

INFORME DE BÚSQUEDA DE PATENTES PARA EL Radicado N° 14-0191567-00000-0000

CRITERIOS PARA LA BÚSQUEDA (anexar pantallazo o reporte en PDF, junto con los boleanos utilizados)

Palabras clave utilizadas	Polynucleotide EPSP synthase genes, herbicide resistance, molecules encoding herbicide resistance or tolerance polypeptides.
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CLASIFICACIONES INTERNACIONALES UTILIZADAS PARA LA BÚSQUEDA	A01H 5/00, C12N 15/29 // 15/82.
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BASES DE DATOS CONSULTADAS.

Patentscope	Google/patents		
NCBI	PatBase		
Espacenet	ScienceDirect		
Lens			

INFORMES DE EXÁMENES REALIZADOS EN OTRAS OFICINAS (documentos patentes, literatura no patente etc...)

Oficina	Fecha del examen o de reporte de búsqueda de documentos	Anterioridades encontradas para el examen o reportados en el examen de búsqueda(relacionarlos todos)	Reiv. afectadas	RELEVANCIA (requisito que afecta)	FUERON TENIDOS EN CUENTA PARA EL EXAMEN EN LA OFICINA COLOMBIANA	
					SI	NO
INTERNATIONAL SEARCH REPORT EPO	31/Agosto/ 2015	DATABASE EMBL 1 JUNE 2010 "Streptomyces sviveus ATCC 29083. 3-phosphoshikimate 1-carboxyvinyltransferase. EMBL: EDY54343.	1 - 3	Novedad	X	
		DATABASE EMBL 1 JULY 2011 "Amycolatopsis mediterranei S699. 3-phosphoshikimate 1-carboxyvinyltransferase. EMBL: AEK46452.	1 - 3	Novedad		X
		Verma <i>et al.</i> , 2011. Whole Genome Sequence of the Rifamycin B-Producing Stain Amycolatopsis mediterranei S699.	4 - 13	Nivel inventivo		X
		DATABASE EMBL 26 JANUARY 2011 "Streptomyces pratensis ATCC 33331. 3-phosphoshikimate 1-carboxyvinyltransferase. EMBL: ADW03091	1 - 3	Novedad		X
USPTO	18/Septiembre/ 2015	US2007300326	1, 2, 4 - 9, 10 - 24, 29 - 37	Nivel inventivo	X	
		US2009093366	1, 2, 4 - 9, 10 - 24, 29 - 37	Nivel inventivo	X	

DOCUMENTOS ADICIONALES ENCONTRADOS POR EL EXAMINADOR DE ACUERDO A LOS CRITERIOS DE BÚSQUEDA.

US20110209246
US7517684
WO2009099580
US7507875
US2009093366
US2007300326
US7169970
US5510471

US20110023179					
US5633435					
US2007289035					
US2006150270					
US2006253921					
WO2007053482					
US2006225147					
US2003009783					
WO0012732					
WO0031282					
US2006242727					
US2010186125					
US2011321187					
US2010251432					
Vaithanomsat & Brown, 2007. Isolation and mutation of recombinant EPSP synthase from pathogenic bacteria <i>Pseudomonas aeruginosa</i>					
BÚSQUEDA DE SECUENCIAS Número de depósito / patente y N° de secuencia % de identidad					
SEQ ