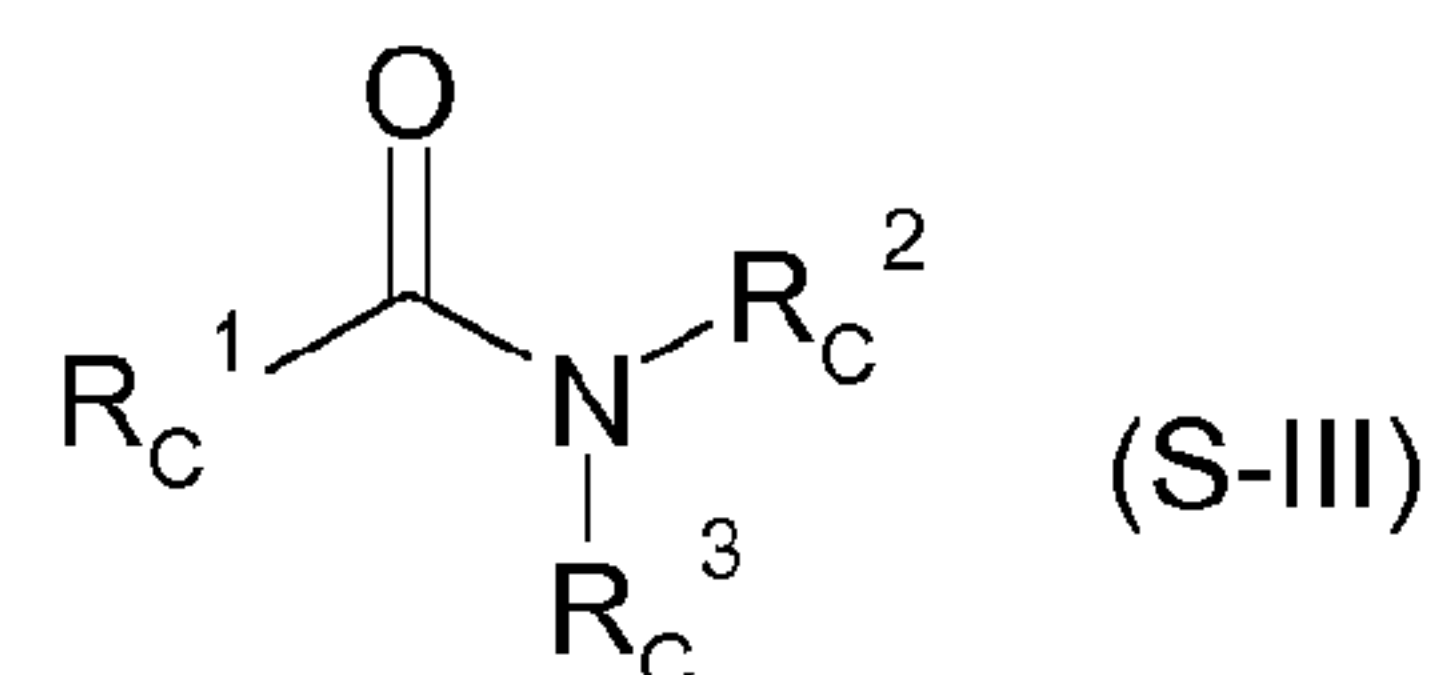
methyl (5-chloro-8-quinolinoxy)acetate (S2-6),

allyl (5-chloro-8-quinolinoxy)acetate (S2-7),

15 2-(2-propylideneiminoxy)-1-ethyl (5-chloro-8-quinolinoxy)acetate (S2-8), 2-oxoprop-1-yl (5-chloro-8-quinolinoxy)acetate (S2-9) and related compounds, as described in EP-A-86 750, EP-A-94 349 and EP-A-191 736 or EP-A-0 492 366, and also their hydrates and salts, as described in WO-A-2002/034048.

20 b) Compounds of the type of the (5-chloro-8-quinolinoxy)malonic acid, preferably compounds such as diethyl (5-chloro-8-quinolinoxy)malonate, diallyl (5-chloro-8-quinolinoxy)malonate, methyl ethyl (5-chloro-8-quinolinoxy)malonate and related compounds, as described in EP-A-0 582 198.

25 C) Compounds of the formula (S-III)



where the symbols and indices have the following meanings:

R_C^1 is (C₁-C₄)-alkyl, (C₁-C₄)-haloalkyl, (C₂-C₄)-alkenyl, (C₂-C₄)-haloalkenyl, (C₃-C₇)-cycloalkyl, preferably dichloromethyl;

30 R_C^2 , R_C^3 are identical or different and are hydrogen, (C₁-C₄)-alkyl, (C₂-C₄)-alkenyl,

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(C₂-C₄)-alkynyl, (C₁-C₄)-haloalkyl, (C₂-C₄)-haloalkenyl, (C₁-C₄)-alkylcarbamoyl-(C₁-C₄)-alkyl, (C₂-C₄)-alkenylcarbamoyl-(C₁-C₄)-alkyl, (C₁-C₄)-alkoxy-(C₁-C₄)-alkyl, dioxolanyl-(C₁-C₄)-alkyl, thiazolyl, furyl, furylalkyl, thienyl, piperidyl, substituted or unsubstituted phenyl, or R_C² and R_C³ together form a substituted or unsubstituted heterocyclic ring,

5 preferably an oxazolidine, thiazolidine, piperidine, morpholine, hexahydropyrimidine or benzoxazine ring;

preferably:

Active compounds of the type of the dichloroacetamides which are frequently used as pre-emergence safener (soil-acting safeners), such as, for example,

"dichlormid" (see Pestic.Man.) (= N,N-diallyl-2,2-dichloroacetamide),

"R-29148" (= 3-dichloroacetyl-2,2,5-trimethyl-1,3-oxazolidine from Stauffer),

"R-28725" (= 3-dichloroacetyl-2,2,-dimethyl-1,3-oxazolidine from Stauffer),

"benoxacor" (see Pestic. Man.) (= 4-dichloroacetyl-3,4-dihydro-3-methyl-2H-1,4-

15 benzoxazine),

"PPG-1292" (= N-allyl-N-[(1,3-dioxolan-2-yl)methyl]dichloroacetamide from PPG Industries),

"DKA-24" (= N-allyl-N-[(allylaminocarbonyl)methyl]dichloroacetamide from Sagro-Chem),

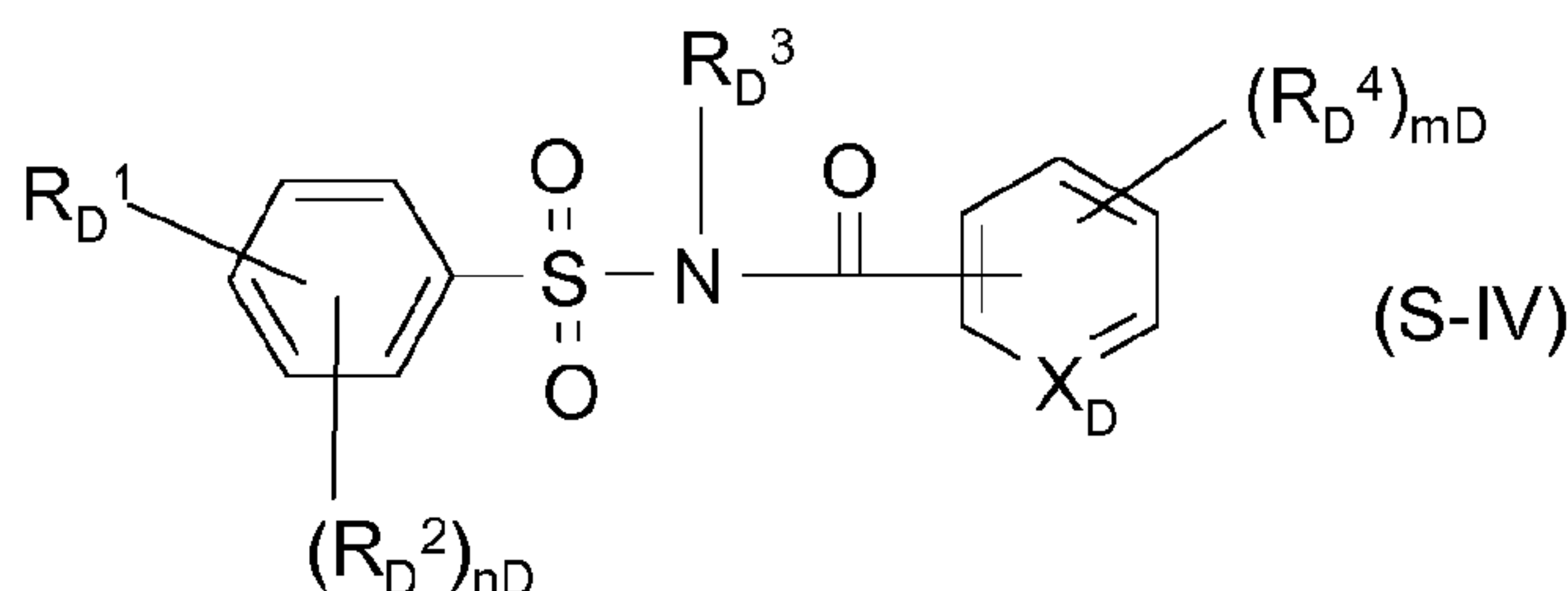
"AD-67" or "MON 4660" (= 3-dichloroacetyl-1-oxa-3-aza-spiro[4,5]decane from Nitrokemia or Monsanto),

"TI-35" (= 1-dichloroacetylazepane from TRI-Chemical RT)

"diclonon" (dicyclonone) or "BAS145138" or "LAB145138" (= 3-dichloroacetyl-2,5,5-trimethyl-1,3-diazabicyclo[4.3.0]nonane from BASF) and

"furilazole" or "MON 13900" (see Pestic. Man.) (= (RS)-3-dichloroacetyl-5-(2-furyl)-2,2-dimethyloxazolidine).

D) N-Acylsulfonamides of the formula (S-IV) and their salts



in which

X_D is CH or N;

R_D^1 is $CO-NR_D^5R_D^6$ or $NHCO-R_D^7$;

R_D^2 is halogen, (C_1-C_4) -haloalkyl, (C_1-C_4) -haloalkoxy, nitro, (C_1-C_4) -alkyl, (C_1-C_4) -alkoxy, (C_1-C_4) -alkylsulfonyl, (C_1-C_4) -alkoxycarbonyl or (C_1-C_4) -alkylcarbonyl;

R_D^3 is hydrogen, (C_1-C_4) -alkyl, (C_2-C_4) -alkenyl or (C_2-C_4) -alkynyl;

5 R_D^4 is halogen, nitro, (C_1-C_4) -alkyl, (C_1-C_4) -haloalkyl, (C_1-C_4) -haloalkoxy, (C_3-C_6) -cycloalkyl, phenyl, (C_1-C_4) -alkoxy, cyano, (C_1-C_4) -alkylthio, (C_1-C_4) -alkylsulfinyl, (C_1-C_4) -alkylsulfonyl, (C_1-C_4) -alkoxycarbonyl or (C_1-C_4) -alkylcarbonyl;

R_D^5 is hydrogen, (C_1-C_6) -alkyl, (C_3-C_6) -cycloalkyl, (C_2-C_6) -alkenyl, (C_2-C_6) -alkynyl, (C_5-C_6) -cycloalkenyl, phenyl or 3- to 6-membered heterocyclyl containing v_D heteroatoms from
10 the group consisting of nitrogen, oxygen and sulfur, where the seven last-mentioned radicals are substituted by v_D substituents from the group consisting of halogen, (C_1-C_6) -alkoxy, (C_1-C_6) -haloalkoxy, (C_1-C_2) -alkylsulfinyl, (C_1-C_2) -alkylsulfonyl, (C_3-C_6) -cycloalkyl, (C_1-C_4) -alkoxycarbonyl, (C_1-C_4) -alkylcarbonyl and phenyl and, in the case of cyclic radicals, also (C_1-C_4) -alkyl and (C_1-C_4) -haloalkyl;

15 R_D^6 is hydrogen, (C_1-C_6) -alkyl, (C_2-C_6) -alkenyl or (C_2-C_6) -alkynyl, where the three last-mentioned radicals are substituted by v_D radicals from the group consisting of halogen, hydroxy, (C_1-C_4) -alkyl, (C_1-C_4) -alkoxy and (C_1-C_4) -alkylthio, or

20 R_D^5 and R_D^6 together with the nitrogen atom carrying them form a pyrrolidinyl or piperidinyl radical;

R_D^7 is hydrogen, (C_1-C_4) -alkylamino, di- (C_1-C_4) -alkylamino, (C_1-C_6) -alkyl, (C_3-C_6) -cycloalkyl, where the 2 last-mentioned radicals are substituted by v_D substituents from the
25 group consisting of halogen, (C_1-C_4) -alkoxy, halogen- (C_1-C_6) -alkoxy and (C_1-C_4) -alkylthio and, in the case of cyclic radicals, also (C_1-C_4) -alkyl and (C_1-C_4) -haloalkyl;

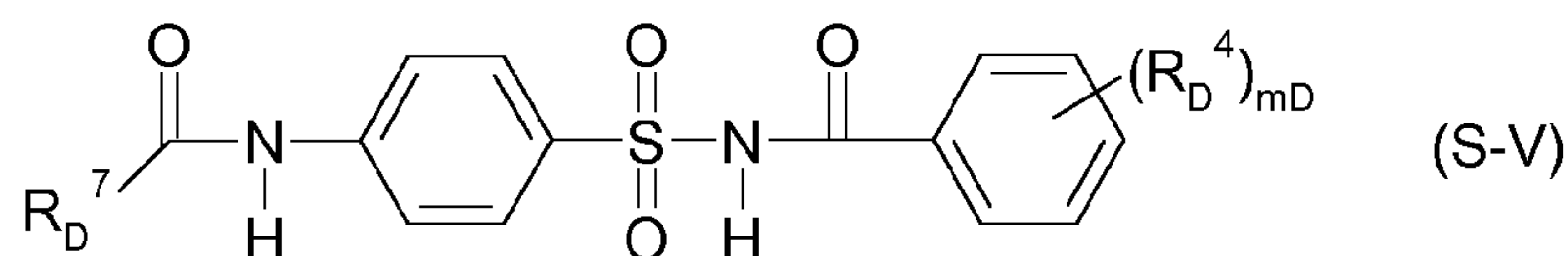
n_D is 0, 1 or 2;

m_D is 1 or 2;

30 v_D is 0, 1, 2 or 3;

from among these, preference is given to compounds of the type of the N-acylsulfonamides, for example of the formula (S-V) below, which are known, for example, from WO 97/45016

225



in which

R_D^7 is (C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl, where the 2 last-mentioned radicals are substituted by v_D substituents from the group consisting of halogen, (C₁-C₄)-alkoxy, halogen-(C₁-C₆)-alkoxy and (C₁-C₄)-alkylthio and, in the case of cyclic radicals, also (C₁-C₄)-alkyl and (C₁-C₄)-haloalkyl;

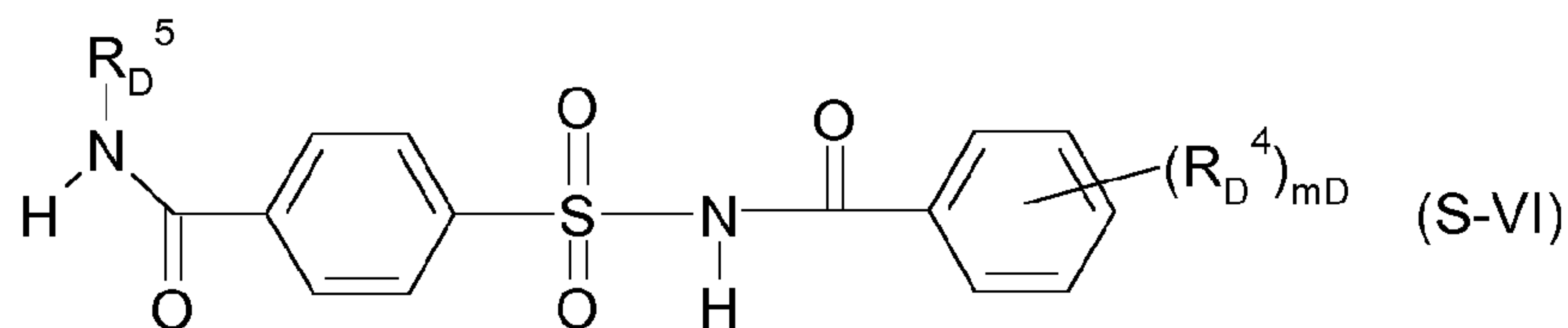
R_D^4 is halogen, (C₁-C₄)-alkyl, (C₁-C₄)-alkoxy, CF₃;

m_D is 1 or 2;

v_D is 0, 1, 2 or 3;

and also

acylsulfamoylbenzamides, for example of the formula (S-VI) below, which are known, for example, from WO 99/16744,



for example those in which

R_D^5 = cyclopropyl and (R_D^4) = 2-OMe ("cyprosulfamide", S3-1),

R_D^5 = cyclopropyl and (R_D^4) = 5-Cl-2-OMe (S3-2),

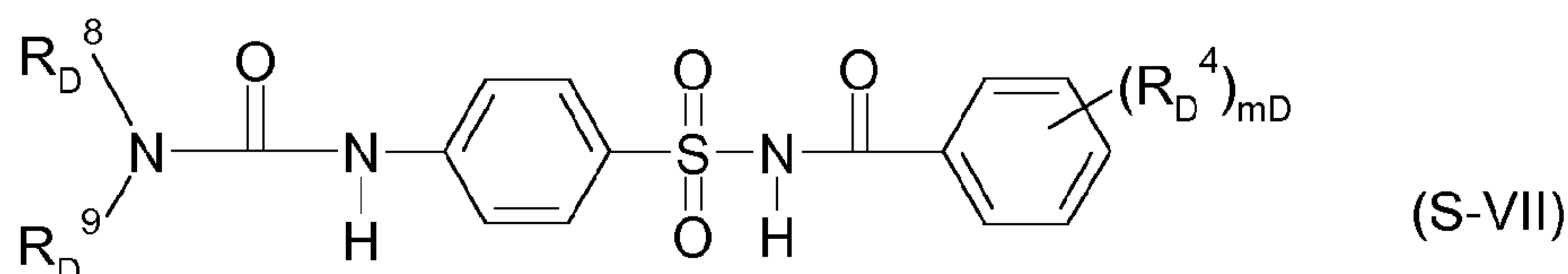
R_D^5 = ethyl and (R_D^4) = 2-OMe (S3-3),

R_D^5 = isopropyl and (R_D^4) = 5-Cl-2-OMe (S3-4) and

R_D^5 = isopropyl and (R_D^4) = 2-OMe (S3-5);

and also

compounds of the type of the N-acylsulfamoylphenylureas of the formula (S-VII), which are known, for example, from EP-A-365484



in which

R_D^8 and R_D^9 independently of one another are hydrogen, (C₁-C₈)-alkyl, (C₃-C₈)-cycloalkyl, (C₃-C₆)-alkenyl, (C₃-C₆)-alkynyl,

R_D^4 is halogen, (C₁-C₄)-alkyl, (C₁-C₄)-alkoxy, CF₃

m_D is 1 or 2;

5

from among these in particular

1-[4-(N-2-methoxybenzoylsulfamoyl)phenyl]-3-methylurea,

1-[4-(N-2-methoxybenzoylsulfamoyl)phenyl]-3,3-dimethylurea,

1-[4-(N-4,5-dimethylbenzoylsulfamoyl)phenyl]-3-methylurea,

10 1-[4-(N-naphthoylsulfamoyl)phenyl]-3,3-dimethylurea,

G) active compounds from the class of the hydroxyaromatics and aromatic-aliphatic carboxylic acid derivatives, for example

ethyl 3,4,5-triacetoxybenzoate, 3,5-dimethoxy-4-hydroxybenzoic acid, 3,5-

15 dihydroxybenzoic acid, 4-hydroxysalicylic acid, 4-fluorosalicylic acid, 1,2-dihydro-2-oxo-6-trifluoromethylpyridine-3-carboxamide, 2-hydroxycinnamic acid, 2,4-dichlorocinnamic acid, as described in WO 2004084631, WO 2005015994, WO 2006007981, WO 2005016001;

H) active compounds from the class of the 1,2-dihydroquinoxalin-2-ones, for example

20 1-methyl-3-(2-thienyl)-1,2-dihydroquinoxalin-2-one, 1-methyl-3-(2-thienyl)-1,2-dihydroquinoxaline-2-thione, 1-(2-aminoethyl)-3-(2-thienyl)-1,2-dihydroquinoxalin-2-one hydrochloride, 1-(2-methylsulfonylaminoethyl)-3-(2-thienyl)-1,2-dihydro-quinoxalin-2-one, as described in WO 2005112630,

25 I) active compounds which, in addition to a herbicidal action against harmful plants, also have safener action on crop plants such as rice, such as, for example, "dimepiperate" or "MY-93" (see Pestic. Man.) (=S-1-methyl-1-phenylethyl piperidine-1-thiocarboxylate), which is known as safener for rice against damage by the herbicide molinate,

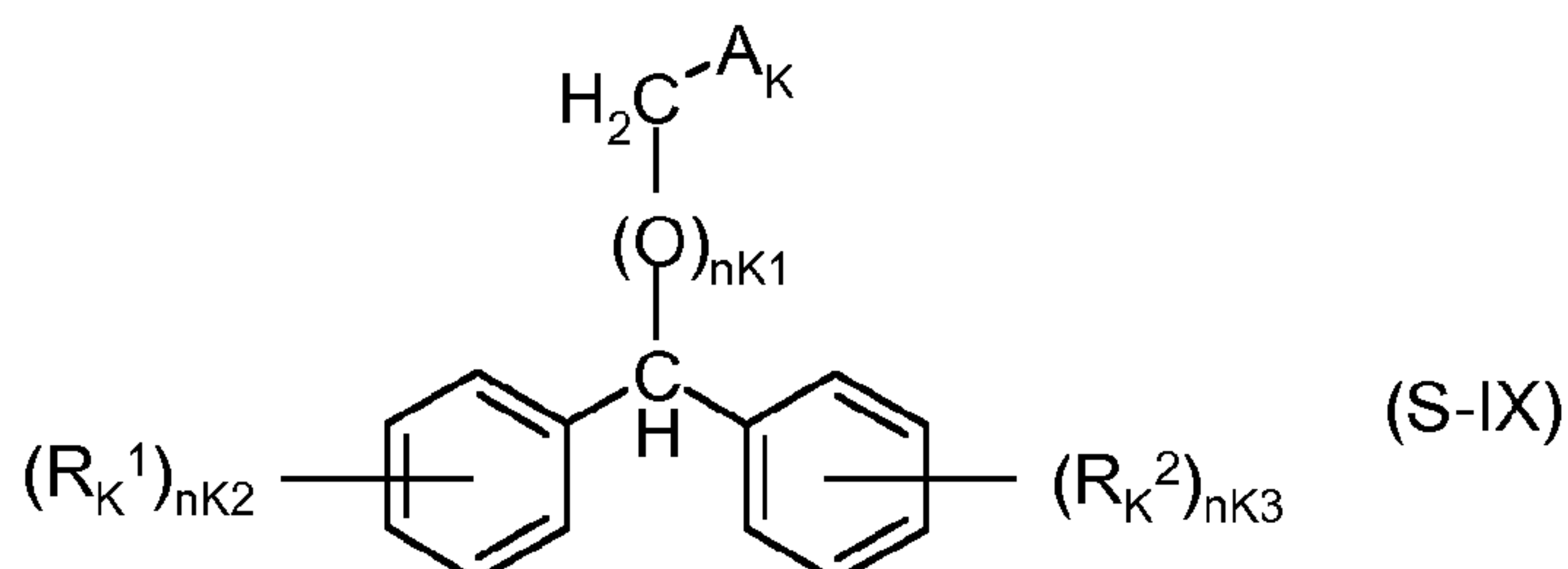
30 "daimuron" or "SK 23" (see Pestic. Man.) (= 1-(1-methyl-1-phenylethyl)-3-p-tolylurea), which is known as safener for rice against damage by the herbicide imazosulfuron, "cumyluron" = "JC-940" (= 3-(2-chlorophenylmethyl)-1-(1-methyl-1-phenyl-ethyl)urea, see JP-A-60087254), which is known as safener for rice against damage by a number of herbicides,

227

"methoxyphenone" or "NK 049" (= 3,3'-dimethyl-4-methoxybenzophenone), which is known as safener for rice against damage by a number of herbicides,
 "CSB" (= 1-bromo-4-(chloromethylsulfonyl)benzene) (CAS Reg. No. 54091-06-4 from Kumiai), which is known as safener against damage by a number of herbicides in rice,

5

K) compounds of the formula (S-IX),
 as described in WO-A-1998/38856



in which the symbols and indices have the following meanings:

10 R_K^1, R_K^2 independently of one another are halogen, (C₁-C₄)-alkyl, (C₁-C₄)-alkoxy, (C₁-C₄)-haloalkyl, (C₁-C₄)-alkylamino, di-(C₁-C₄)-alkylamino, nitro;

A_K is COOR_K³ or COOR_K⁴

R_K^3, R_K^4 independently of one another are hydrogen, (C₁-C₄)-alkyl, (C₂-C₆)-alkenyl, (C₂-C₄)-alkynyl, cyanoalkyl, (C₁-C₄)-haloalkyl, phenyl, nitrophenyl, benzyl, halobenzyl,

15 pyridinylalkyl or alkylammonium,

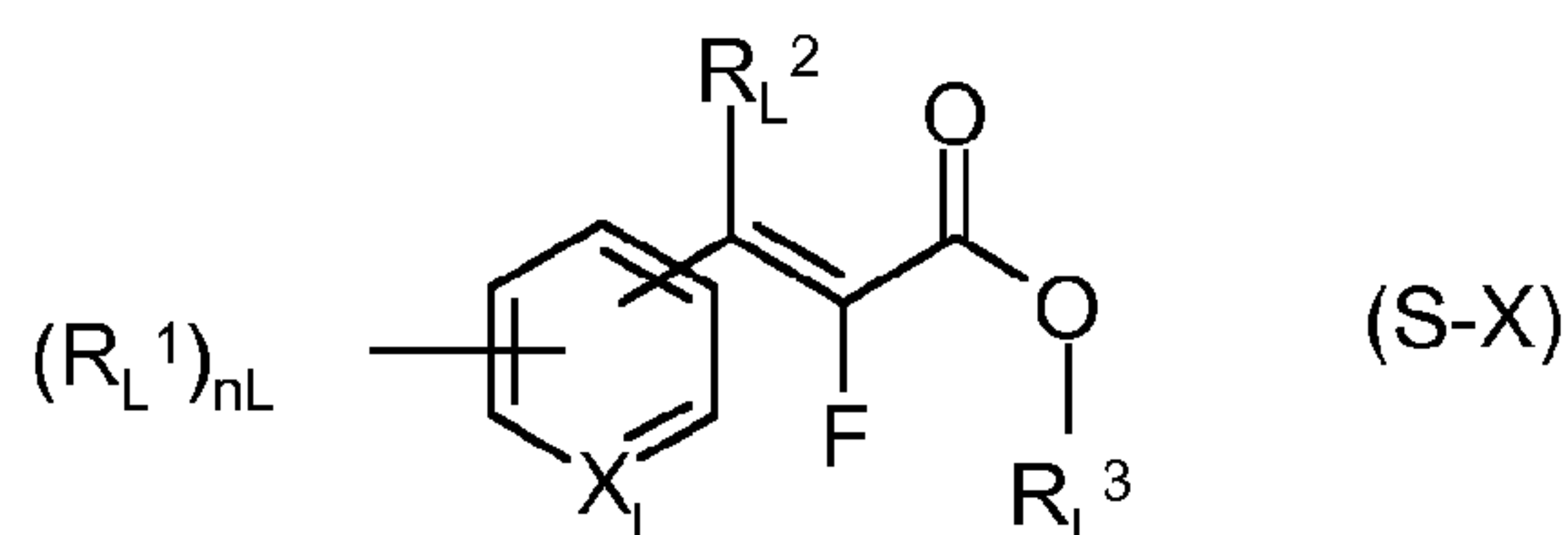
n_K^1 is 0 or 1,

n_K^2, n_K^3 independently of one another are 0, 1 or 2

preferably: methyl (diphenylmethoxy)acetate (CAS Reg. No.: 41858-19-9),

20

L) compounds of the formula (S-X),
 as described in WO A-98/27049



in which the symbols and indices have the following meanings:

25 X_L is CH or N,

n_L is, in the case that X=N, an integer from 0 to 4 and,

in the case that $X=CH$, an integer from 0 to 5,

R_L^1 is halogen, (C_1-C_4) -alkyl, (C_1-C_4) -haloalkyl, (C_1-C_4) -alkoxy, (C_1-C_4) -haloalkoxy, nitro, (C_1-C_4) -alkylthio, (C_1-C_4) -alkylsulfonyl, (C_1-C_4) -alkoxycarbonyl, optionally substituted phenyl, optionally substituted phenoxy,

5 R_L^2 is hydrogen or (C_1-C_4) -alkyl,

R_L^3 is hydrogen, (C_1-C_8) -alkyl, (C_2-C_4) -alkenyl, (C_2-C_4) -alkynyl or aryl, where each of the carbon-containing radicals mentioned above is unsubstituted or substituted by one or more, preferably by up to three, identical or different radicals from the group consisting of halogen and alkoxy; or salts thereof,

10

M) active compounds from the class of the 3-(5-tetrazolylcarbonyl)-2-quinolones, for example

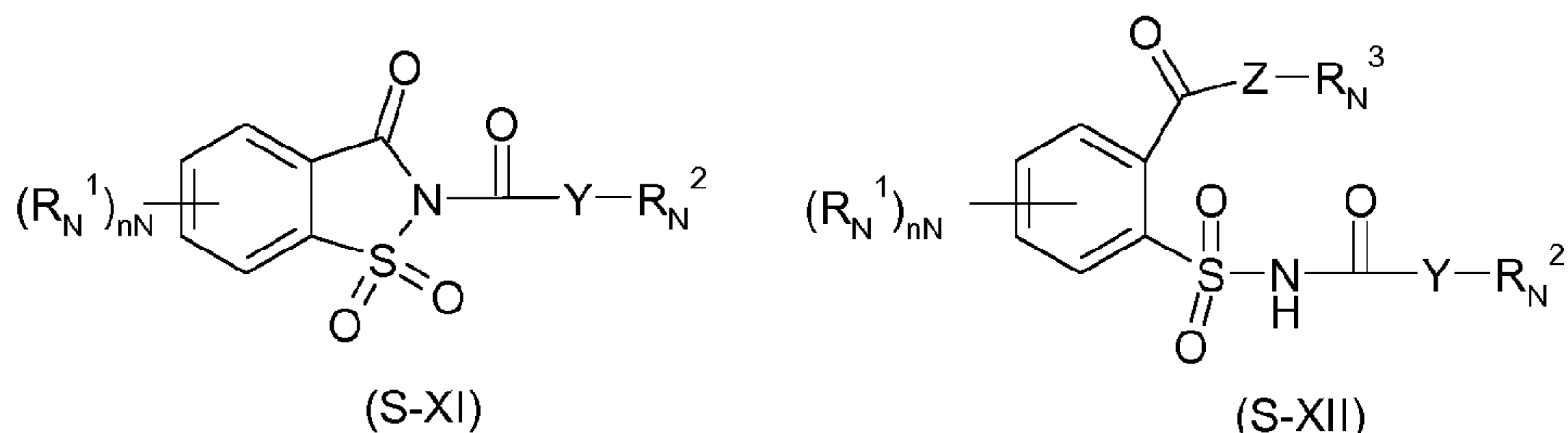
1,2-dihydro-4-hydroxy-1-ethyl-3-(5-tetrazolylcarbonyl)-2-quinolone (CAS Reg. No.:

219479-18-2), 1,2-dihydro-4-hydroxy-1-methyl-3-(5-tetrazolylcarbonyl)-2-quinolone (CAS

15 Reg. No.: 95855-00-8), as described in WO-A-1999000020,

N) compounds of the formula (S-XI) or (S-XII),

as described in WO-A-2007023719 and WO-A-2007023764



20 in which

R_N^1 is halogen, (C_1-C_4) -alkyl, methoxy, nitro, cyano, CF_3 , OCF_3

Y, Z independently of one another are O or S,

n_N is an integer from 0 to 4,

R_N^2 is (C_1-C_{16}) -alkyl, (C_2-C_6) -alkenyl, (C_3-C_6) -cycloalkyl, aryl, benzyl, halobenzyl,

25 R_N^3 is hydrogen, (C_1-C_6) alkyl,

O) one or more compounds from the group consisting of:

1,8-naphthalic anhydride,

O,O-diethyl S-2-ethylthioethyl phosphorodithioate (disulfoton),

4-chlorophenyl methylcarbamate (mephenate),
 O,O-diethyl O-phenyl phosphorothioate (dietholate),
 4-carboxy-3,4-dihydro-2H-1-benzopyran-4-acetic acid (CL-304415, CAS Reg. No.: 31541-57-8),

5 2-propenyl 1-oxa-4-azaspiro[4.5]decane-4-carbodithioate (MG-838, CAS Reg. No.: 133993-74-5),

methyl [(3-oxo-1H-2-benzothiopyran-4(3H)-ylidene)methoxy]acetate (from WO-A-98/13361; CAS Reg. No.: 205121-04-6),

cyanomethoxyimino(phenyl)acetonitrile (cyometrinil),

10 1,3-dioxolan-2-ylmethoxyimino(phenyl)acetonitrile (oxabetrinil),

4'-chloro-2,2,2-trifluoroacetophenone O-1,3-dioxolan-2-ylmethyloxime (fluxofenim),

4,6-dichloro-2-phenylpyrimidine (fencloirim),

benzyl 2-chloro-4-trifluoromethyl-1,3-thiazole-5-carboxylate (flurazole),

2-dichloromethyl-2-methyl-1,3-dioxolane (MG-191),

15

including the stereoisomers, and the salts customary in agriculture.

A mixture of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above or their salts to be applied in connection with other known active compounds, such as fungicides,

20 insecticides, acaricides, nematocides, bird repellents, plant nutrients and soil structure improvers to transgenic plants containing one or more chimeric gene(s) (I) comprising a

DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined

25 by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably

30 comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined

by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No

33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named
5 Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being
10 disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being
15 disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln)
20 replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), is likewise possible.

Some of the safeners are already known as herbicides and accordingly, in addition to the
25 herbicidal action against harmful plants, also act by protecting the crop plants.

The weight ratios of herbicide (mixture) to safener generally depend on the herbicide application rate and the effectiveness of the safener in question and may vary within wide limits, for example in the range from 200:1 to 1:200, preferably from 100:1 to 1:100, in particular from 20:1 to 1:20. The safeners may be formulated analogously to the
30 compounds of the formula (I) or their mixtures with other herbicides/pesticides and be provided and used as a finished formulation or as a tank mix with the herbicides.

The required application rate of the N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides as defined above to areas where such transgenic plants containing one or more chimeric gene(s) (I)

comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) (I) derived from a member of a group of organisms, consisting of (a) *Avena*, preferably *Avena sativa*, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) *Pseudomonas*, preferably *Pseudomonas fluorescens*,
5 more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) *Synechococcoideae*, preferably *Synechococcus* sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) *Blepharismidae*, preferably *Blepharisma japonicum*, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID
10 No. 9, (e) *Rhodococcus*, preferably *Rhodococcus* sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or *Rhodococcus* sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) *Picrophilaceae*, preferably *Picrophilus torridus*, more preferably
15 comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) *Kordia*, preferably *Kordia algicida*, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968,
20 WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (*Zea mays*) or soybean (*Glycine max*), especially preferable HPPD encoding genes from maize (*Zea mays*) or (III) comprising a mutated DNA sequence described in
25 PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at
30 position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and

an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas* (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas agarici* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598, and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 and being disclosed in present application as the HPPD

protein sequence under SEQ ID No 37) varies depending, inter alia, on external conditions such as temperature, humidity and the type of herbicide used. It can vary within wide limits, for example between 0.001 and 10 000 g/ha or more of active substance; however, it is preferably between 0.5 and 5000 g/ha, particularly preferably between 0.5 and 1000 g/ha and very particularly preferably between 0.5 and 500 g/ha.

SEQUENCES LISTING

- | | | |
|----|----------------|---|
| 10 | SEQ ID No. 1: | Nucleic acid sequence encoding <i>Avena sativa</i> HPPD optimized for the expression in <i>E. coli</i> cells |
| | SEQ ID No. 2: | Protein encoded by SEQ ID No. 1 |
| | SEQ ID No. 3: | Nucleic acid sequence encoding <i>Pseudomonas fluorescens</i> HPPD mutated at position 336; mutation Gly => Trp (Pfw336) |
| | SEQ ID No. 4: | Protein encoded by SEQ ID No. 3 (PfHPPD336W) |
| 15 | SEQ ID No. 5: | Nucleic acid sequence encoding <i>Pseudomonas fluorescens</i> HPPD mutated at position 336; mutation Gly => Trp; optimized for the expression in soybean and cotton |
| | SEQ ID No. 6: | Nucleic acid sequence encoding <i>Synechococcus</i> sp. HPPD |
| | SEQ ID No. 7: | Protein encoded by SEQ ID No. 6 |
| 20 | SEQ ID No. 8: | Nucleic acid sequence encoding <i>Blepharisma japonicum</i> HPPD (FMP37) |
| | SEQ ID No. 9: | Protein encoded by SEQ ID No. 8 |
| | SEQ ID No. 10: | Nucleic acid sequence encoding <i>Rhodococcus</i> sp. (strain RHA1), isolate ro03041 HPPD (FMP22) |
| 25 | SEQ ID No. 11: | Protein encoded by SEQ ID No. 10 |
| | SEQ ID No. 12: | Nucleic acid sequence encoding <i>Rhodococcus</i> sp. (strain RHA1), isolate ro02040 HPPD |
| | SEQ ID No. 13: | Protein encoded by SEQ ID No. 12 |
| | SEQ ID No. 14: | Nucleic acid sequence encoding <i>Picrophilus torridus</i> HPPD |
| 30 | SEQ ID No. 15: | Protein encoded by SEQ ID No. 14 |
| | SEQ ID No. 16: | Nucleic acid sequence encoding <i>Kordia algicida</i> HPPD (FMP27) |
| | SEQ ID No. 17: | Protein encoded by SEQ ID No. 16 |
| | SEQ ID No. 18: | Nucleic acid sequence encoding <i>Synechococcus</i> sp. HPPD optimized for the expression in soybean and cotton |

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- SEQ ID No. 19: Nucleic acid sequence encoding *Blepharisma japonicum* HPPD optimized for the expression in soybean and cotton
- SEQ ID No. 20: Nucleic acid sequence encoding *Rhodococcus* sp. (strain RHA1), isolate ro0341 HPPD optimized for the expression in soybean and cotton
- 5 SEQ ID No. 21: Nucleic acid sequence encoding *Rhodococcus* sp. (strain RHA1), isolate ro0240 HPPD optimized for the expression in soybean and cotton
- SEQ ID No. 22: Nucleic acid sequence encoding *Picrophilus torridus* HPPD optimized for the expression in soybean and cotton
- 10 SEQ ID No. 23: Nucleic acid sequence encoding *Kordia algicida* HPPD optimized for the expression in soybean and cotton
- SEQ ID No 24 Nucleic acid sequence encoding *Pseudomonas fluorescens* HPPD (PfHPPD-Evo33)
- 15 mutated at position 335, mutation Glu => Pro; and mutated at position 336; mutation Gly => Trp
- SEQ ID No 25 Protein encoded by SEQ ID No 24.
- SEQ ID No 26 Nucleic sequence encoding *Pseudomonas fluorescens* HPPD (PfHPPD-Evo40) mutated at position 335, mutation Glu-->Pro, mutated at position 336, mutation Gly-->Ser, and mutated at position 340, mutation Ala-->Glu
- 20 SEQ ID No 27 Protein encoded by SEQ ID No 26.
- SEQ ID No 28 Nucleic acid sequence encoding *Pseudomonas fluorescens* HPPD (PfHPPD-Evo41)
- 25 mutated at position 335, mutation Glu-->Pro, mutated at position 336, mutation Gly-->Trp, mutated at position 339, mutation Lys-->Ala, and mutated at position 340, mutation Ala-->Gln
- SEQ ID No 29 Protein encoded by SEQ ID No 28.
- 30 SEQ ID No 30 Nucleic acid sequence encoding *Pseudomonas* (=Comamonas) testosterone Axmi428H HPPD
- SEQ ID No 31 Protein encoded by SEQ ID No 30.
- SEQ ID No 32 Protein sequence of *Pseudomonas* (=Comamonas) testosterone Axmi428H HPPD (Axmi428-Evo40)

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Mutated at position 351, mutation Glu-->Pro,
 mutated at position 352, mutation Gly--> Ser, and
 mutated at position 356, mutation Ala -->Glu

SEQ ID No 33 Protein sequence of Pseudomonas (=Comamonas) testosteroni
 Axmi428H HPPD (Axmi428-Evo41)

mutated at position 351, mutation Glu-->Pro,
 mutated at position 352, mutation Gly--> Trp,
 mutated at position 355, mutation Lys-->Ala, and
 mutated at position 356, mutation Ala -->Gln

10 SEQ ID No 34 Nucleic acid sequence encoding Pseudomonas agarici
 Axmi309H HPPD.

SEQ ID No 35 Protein encoded by SEQ ID No 34.

SEQ ID No 36 Protein sequence of Pseudomonas agarici Axmi309H HPPD
 (Axmi309-Evo40)

15 mutated at position 335, mutation Glu-->Pro,
 mutated at position 336, mutation Gly--> Ser, and
 mutated at position 340, mutation Ala -->Glu

SEQ ID No 37 Protein sequence of Pseudomonas agarici Axmi309H HPPD
 (Axmi309-Evo41)

20 mutated at position 335, mutation Glu-->Pro,
 mutated at position 336, mutation Gly--> Trp,
 mutated at position 339, mutation Lys-->Ala, and
 mutated at position 340, mutation Ala -->Gln

SEQ ID No 38 Nucleic acid encoding of Pseudomonas aeruginosa Axmi305H
 HPPD.

25 SEQ ID No 39 Protein encoded by SEQ ID No 38.

SEQ ID No 40 Protein sequence of Pseudomonas aeruginosa Axmi305H
 (Axmi305-Evo40)

mutated at position 337, mutation Glu-->Pro,
 mutated at position 338, mutation Gly--> Ser, and
 mutated at position 342, mutation Ala -->Glu

30 SEQ ID No 41 Protein sequence of Pseudomonas aeruginosa Axmi305H
 (Axmi305-Evo41)

mutated at position 337, mutation Glu-->Pro,

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mutated at position 338, mutation Gly--> Trp,
 mutated at position 341, mutation Lys-->Ala, and
 mutated at position 342, mutation Ala -->Gln

- SEQ ID NO 42 HPPD protein encoded by Avena sativa
- 5 SEQ ID No 43 HPPD protein as of SEQ ID No 42 having a deletion at position 109
 (Avena sativa Δ A109).
- SEQ ID No 44 HPPD protein encoded by Zea mays.
- SEQ ID No 45 Nucleic acid encoding of Pseudomonas fluorescens HPPD
 (PfHPPD).
- 10 SEQ ID No 46 Protein encoded by SEQ ID No 45.

Examples

- 15 A. Cloning of Avena HPPD (according WO02/46387)

A1- Cloning for expression in E. coli cells

- cDNA coding for Avena sativa HPPD (AvHPPD; SEQ ID No. 1) was ordered at GeneArt
 (Regensburg, Germany) using the codon usage optimized for the expression of the gene
 20 in Escherichia coli cells. Upstream to the start codon ATG, was added the sequence
 corresponding to the recognition site of the restriction enzyme BamHI, and downstream to
 the stop codon was added the sequence stretch corresponding to the recognition site of
 the enzyme HindIII. The synthesized fragment was cloned using the restriction enzymes
 BamHI and HindIII in the previously opened vector pET32a (Novagen, Darmstadt,
 25 Germany), in order to obtain a fusion with the HisTag present in the vector at the N-
 Terminal extremity from the AvHPPD protein (SEQ ID No. 2). The resulting vector was
 named pET32a-AvHPPDe.

The protein was produced in E.coli and isolated following the standard protocol (as
 described for example in WO2009/144079).

30

B Cloning of PfHPPD-G336W

B1- Cloning of PfHPPD-G336W for the expression in E. coli cells

The gene coding for the mutant HPPD G336W (SEQ ID No. 3) (US 6,245,968) from *Pseudomonas fluorescens* in the plasmid pKK233-2 (Clontech) (US 6245968) was used as template for a PCR to add to the sequence at its 5' extremity the sequence corresponding to the recognition site of the enzyme NcoI and at its 3' extremity the sequence corresponding to the recognition site of the enzyme XbaI. (see WO 2009/144079). The cloning was made in order to obtain a His tag fusion protein at the N-terminal extremity of the *Pseudomonas* HPPD G336W, also called PfW336 or PfG336W or PfHPPDW336 (SEQ ID No. 4) named "pSE420(RI)NX-PfG336W".

10 B2 - Cloning of PfHPPD-G336W for the expression in plants

A binary vector for tobacco or soybean transformation is, for example, constructed with the CaMV35 promoter driving the expression of the gene PfHPPD-G336W (SEQID No 5), with a codon usage optimized for the expression in dicotyledoneous plants and at its 5'extremity was added a sequence coding for an OTP, and further upstream a sequence TEV (Tobacco etch virus) to improve the stability of the mRNA in plants followed by the CaMV35S terminator. Additionally, the transformation vector also contains a PAT gene cassette in which the gene is driven by a CaVM35S promoter and followed by a CaMV35S terminator for glufosinate based selection during the transformation process and a 2mEPSPS gene cassette in which the gene is driven by an histone promoter from Arabidopsis to confer tolerance to the herbicide glyphosate to the transformed plants. The binary vector was called pFCO117.

All other mutated *Pseudomonas* genes and genes obtained from other organisms according to this invention can be cloned in analogy to the above.

25 B3 – Alternative approach for cloning of HPPD genes into a plant expression cassette.

For each of the HPPD genes described herein, the open reading frame (ORF) is amplified by PCR from a full-length DNA template. Hind III restriction sites are added to each end of the ORFs during PCR. Additionally, the nucleotide sequence ACC is added immediately 5' to the start codon of the gene to increase translational efficiency (Kozak (1987) Nucleic Acids Research 15:8125-8148; Joshi (1987) Nucleic Acids Research 15:6643-6653). The PCR product is cloned and sequenced using techniques well known in the art to ensure that no mutations are introduced during PCR.

The plasmid containing the PCR product is digested with Hind III and the fragment containing the intact ORF is isolated. This fragment is cloned into the Hind III site of a

plasmid such as pAX200, a plant expression vector containing the rice actin promoter (McElroy et al. (1991) Molec. Gen. Genet. 231:150-160) and the PinII terminator (An et al. (1989) The Plant Cell 1:115-122). The promoter – gene – terminator fragment from this intermediate plasmid is then sub cloned into plasmid pSB11 (Japan Tobacco, Inc.) to form
5 a final pSB11-based plasmid. These pSB11-based plasmids are typically organized such that the DNA fragment containing the promoter – gene– terminator construct may be excised by double digestion by restriction enzymes, such as Kpn I and Pme I, and used for transformation into plants by aerosol beam injection. The structure of the resulting pSB11-based clones is verified by restriction digest and gel electrophoresis, and by sequencing
10 across the various cloning junctions.

The plasmid is mobilized into *Agrobacterium tumefaciens* strain LBA4404 which also harbors the plasmid pSB1 (Japan Tobacco, Inc.), using triparental mating procedures well known in the art, and plating on media containing spectinomycin. The pSB11-based
15 plasmid clone carries spectinomycin resistance but is a narrow host range plasmid and cannot replicate in *Agrobacterium*. Spectinomycin resistant colonies arise when pSB11-based plasmids integrate into the broad host range plasmid pSB1 through homologous recombination. The cointegrate product of pSB1 and the pSB11-based plasmid is verified by Southern hybridization. The *Agrobacterium* strain harboring the cointegrate is used to
20 transform maize by methods known in the art, such as, for example, the PureIntro method (Japan Tobacco).

C Mutation of the various HPPD enzymes

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C1- Generation point mutants (as described in detail in PCT/US2013/59598)
The Pfw336 mutant was further mutagenized at several positions. Randomization of these positions was carried out using the QUIKCHANGE® lightning kit. The theoretical diversity of the library was about 300. Mutants were pooled and transformed into DH5α *E. coli* cells.
30 Six hundred individual clones were screened for tolerance to the HPPD inhibitor tembotrione (TBT). The clones were grown in LB media plus kanamycin at 37 degrees C in a shaker until an OD600 nm of 0.3 was reached. Cultures were then switched to 30 degrees C and incubated for an additional 17 hours. Cultures were spun down and cell

pellets resuspended in 10 mM Hepes/KOH pH 7.6, 4 mM MgCl₂, 1 mM DTT. The cells were lysed by bead beating and soluble cell extracts were obtained after centrifugation. The mutants were analyzed using a brown color assay. Specifically, the HPPD extracts were assayed in 96 well format for HPPD inhibitor tolerance by spotting on solid media containing LB-agar, kanamycin, 5 mM tyrosine, 42 mM succinate and an HPPD inhibitor. In the primary screen, 20 ul extract was spotted in triplicate on plates containing 250 uM tembotrione. Plates were covered with airpore tape and incubated at 37 degrees C. After 24 hours, brown pigment formation was visually compared to a sample containing PfHPPD336W. Variants showing increased pigment formation in the presence of TBT were re-assayed on 250 uM TBT and 250 uM diketonitrile (DKN) active compound of isoxaflutole (IFT). Those variants that again showed improved inhibitor tolerance were again expressed, and extract was titrated on 250 uM TBT and 250 uM DKN to determine the extent of improvement. Extract samples were also analyzed by SDS-PAGE and the extracts were found to contain equal amounts of HPPD protein.

C2 - Generation of permutational library (as described in detail in PCT/US2013/59598)

The sequences of the top performing first-generation variants were analyzed and a permutational library in the region combining positions 335, 336, 339, 340 was generated. Screening was carried out as described under C1, above. Titration data below shows variant PfHPPDEvo40 had improved tolerance to TBT and DKN compared to PfHPPD336W. SDS-PAGE analysis was carried out and showed no differences in HPPD expression levels between variants.

Variants were also tested by plating whole *E. coli* cells expressing HPPDs on media containing various HPPD inhibitors. For these experiments, DH5 α cells containing HPPD expressing plasmids were grown in LB media + kanamycin until an OD_{600nm}=0.5 was reached. Serial dilutions of cells were prepared in LB media + kanamycin corresponding to OD₆₀₀ values of 0.016, 0.008, 0.004, and 0.002. Ten microliters of each dilution were plated in triplicate on plates containing no HPPD inhibitor, 250 uM TBT, 250 uM DKN and 250 uM mesotrione (MST). Plates were incubated for 18 hours at 37 degrees C. SDS-PAGE analysis was carried out and showed no differences in HPPD expression levels between variants.

C3 - Preparation of *Pseudomonas fluorescens* HPPD mutant G336W (Pfw336) and kinetic characterization of the HPPD enzymes.

The native *Pseudomonas fluorescens* HPPD nucleotide sequence (PfHPPD, 1077 bp, as described in WO2009144079), which encodes the amino acid sequence listed herein as SEQ ID No 45, and as described in WO2009144079, WO 96/38567, and in Rüetschi et al. (*Eur. J. Biochem.*, 205, 459-466, 1992), was initially cloned into the unique NcoI site of the
5 expression vector pKK233-2 (Pharmacia) that provides a start codon.

At the 5' end, directly downstream to the ATG, a nucleic acid sequence encoding an alanine amino acid and a nucleic acid sequence encoding an N-terminal HIS6-Tag was inserted. Upstream to the ATG, two additional cytosine base pairs were added in order to obtain a sequence corresponding to the recognition site of the restriction enzyme NcoI and
10 downstream to the stop codon the sequences corresponding to the recognition site of the restriction enzyme XbaI were added. The DNA sequence corresponding to the gene, including the sequence encoding the HIS-TAG, was cut with the restriction enzymes NcoI and XbaI, and then cloned into the modified expression vector pSE420(RI)NX (5261 bp).

The cloning and expression vector pSE420(RI)NX (5261 bp) is based on the plasmid
15 pSE420 by Invitrogen (Karlsruhe, Germany). Modifications of this vector include the addition of a nptII gene (neomycin phosphotransferase; Sambrook and Russell, 2001, *Molecular Cloning: a laboratory manual* (Third edition)) conferring tolerance to the antibiotic kanamycin and which is missing the majority of the superlinker region (multiple cloning site).

20 The plasmid possesses the trp-lac (trc) promoter and the lacI^q gene that provides the lac repressor in every *E. coli* host strain. The lac repressor binds to the lac operator (lacO) and restricts expression of the target gene; this inhibition can be alleviated by induction with Isopropyl β -D-1-thiogalactopyranoside (IPTG).

The resulting vector was called pSE420(RI)NX-PfHPPD and it was used to transform
25 *Escherichia coli* BL21 cells (Merck, Darmstadt, Germany).

Expression of HPPD was carried out in *E. coli* K-12 BL21 containing pSE420(RI)NX-PfHPPD or pSE420(RI)NX-Pfw336 (for details, see under B1, above). Cells were allowed to grow until OD reached 0.5, then expression was initiated from the trp-lac (trc) promoter by induction with 1 mM IPTG which binds to the lac repressor and causes its dissociation
30 from the lac operon. Expression was carried out over 15 h at 28 °C.

To prepare the pre-starter culture, 2 mL of TB medium (100 $\mu\text{g}\cdot\text{mL}^{-1}$ carbenicillin) were inoculated with 50 μL of an *E. coli* K-12 BL21 glycerol stock. The pre-starter culture was incubated at 37 °C with shaking at 140 rpm for 15 h. 200 μL of the pre-starter culture was

used to initiate the starter culture (5mL TB supplement with $100 \mu\text{g}\cdot\text{L}^{-1}$), which was incubated 3 h at 37°C .

To prepare the main culture, 400 mL of TB medium ($100 \mu\text{g}\cdot\text{mL}^{-1}$ carbenicillin) were inoculated with 4 mL of the starter culture. This starter culture was incubated at 37°C with shaking at 140 rpm until OD_{600} 0.5 was reached. Then recombinant protein expression was induced with 400 μL of 1M IPTG solution. The cells were allowed to grow for an additional hour under these conditions, then the temperature was lowered to 28°C and the culture was shaken at 140 rpm for 15 h. Cells were harvested by centrifugation at $6000 \times g$ for 15 min at 4°C . Then cell pellets were stored at -80°C .

D - Production of HPPD protein in E coli, purification via His-Tag

All above defined E. coli expression vectors were used to transform *Escherichia coli* BL21 cells (Merck, Darmstadt, Germany).

Expression of HPPD was carried out in *E. coli* K-12 BL21 containing pQE30-*AtHPPD*, pET32a-AvHPPDe, pSE420(RI)NX-Pfw336, pSE420(RI)NX-FMP27 (see WO2011/076889 or pSE420(RI)NX-FMP37 (see WO2011/076882). Cells were allowed to grow until OD reached 0.5, then expression was initiated from the trp-lac (trc) promoter by induction with 1 mM IPTG which binds to the *lac* repressor and causes its dissociation from the *lac* operon. Expression was carried out over 15 h at 28°C .

To prepare the pre-starter culture, 2 mL of TB medium ($100 \mu\text{g}\cdot\text{mL}^{-1}$ carbenicillin) were inoculated with 50 μL of an *E. coli* K-12 BL21 glycerol stock. The pre-starter culture was incubated at 37°C with shaking at 140 rpm for 15 h. 200 μL of the pre-starter culture was used to initiate the starter culture (5mL TB supplement with $100 \mu\text{g}\cdot\text{L}^{-1}$), which was incubated 3 h at 37°C .

To prepare the main culture, 400 mL of TB medium ($100 \mu\text{g}\cdot\text{mL}^{-1}$ carbenicillin) were inoculated with 4 mL of the starter culture. This starter culture was incubated at 37°C with shaking at 140 rpm until OD_{600} 0.5 was reached. Then recombinant protein expression was induced with 400 μL of 1M IPTG solution. The cells were allowed to grow for an additional hour under these conditions, then the temperature was lowered to 28°C and the culture was shaken at 140 rpm for 15 h. Cells were harvested by centrifugation at $6000 \times g$ for 15 min at 4°C . Then cell pellets were stored at -80°C .

D1 - Isolation and purification of His₆-tagged HPPD in native form

Lysis of cells

Cells were lysed using Lysozyme, an enzyme that cleaves the 1,4- β -linkages between N-acetylmuramic acid and N-acetyl-D-glucosamine residues in peptidoglycan which forms the bacterial cell wall. Cell membranes were then disrupted by the internal pressure of the bacterial cell. In addition, the lysis buffer contained Benzonase[®] Nuclease, an endonuclease that hydrolyzes all forms of DNA and RNA without damaging proteins and thereby largely reduces viscosity of the cell lysate. Lysis under native conditions was carried out on ice.

For purification of His₆-tagged proteins the QIAexpress[®] Ni-NTA Fast Start Kit was used following the user manual instruction.

D2 - Purification of His₆-tagged proteins by immobilized metal ion affinity chromatography (IMAC)

The cleared cell lysate (10 mL) obtained after centrifugation of the lysis reaction was loaded onto a Ni-NTA Fast Start Column from the QIAexpress[®] Ni-NTA Fast Start Kit (Qiagen, Hilden, Germany) and purification was carried out according to the instruction manual. The His₆-tagged protein was eluted with 2.5 mL of elution buffer.

D3 - Desalting of HPPD solutions by gel filtration

HPPD solutions eluted from a Ni-NTA Fast Start Column with 2.5 mL of elution buffer were applied to a Sephadex G-25 PD-10 column (GE Healthcare, Freiburg, Germany) following the user manual instruction. After the whole sample had entered the gel bed, elution was performed with 3.5 mL of storage buffer.

The HPPD solutions eluted from the desalting column were frozen at -80 °C in 1 mL aliquots.

D4 - Determination of HPPD protein concentration using the Bradford protein assay

Protein concentration was determined using the standard Bradford assay (Bradford, (1976), Anal Biochem 72: 248-254).

D5 - Determination of purity of HPPD solutions using SDS-PAGE

The integrity of the eluted protein was checked by SDS-PAGE protein gel electrophoresis using the gel NuPAGE® Novex 4-12 % Bis-Tris Gels (Invitrogen, Karlsruhe, Germany), approximately 10 µg of protein were loaded. 10 µL of Laemmli Sample Buffer was added to 1-10 µL of protein solution and the mixture was incubated at 90 °C for 10 min. After
5 short centrifugation step, the whole mixture was loaded into a slot of an SDS gel previously fixed in a XCell SureLock™ Novex Mini-Cell gel chamber filled with NuPAGE® MOPS SDS Running Buffer (diluted from the 20 x-solution with ddH₂O). A voltage of 150 was then applied to the gel chamber for 1 h. For staining of protein bands, the gel was immersed in Coomassie Brilliant Blue R-250 Staining Solution. For destaining of the
10 polyacrylamide gel, it was immersed in Coomassie Brilliant Blue R-250 Destaining Solution until protein bands appear blue on a white gel.

E - Determination of HPPD activity in presence of N-(1,3,4-Oxadiazol-2-
15 yl)arylcarboxamides

HPPD activity was measured at room temperature by adding appropriate amounts of HPPD to a solution of 200 mM Tris-HCl pH 7.6, 10 mM ascorbate, 20 µM FeSO₄, 650 units of catalase, 8 µg HGA dioxygenase (HGA: homogentisate) and 600 µM HPP in a total
20 volume of 1 ml. Initial reaction rates in the absence or presence of inhibitors were determined from the increase in absorbance at 318 nm due to the formation of maleylacetoacetate ($\epsilon_{318} = 11,900 \text{ M}^{-1} \text{ cm}^{-1}$). pI_{50} -values (the negative log values of the concentration of inhibitor necessary to inhibit 50% of the enzyme activity in molar concentration were determined from dose-response plots of HPPD activity versus inhibitor
25 concentrations tested (0.1 to 100 µM) using the 4 Parameter Logistic Model or Sigmoidal Dose-Response Model of the ID Business Solutions Ltd. XLfit software suite. Due to the UV absorption of the HPPD inhibitors tested, inhibitor concentrations >100 µM could not be tested. In cases, the symbol ">" is used this means that the value was far higher than the one indicated but could not be precisely calculated within in the range of concentration
30 of inhibitor tested.

All results are shown in Table 8.

In the 1st column of Table 8, the chemical compound employed in the assay is named (according to the numbering of the Tables 1 to 7, above). In columns 2, 3, 4, and 5 the

245

pI50-values of the corresponding chemical compounds against various HPPD enzymes (name and SEQ ID Nos are indicated, respectively) are given.

Table 8

Com- pound	Avena HPPD SEQ ID No 2	FMP 37 SEQ ID No 9	PfHPPD Evo 40 SEQ ID No 27	PfHPPD Evo 41 SEQ ID No 29
5-145	5.5	5.0	>5.3	>5.3
2-145	5.8	5.0	5.3	5.3
6-37	4.4	3.8	3.9	3.8
7-132	4.8	5.1	3.7	3.6
2-360	5.4	4.7	4.8	4.7
2-361	5.8	4.9	5.3	5.1
2-363	5.8	5.0	5.2	4.9
2-144	5.4	4.9	5.2	5.0
2-364	5.8	5.1	4.9	4.5

5

These data show that the HPPD derived from various organisms do show an acceptable tolerance levels to several N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides.

F - Soybean transformation and herbicide tolerance evaluation of transgenic plants expressing mutated DNA sequences of HPPD encoding genes

F1- Soybean transformation and T0 plant establishment

5 Soybean transformation was achieved by using methods by best mode well known in the art, such as the one described using the *Agrobacterium tumefaciens* mediated transformation soybean half-seed explants using essentially the method described by Paz et al. (2006), Plant cell Rep. 25:206. Transformants were identified using various HPPD inhibitors tembotrione or isoxaflutole as selection marker. The appearance of green shoots
10 can be observed, and documented as an indicator of tolerance to the respective herbicide. The tolerant transgenic shoots showed normal greening comparable to wild-type soybean shoots not treated with the respective HPPD inhibitor, whereas wild-type soybean shoots treated with the same amount of the respective HPPD inhibitor was entirely bleached. This indicates that the presence of the HPPD protein enables the tolerance to HPPD inhibitor
15 herbicides.

Tolerant green shoots are transferred to rooting media or grafted. Rooted plantlets are transferred to the greenhouse after an acclimation period. Plants containing the transgene are then sprayed with HPPD inhibitor herbicides, as for example with tembotrione at a rate
20 of 100 to 200g AI/ha supplemented with ammonium sulfate and methyl ester raps oil or with mesotrione at a rate of 100 to 400g AI/ha supplemented with ammonium sulfate and methyl ester raps oil . Ten days after the application the symptoms due to the application of the herbicide are evaluated and compared to the symptoms observed on a wild type plants under the same conditions. Tolerant T0 soybean plants obtained according to the
25 above were advanced to the T1 generation.

F2 - Greenhouse trials with transgenic soybean T2 plants

In this herbicide efficacy testing the established T2 plants harbor an expression vector, which contained at least one chimeric gene encoding a mutated DNA sequence described
30 in PCT/US2013/59598, more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 25), or comprising an E (Glu) -> P (Pro) replacement at

position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or expressing the variant of the *Pseudomonas fluorescens* HPPD protein PfHPPD-G336W described in patent WO99/24585,

T2 events were germinated and grown in the greenhouse and sprayed at the V2-V3 stage of soybean development with one exemplary N-(1,3,4-Oxadiazol-2-yl)arylcarboxamide of formulation type WP20 (concentration range of 6.25g AI/ha – 75g AI/ha) supplemented with ammonium sulfate and methylated rape seed oil (Actirob).

As a spray control, wild type soybean (Merlin and Thorne) and the above mentioned transgenic T2 soybean plants have been sprayed with the spray mixture lacking the herbicide. Herbicide tolerance of all plants in the experiment was evaluated fourteen days after treatment (DAT). Plants were rated visually with the following herbicide tolerance classes: “0”= marginal tolerance; 41% - 100% damaged leaf area; “1”= moderate tolerance; 26% - 40% damaged leaf area; “2”= good tolerance; 16% - 25% damaged leaf area; “3”= high tolerance; less than or equal to 15% damaged leaf area.

Table 9

Evaluation of the HPPD inhibitor tolerance from T2 soybean transgenic events expressing the variant of the *Pseudomonas fluorescens* HPPD protein PfHPPD-G336W (WO99/24585), or PfHPPD-Evo33, or PfHPPD-Evo40, or PfHPPD-Evo41 (PCT/US2013/59598) versus wild type (wt) soybean plants (Merlin and Thorne). Plants were treated with one exemplary N-(1, 3,4-Oxadiazol-2-yl)arylcarboxamide (Compound “2-145”; Table 2) with a final concentration of 6.25, 25, 50, or 75 g AI/ha. Herbicide tolerance has been scored after 14 days of treatment. As a control, wild type soybean and transgenic soybean T2 plants were treated with a spray mix lacking the herbicide. All these control plants did not show bleached leaf area. Following leaf area damage classes have been defined for herbicide tolerance scoring: “0”= marginal tolerance; 41% - 100% damaged leaf area; “1”= moderate tolerance; 26% - 40% damaged leaf area; “2”= good

tolerance; 16% - 25% damaged leaf area; “3”= high tolerance; 0% - less than or equal to 15% damaged leaf area.

Soybean Events	Herbicide tolerance scoring				
	“0”	“1”	“2”	“3”	
Treatment: Compound “2-145” with 6.25 g AI/ha					
	Number of plants tested and categorized				Total number events
Merlin (wt)	4	0	0	0	4
Thorne (wt)	4	0	0	0	4
PfHPPD-Evo33	0	0	0	12	12
PfHPPD-Evo40	0	0	0	8	8
PfHPPD-Evo41	0	1	0	11	12
PfHPPD-W336	1	0	0	11	12
Treatment: Compound “2-145” with 25 g AI/ha					
Merlin	4	0	0	0	4
Thorne	4	0	0	0	4
PfHPPD-Evo33	1	1	0	14	16
PfHPPD-Evo40	0	0	0	12	12
PfHPPD-Evo41	0	0	0	16	16
PfHPPD-W336	0	2	3	11	16
Treatment: Compound “2-145” with 50 g AI/ha					
PfHPPD-Evo33	0	0	1	3	4
PfHPPD-Evo40	0	0	0	4	4
PfHPPD-Evo41	0	0	2	2	4
PfHPPD-W336	0	0	1	3	4
Treatment: Compound “2-145” with 75 g AI/ha					
PfHPPD-Evo33	0	0	0	4	4
PfHPPD-Evo40	0	0	0	4	4
PfHPPD-Evo41	0	0	0	4	4
PfHPPD-W336	0	1	0	3	4

The transgenic T2 soybean plants expressing the mutated DNA sequences of HPPD encoding genes had a superior tolerance compared to the controls with several events tolerant to agronomic relevant levels of the exemplary N-(1,3,4-Oxadiazol-2-yl)arylcarboxamide.

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G - Cotton transformation, selection and herbicide tolerance evaluation of transgenic plants expressing mutated DNA sequences of HPPD encoding genes

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G1- Cotton transformation and T0 plant establishment

Cotton transformation is achieved by using methods well known in the art, especially preferred method in the one described in the PCT patent publication WO 00/71733.

Regenerated plants were transferred to the greenhouse. Following an acclimation period,

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sufficiently grown plants were sprayed with HPPD inhibitor herbicides as for example

tembotrione equivalent to 100 gAI/ha or with mesotrione equivalent to 100 to 200 g AI/ha

supplemented with ammonium sulfate and methyl ester raps oil. Seven days after the

spray application, the symptoms due to the treatment with the herbicide were evaluated

and compared to the symptoms observed on wild type cotton plants subjected to the same

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treatment under the same conditions. Obtained tolerant T0 plants were selected and

advanced for T1 generation.

G2 - Field studies of HPPD inhibitor tolerant T3 transgenic cotton plants

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To further test the performance of generated HPPD tolerant cotton plants under field conditions a study was conducted at two locations.

In particular, several independent events harbor a cotton optimized plant expression

cassette, which contained and expressed at least one chimeric gene encoding a mutated

DNA sequence described in PCT/US2013/59598, more specifically a mutated sequence

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of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro)

replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336

(named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598

and being disclosed in present application under SEQ ID No. 25), or (iii) comprising an E

(Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position

336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 and being disclosed in present application under SEQ ID No. 29), or expressing the variant of the *Pseudomonas fluorescens* HPPD protein PfHPPD-G336W describe in patent WO99/24585, were analyzed.

The studies were designed as follows and well known to those skilled in the art: The plots were kept free of weed with a pre-planting treatment of a non-selective herbicide. Control rows were set-up with the non-transgenic cotton variety "Cocker" and the respective transgenic cotton events, which have been treated with a spray mix lacking the different herbicides. Cotton plants were treated with herbicides at V3 stage. Up to three replications have been set-up and conducted and the average maximum phytotoxicity has been summarized in Table 10, below.

Post-emergence application has been conducted with the N-(1,3,4-Oxadiazol-2-yl)arylcarboxamide compound "2-145" with a final concentration of 200 g AI/ha and scored after 14 days (Table 10).

The control treatments did not show bleached leaf area. The variety "Cocker" showed at least 87% and up to 98% leaf damage. The following leaf area damage (phytotoxicity) classes have been defined based on visually herbicide tolerance scoring:

- "0"= marginal / agronomic non-relevant tolerance; greater than 20% damaged leaf area;
- "1"= moderate tolerance / agronomic non-relevant tolerance; 16% - 20% damaged leaf area;
- "2"= good tolerance; greater than 10% and up to 15% damaged leaf area;
- "3"= high tolerance; less than or equal to 10% damaged leaf area.

Table 10

Evaluation of the HPPD inhibitor tolerance from T3 cotton transgenic events expressing the variant of the *Pseudomonas fluorescens* HPPD protein PfHPPD-G336W (WO99/24585), or PfHPPD-Evo33, or PfHPPD-Evo41 (PCT/US2013/59598). The control variety "Cocker" showed under all treatment conditions at least 87% leaf damage with up to 98%. Results are shown for plants treated with N-(1,3,4-Oxadiazol-2-yl)arylcarboxamide compound "2-145" (Table 2) with a final concentration of 200 g AI/ha. Plants have been

treated after emergence in developmental stage V3 (post-emergence) and scored after 14 days

As a control non-transgenic and transgenic cotton plants were always treated with a spray mix lacking the herbicide. All these control plants did not show bleached leaf area.

- 5 Following leaf area damage (phytotoxicity) classes have been defined for herbicide tolerance scoring: “0”= marginal tolerance; >20% damaged leaf area; “1”= moderate tolerance; 16% - 20% damaged leaf area; “2”= good tolerance; 11% - 15% damaged leaf area; “3”= high tolerance; 0% - 10% damaged leaf area.

Independent cotton events harboring the variant of the PfHPPD protein	Average maximum phytotoxicity scoring with Compound “2-145” [200 g AI / ha]
PfHPPD-Evo33	
Evo33/1	3
Evo33/2	3
Evo33/3	3
Evo33/4	3
Evo33/5	3
Evo33/6	3
PfHPPD-Evo41	
Evo41/1	3
Evo41/2	3
Evo41/3	3
Evo41/4	3
Evo41/5	3
Evo41/6	3
Evo41/7	3
Evo41/8	3
Evo41/9	3
Evo41/10	3
Evo41/11	3
Evo41/12	2
Evo41/13	3

Independent cotton events harboring the variant of the PfHPPD protein	Average maximum phytotoxicity scoring with Compound "2-145" [200 g AI / ha]
Evo41/14	3
Evo41/15	3
PfHPPD-W336	
W336/1	2
W336/2	2
W336/3	2

Most of the transgenic cotton plants expressing a variant of HPPD encoding genes had an agronomic relevant tolerance level against N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides.

These field studies showed for the first time that it is possible to generate crop plants

5 tolerant to N-(1,3,4-Oxadiazol-2-yl) arylcarboxamides by over-expressing mutated HPPD encoding genes in the crop of interest.

H - Transformation of Maize Plant Cells by Agrobacterium-Mediated Transformation

Ears are best collected 8-12 days after pollination. Embryos were isolated from the ears,

10 and those embryos 0.8-1.5 mm in size were preferred for use in transformation. Embryos were plated scutellum side-up on a suitable incubation media, and incubated overnight at 25°C in the dark.

However, it is not necessary per se to incubate the embryos overnight. Embryos were

15 contacted with an Agrobacterium strain containing the appropriate vectors having a nucleotide sequence of the present invention for Ti plasmid mediated transfer for about 5-10 min, and then plated onto co-cultivation media for about 3 days (25°C in the dark). After co-cultivation, explants were transferred to recovery period media for about five days (at 25°C in the dark). Explants were incubated in selection media for up to eight weeks,

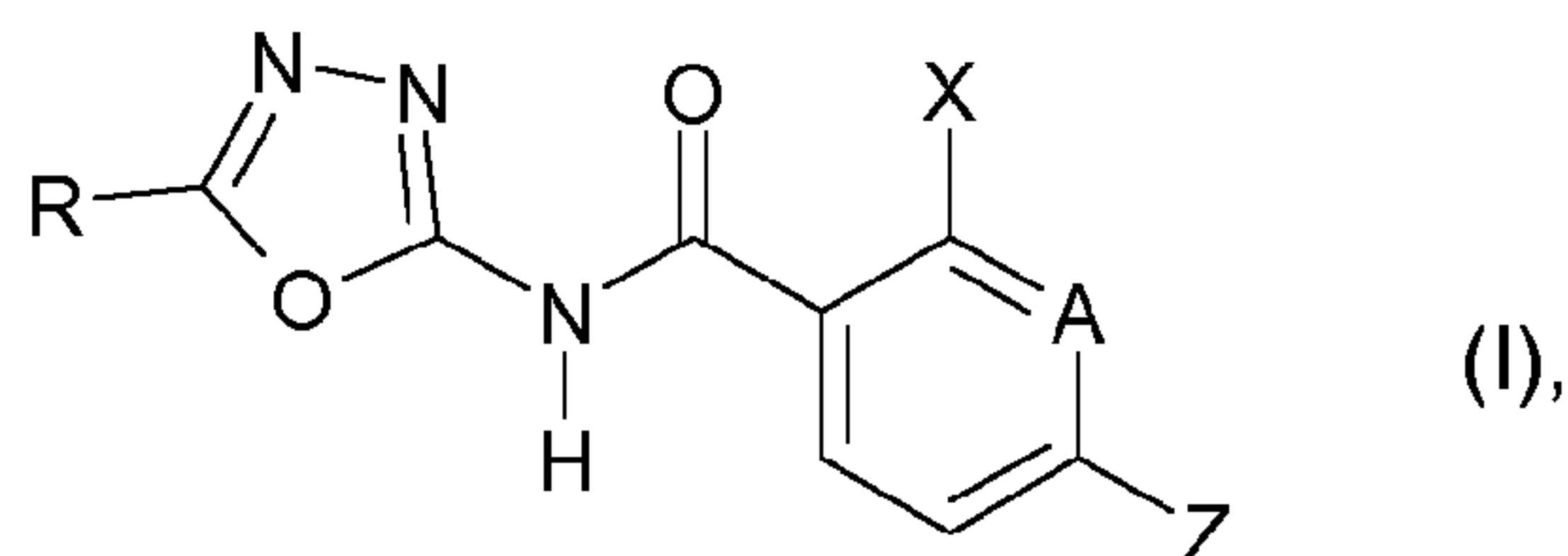
20 depending on the nature and characteristics of the particular selection utilized. After the selection period, the resulting callus were transferred to embryo maturation media, until the formation of mature somatic embryos were observed. The resulting mature somatic embryos were then placed under low light, and the process of regeneration was initiated the best mode as known in the art. The resulting shoots are allowed to root on rooting

media, and the resulting plants are transferred to nursery pots and propagated as transgenic plants.

- All publications and patent applications mentioned in the specification are indicative of the level of skill of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.
- 10 Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

Claims

1. The use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides of the formula (I) or their salts



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in which

A is N or CY,

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R is hydrogen, (C₁–C₆)-alkyl, R¹O-(C₁–C₆)-alkyl, CH₂R⁶, (C₃–C₇)-cycloalkyl, halo-(C₁–C₆)-alkyl, (C₂–C₆)-alkenyl, halo-(C₂–C₆)-alkenyl, (C₂–C₆)-alkynyl, halo-(C₂–C₆)-alkynyl, OR¹, NHR¹, methoxycarbonyl, ethoxycarbonyl, methoxycarbonylmethyl, ethoxycarbonylmethyl, methylcarbonyl, trifluoromethylcarbonyl, dimethylamino, acetylamino, methylsulfenyl, methylsulfinyl, methylsulfonyl, or heteroaryl, heterocyclyl, benzyl or phenyl each substituted by s radicals from the group of halogen, nitro, cyano, (C₁–C₆)-alkyl, halo-(C₁–C₆)-alkyl, (C₃–C₆)-cycloalkyl, S(O)_n-(C₁–C₆)-alkyl, (C₁–C₆)-alkoxy, halo-(C₁–C₆)-alkoxy, (C₁–C₆)-alkoxy-(C₁–C₄)-alkyl,

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X is nitro, halogen, cyano, formyl, thiocyanato, (C₁–C₆)-alkyl, halo-(C₁–C₆)-alkyl, (C₂–C₆)-alkenyl, halo-(C₂–C₆)-alkenyl, (C₂–C₆)-alkynyl, halo-(C₃–C₆)-alkynyl, (C₃–C₆)-cycloalkyl, halo-(C₃–C₆)-cycloalkyl, (C₃–C₆)-cycloalkyl-(C₁–C₆)-alkyl, halo-(C₃–C₆)-cycloalkyl-(C₁–C₆)-alkyl, COR¹, COOR¹, OCOOR¹, NR¹COOR¹, C(O)N(R¹)₂, NR¹C(O)N(R¹)₂, OC(O)N(R¹)₂, C(O)NR¹OR¹, OR¹, OCOR¹, OSO₂R², S(O)_nR², SO₂OR¹, SO₂N(R¹)₂, NR¹SO₂R², NR¹COR¹, (C₁–C₆)-alkyl-S(O)_nR², (C₁–C₆)-alkyl-OR¹, (C₁–C₆)-alkyl-OCOR¹, (C₁–C₆)-alkyl-OSO₂R², (C₁–C₆)-alkyl-CO₂R¹, (C₁–C₆)-alkyl-SO₂OR¹, (C₁–C₆)-alkyl-CON(R¹)₂, (C₁–C₆)-alkyl-SO₂N(R¹)₂, (C₁–C₆)-alkyl-NR¹COR¹, (C₁–C₆)-alkyl-NR¹SO₂R², NR¹R², P(O)(OR⁵)₂, CH₂P(O)(OR⁵)₂, (C₁–C₆)-alkylheteroaryl, (C₁–C₆)-

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alkylheterocyclyl, where the two latter radicals are each substituted by s

halogen, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, S(O)_n-(C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, halo-(C₁-C₆)-alkoxy radicals, and where heterocyclyl bears n oxo groups,

Y is hydrogen, nitro, halogen, cyano, thiocyanato, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, (C₂-C₆)-alkenyl, halo-(C₂-C₆)-alkenyl, (C₂-C₆)-alkynyl, halo-(C₂-C₆)-alkynyl, (C₃-C₆)-cycloalkyl, (C₃-C₆)-cycloalkenyl, halo-(C₃-C₆)-cycloalkyl, (C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, halo-(C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, COR¹, COOR¹, OCOOR¹, NR¹COOR¹, C(O)N(R¹)₂, NR¹C(O)N(R¹)₂, OC(O)N(R¹)₂, CO(NOR¹)R¹, NR¹SO₂R², NR¹COR¹, OR¹, OSO₂R², S(O)_nR², SO₂OR¹, SO₂N(R¹)₂, (C₁-C₆)-alkyl-S(O)_nR², (C₁-C₆)-alkyl-OR¹, (C₁-C₆)-alkyl-OCOR¹, (C₁-C₆)-alkyl-OSO₂R², (C₁-C₆)-alkyl-CO₂R¹, (C₁-C₆)-alkyl-CN, (C₁-C₆)-alkyl-SO₂OR¹, (C₁-C₆)-alkyl-CON(R¹)₂, (C₁-C₆)-alkyl-SO₂N(R¹)₂, (C₁-C₆)-alkyl-NR¹COR¹, (C₁-C₆)-alkyl-NR¹SO₂R², N(R¹)₂, P(O)(OR⁵)₂, CH₂P(O)(OR⁵)₂, (C₁-C₆)-alkylphenyl, (C₁-C₆)-alkylheteroaryl, (C₁-C₆)-alkylheterocyclyl, phenyl, heteroaryl or heterocyclyl, where the 6 latter radicals are each substituted by s radicals from the group of halogen, nitro, cyano, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl, S(O)_n-(C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, halo-(C₁-C₆)-alkoxy, (C₁-C₆)-alkoxy-(C₁-C₄)-alkyl and cyanomethyl, and where heterocyclyl bears n oxo groups,

Z is hydrogen, halogen, cyano, thiocyanato, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, halo-(C₁-C₆)-alkyl, (C₂-C₆)-alkenyl, halo-(C₂-C₆)-alkenyl, (C₂-C₆)-alkynyl, halo-(C₂-C₆)-alkynyl, (C₃-C₆)-cycloalkyl, halo-(C₃-C₆)-cycloalkyl, (C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, halo-(C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, COR¹, COOR¹, OCOOR¹, NR¹COOR¹, C(O)N(R¹)₂, NR¹C(O)N(R¹)₂, OC(O)N(R¹)₂, C(O)NR¹OR¹, OSO₂R², S(O)_nR², SO₂OR¹, SO₂N(R¹)₂, NR¹SO₂R², NR¹COR¹, (C₁-C₆)-alkyl-S(O)_nR², (C₁-C₆)-alkyl-OR¹, (C₁-C₆)-alkyl-OCOR¹, (C₁-C₆)-alkyl-OSO₂R², (C₁-C₆)-alkyl-CO₂R¹, (C₁-C₆)-alkyl-SO₂OR¹, (C₁-C₆)-alkyl-CON(R¹)₂, (C₁-C₆)-alkyl-SO₂N(R¹)₂, (C₁-C₆)-alkyl-NR¹COR¹, (C₁-C₆)-alkyl-NR¹SO₂R², N(R¹)₂, P(O)(OR⁵)₂, heteroaryl, heterocyclyl or phenyl, where the three latter radicals are each substituted by s radicals from the group of halogen, nitro, cyano, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl, S(O)_n-(C₁-C₆)-alkyl, (C₁-C₆)-alkoxy or halo-(C₁-C₆)-alkoxy, and where heterocyclyl bears n oxo groups,

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- R^1 is hydrogen, (C₁-C₆)-alkyl, (C₁-C₆)-haloalkyl, (C₂-C₆)-alkenyl, (C₂-C₆)-haloalkenyl, (C₂-C₆)-alkynyl, (C₂-C₆)-haloalkynyl, (C₃-C₆)-cycloalkyl, (C₃-C₆)-cycloalkenyl, (C₃-C₆)-halocycloalkyl, (C₁-C₆)-alkyl-O-(C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, phenyl, phenyl-(C₁-C₆)-alkyl, heteroaryl, (C₁-C₆)-alkylheteroaryl, heterocyclyl, (C₁-C₆)-alkylheterocyclyl, (C₁-C₆)-alkyl-O-heteroaryl, (C₁-C₆)-alkyl-O-heterocyclyl, (C₁-C₆)-alkyl-NR³-heteroaryl, (C₁-C₆)-alkyl-NR³-heterocyclyl, where the 21 latter radicals are substituted by s radicals from the group consisting of cyano, halogen, nitro, thiocyanato, OR³, S(O)_nR⁴, N(R³)₂, NR³OR³, COR³, OCOR³, SCOR⁴, NR³COR³, NR³SO₂R⁴, CO₂R³, COSR⁴, CON(R³)₂ and (C₁-C₄)-alkoxy-(C₂-C₆)-alkoxycarbonyl, and where heterocyclyl bears n oxo groups,
- R^2 is (C₁-C₆)-alkyl, (C₁-C₆)-haloalkyl, (C₂-C₆)-alkenyl, (C₂-C₆)-haloalkenyl, (C₂-C₆)-alkynyl, (C₂-C₆)-haloalkynyl, (C₃-C₆)-cycloalkyl, (C₃-C₆)-cycloalkenyl, (C₃-C₆)-halocycloalkyl, (C₁-C₆)-alkyl-O-(C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, phenyl, phenyl-(C₁-C₆)-alkyl, heteroaryl, (C₁-C₆)-alkylheteroaryl, heterocyclyl, (C₁-C₆)-alkylheterocyclyl, (C₁-C₆)-alkyl-O-heteroaryl, (C₁-C₆)-alkyl-O-heterocyclyl, (C₁-C₆)-alkyl-NR³-heteroaryl, (C₁-C₆)-alkyl-NR³-heterocyclyl, where the 21 latter radicals are substituted by s radicals from the group consisting of cyano, halogen, nitro, thiocyanato, OR³, S(O)_nR⁴, N(R³)₂, NR³OR³, COR³, OCOR³, SCOR⁴, NR³COR³, NR³SO₂R⁴, CO₂R³, COSR⁴, CON(R³)₂ and (C₁-C₄)-alkoxy-(C₂-C₆)-alkoxycarbonyl, and where heterocyclyl bears n oxo groups,
- R^3 is hydrogen, (C₁-C₆)-alkyl, (C₂-C₆)-alkenyl, (C₂-C₆)-alkynyl, (C₃-C₆)-cycloalkyl or (C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl,
- R^4 is (C₁-C₆)-alkyl, (C₂-C₆)-alkenyl or (C₂-C₆)-alkynyl,
- R^5 is methyl or ethyl,
- R^6 is acetoxy, acetamido, N-methylacetamido, benzoyloxy, benzamido, N-methylbenzamido, methoxycarbonyl, ethoxycarbonyl, benzoyl,

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methylcarbonyl, piperidinylcarbonyl, morpholinylcarbonyl, trifluoromethylcarbonyl, aminocarbonyl, methylaminocarbonyl, dimethylaminocarbonyl, (C₁-C₆)-alkoxy, (C₃-C₆)-cycloalkyl, or heteroaryl, heterocyclyl or phenyl each substituted by s radicals from the group of methyl, ethyl, methoxy, trifluoromethyl and halogen,

n is 0, 1 or 2; and

s is 0, 1, 2 or 3.

for controlling unwanted plants in areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides by containing one or more chimeric gene(s) comprising (I) a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) *Avena*, (b) *Pseudomonas*, (c) *Synechococcoideae*, (d) *Blepharismidae*, (e) *Rhodococcus*, (f) *Picrophilaceae*, (g) *Kordia*, or (II) one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, or (III) one or more DNA sequences encoding mutated maize (*Zea mays*) or soybean (*Glycine max*) HPPD each being mutated as described in WO 2012/021785.

2. The use according to claim 1, where in formula (I)

A is N or CY,

R is hydrogen, (C₁-C₆)-alkyl, (C₃-C₇)-cycloalkyl, halo-(C₁-C₆)-alkyl, (C₃-C₇)-cycloalkylmethyl, methoxycarbonylmethyl, ethoxycarbonylmethyl, acetylmethyl, methoxymethyl, methoxyethyl, benzyl, pyrazin-2-yl, furan-2-yl, tetrahydrofuran-2-yl, morpholine, dimethylamino, or phenyl substituted by s radicals from the group of methyl, methoxy, trifluoromethyl and halogen;

X is nitro, halogen, cyano, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl, OR¹, S(O)_nR², (C₁-C₆)-alkyl-S(O)_nR², (C₁-C₆)-alkyl-OR¹, (C₁-C₆)-alkyl-CON(R¹)₂, (C₁-C₆)-alkyl-SO₂N(R¹)₂, (C₁-C₆)-alkyl-NR¹COR¹, (C₁-C₆)-alkyl-

$\text{NR}^1\text{SO}_2\text{R}^2$, $(\text{C}_1\text{-C}_6)$ -alkylheteroaryl, $(\text{C}_1\text{-C}_6)$ -alkylheterocyclyl, where the two latter radicals are each substituted by s halogen, $(\text{C}_1\text{-C}_6)$ -alkyl, halo- $(\text{C}_1\text{-C}_6)$ -alkyl, $\text{S}(\text{O})_n(\text{C}_1\text{-C}_6)$ -alkyl, $(\text{C}_1\text{-C}_6)$ -alkoxy, halo- $(\text{C}_1\text{-C}_6)$ -alkoxy radicals, and where heterocyclyl bears n oxo groups,

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Y hydrogen, nitro, halogen, cyano, $(\text{C}_1\text{-C}_6)$ -alkyl, $(\text{C}_1\text{-C}_6)$ -haloalkyl, OR^1 , $\text{S}(\text{O})_n\text{R}^2$, $\text{SO}_2\text{N}(\text{R}^1)_2$, $\text{N}(\text{R}^1)_2$, $\text{NR}^1\text{SO}_2\text{R}^2$, NR^1COR^1 , $(\text{C}_1\text{-C}_6)$ -alkyl- $\text{S}(\text{O})_n\text{R}^2$, $(\text{C}_1\text{-C}_6)$ -alkyl- OR^1 , $(\text{C}_1\text{-C}_6)$ -alkyl- $\text{CON}(\text{R}^1)_2$, $(\text{C}_1\text{-C}_6)$ -alkyl- $\text{SO}_2\text{N}(\text{R}^1)_2$, $(\text{C}_1\text{-C}_6)$ -alkyl- NR^1COR^1 , $(\text{C}_1\text{-C}_6)$ -alkyl- $\text{NR}^1\text{SO}_2\text{R}^2$, $(\text{C}_1\text{-C}_6)$ -alkylphenyl, $(\text{C}_1\text{-C}_6)$ -alkylheteroaryl, $(\text{C}_1\text{-C}_6)$ -alkylheterocyclyl, phenyl, heteroaryl or heterocyclyl, where the 6 latter radicals are each substituted by s radicals from the group of halogen, nitro, cyano, $(\text{C}_1\text{-C}_6)$ -alkyl, halo- $(\text{C}_1\text{-C}_6)$ -alkyl, $(\text{C}_3\text{-C}_6)$ -cycloalkyl, $\text{S}(\text{O})_n(\text{C}_1\text{-C}_6)$ -alkyl, $(\text{C}_1\text{-C}_6)$ -alkoxy, halo- $(\text{C}_1\text{-C}_6)$ -alkoxy, $(\text{C}_1\text{-C}_6)$ -alkoxy- $(\text{C}_1\text{-C}_4)$ -alkyl and cyanomethyl, and where heterocyclyl bears n oxo groups,

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Z is halogen, cyano, nitro, methyl, halo- $(\text{C}_1\text{-C}_6)$ -alkyl, $(\text{C}_3\text{-C}_6)$ -cycloalkyl, $\text{S}(\text{O})_n\text{R}^2$, 1,2,4-triazol-1-yl, pyrazol-1-yl, or Z may also be hydrogen if Y is the $\text{S}(\text{O})_n\text{R}^2$ radical,

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R^1 is hydrogen, $(\text{C}_1\text{-C}_6)$ -alkyl, $(\text{C}_2\text{-C}_6)$ -alkenyl, $(\text{C}_2\text{-C}_6)$ -alkynyl, $(\text{C}_3\text{-C}_6)$ -cycloalkyl, $(\text{C}_3\text{-C}_6)$ -cycloalkyl- $(\text{C}_1\text{-C}_6)$ -alkyl, $(\text{C}_1\text{-C}_6)$ -alkyl-O- $(\text{C}_1\text{-C}_6)$ -alkyl, phenyl, phenyl- $(\text{C}_1\text{-C}_6)$ -alkyl, heteroaryl, $(\text{C}_1\text{-C}_6)$ -alkylheteroaryl, heterocyclyl, $(\text{C}_1\text{-C}_6)$ -alkylheterocyclyl, $(\text{C}_1\text{-C}_6)$ -alkyl-O-heteroaryl, $(\text{C}_1\text{-C}_6)$ -alkyl-O-heterocyclyl, $(\text{C}_1\text{-C}_6)$ -alkyl- NR^3 -heteroaryl or $(\text{C}_1\text{-C}_6)$ -alkyl- NR^3 -heterocyclyl, where the 16 latter radicals are substituted by s radicals from the group consisting of cyano, halogen, nitro, OR^3 , $\text{S}(\text{O})_n\text{R}^4$, $\text{N}(\text{R}^3)_2$, NR^3OR^3 , COR^3 , OCOR^3 , NR^3COR^3 , $\text{NR}^3\text{SO}_2\text{R}^4$, CO_2R^3 , $\text{CON}(\text{R}^3)_2$ and $(\text{C}_1\text{-C}_4)$ -alkoxy- $(\text{C}_2\text{-C}_6)$ -alkoxycarbonyl, and where heterocyclyl bears n oxo groups,

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R^2 is $(\text{C}_1\text{-C}_6)$ -alkyl, $(\text{C}_3\text{-C}_6)$ -cycloalkyl or $(\text{C}_3\text{-C}_6)$ -cycloalkyl- $(\text{C}_1\text{-C}_6)$ -alkyl, where these three aforementioned radicals are each substituted by s radicals from the group consisting of halogen and OR^3 ,

R^3 is hydrogen or $(\text{C}_1\text{-C}_6)$ -alkyl,

R⁴ is (C₁-C₆)-alkyl,

n is 0, 1 or 2;

s is 0, 1, 2 or 3,

3. The use according to claim 1, where, in formula (I)

A is N or CY,

R is hydrogen, (C₁-C₄)-alkyl, cyclopropyl, halo-(C₁-C₄)-alkyl, (C₃-C₆)-cycloalkylmethyl, methoxymethyl, methoxyethyl, benzyl,;

X is nitro, halogen, cyano, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, cyclopropyl, OR¹, S(O)_nR², (C₁-C₆)-alkyl-S(O)_nR², (C₁-C₆)-alkyl-OR¹, (C₁-C₂)-alkylheteroaryl, (C₁-C₂)-alkylheterocyclyl, where the two latter radicals are each substituted by s halogen, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, S(O)_n-(C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, halo-(C₁-C₆)-alkoxy radicals, and where heterocyclyl bears n oxo groups,

Y hydrogen, nitro, halogen, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-haloalkyl, OR¹, S(O)_nR², SO₂N(R¹)₂, N(R¹)₂, NR¹SO₂R², NR¹COR¹, (C₁-C₆)-alkyl-S(O)_nR², (C₁-C₆)-alkyl-OR¹, (C₁-C₆)-alkyl-CON(R¹)₂, (C₁-C₆)-alkyl-SO₂N(R¹)₂, (C₁-C₆)-alkyl-NR¹COR¹, (C₁-C₆)-alkyl-NR¹SO₂R², (C₁-C₆)-alkylphenyl, (C₁-C₆)-alkylheteroaryl, (C₁-C₆)-alkylheterocyclyl, phenyl, heteroaryl or heterocyclyl, where the 6 latter radicals are each substituted by s radicals from the group of halogen, nitro, cyano, (C₁-C₆)-alkyl, halo-(C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl, S(O)_n-(C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, halo-(C₁-C₆)-alkoxy, (C₁-C₆)-alkoxy-(C₁-C₄)-alkyl and cyanomethyl, and where heterocyclyl bears n oxo groups,

Z is halogen, cyano, nitro, methyl, halo-(C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl, S(O)_nR², 1,2,4-triazol-1-yl, pyrazol-1-yl,

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R¹ is hydrogen, (C₁-C₆)-alkyl, (C₂-C₆)-alkenyl, (C₂-C₆)-alkynyl, (C₃-C₆)-cycloalkyl, (C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, (C₁-C₆)-alkyl-O-(C₁-C₆)-alkyl, phenyl, phenyl-(C₁-C₆)-alkyl, heteroaryl, (C₁-C₆)-alkylheteroaryl, heterocyclyl, (C₁-C₆)-alkylheterocyclyl, (C₁-C₆)-alkyl-O-heteroaryl, (C₁-C₆)-alkyl-O-heterocyclyl, (C₁-C₆)-alkyl-NR³-heteroaryl or (C₁-C₆)-alkyl-NR³-heterocyclyl, where the latter radicals are substituted by s radicals from the group consisting of cyano, halogen, nitro, OR³, S(O)_nR⁴, N(R³)₂, NR³OR³, COR³, OCOR³, NR³COR³, NR³SO₂R⁴, CO₂R³, CON(R³)₂ and (C₁-C₄)-alkoxy-(C₂-C₆)-alkoxycarbonyl, and where heterocyclyl bears n oxo groups,

R² is (C₁-C₆)-alkyl, (C₃-C₆)-cycloalkyl or (C₃-C₆)-cycloalkyl-(C₁-C₆)-alkyl, where these three aforementioned radicals are each substituted by s radicals from the group consisting of halogen and OR³,

R³ is hydrogen or (C₁-C₆)-alkyl,

R⁴ is (C₁-C₆)-alkyl,

n is 0, 1 or 2;

s is 0, 1, 2 or 3.

4. The use of N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides of the formula or its salts according to any one of claims 1 to 3, wherein at least one of the chimeric genes contained in the transgenic crop comprises a DNA encoding a hydroxyphenylpyruvate dioxygenase (HPPD) selected from the group consisting of SEQ ID No.2, SEQ ID No. 4, SEQ ID No. 7, SEQ ID No. 9, SEQ ID No. 11, SEQ ID No. 13, SEQ ID No 15, SEQ ID No. 17, SEQ ID No, 25, and SEQ ID No 27, SEQ ID No. 29, SEQ ID No 31, SEQ ID No 32, SEQ ID No 33, SEQ ID No 35, SEQ ID No 36, SEQ ID No 37, SEQ ID No 39, SEQ ID No 40, SEQ ID No 41, SEQ ID No 43, SEQ ID No 46.

5. A method for controlling unwanted plants comprising the application of one or more N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides according to any one of claims 1 to 3 in

areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides by containing one or more chimeric gene(s) comprising (I) a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) *Avena*, (b) *Pseudomonas*, (c) *Synechococcoideae*, (d) *Blepharismidae*, (e) *Rhodococcus*, (f) *Picrophilaceae*, (g) *Kordia*, or (II) one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms or (III) or (III) one or more DNA sequences encoding mutated maize (*Zea mays*) or soybean (*Glycine max*) HPPD each being mutated as described in WO 2012/021785., and in which the application is performed to (a) the unwanted plants, (b) to the seeds of unwanted plants, and/or (c) to the area on which the plants grow.

6. A method according to claim 5, in which the transgenic crop plant belongs to the group of dicotyledonous crops consisting of *Arachis*, *Beta*, *Brassica*, *Cucumis*, *Cucurbita*, *Helianthus*, *Daucus*, *Glycine*, *Gossypium*, *Ipomoea*, *Lactuca*, *Linum*, *Lycopersicon*, *Nicotiana*, *Phaseolus*, *Pisum*, *Solanum*, and *Vicia*, or to the group of monocotyledonous crops consisting of *Allium*, *Ananas*, *Asparagus*, *Avena*, *Hordeum*, *Oryza*, *Panicum*, *Saccharum*, *Secale*, *Sorghum*, *Triticale*, *Triticum*, *Zea*.

7. A method according to claim 5 or 6 in which one or more N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides according to claim 1 is/are applied in combination with one or more HPPD inhibitor herbicides selected from the group consisting of triketone or pyrazolate herbicide in mixed formulations or in the tank mix, and/or with further known active substances which are based on the inhibition of acetolactate synthase, acetyl-CoA carboxylase, cellulose synthase, enolpyruvylshikimate-3-phosphate synthase, glutamine synthetase, p-hydroxyphenylpyruvate dioxygenase, phytoene desaturase, photosystem I, photosystem II, protoporphyrinogen oxidase, or act as growth regulators.

8. A method according to claim 7, in which one or more N-(1,3,4-Oxadiazol-2-yl)arylcarboxamides is/are applied in combination with one or more HPPD inhibitor herbicides selected from the group consisting of tembotrione, mesotrione, bicyclopyrone, tefuryltrione pyrasulfotole, pyrazolate, diketonitrile, topramezone, benzofenap, or sulcotrione.

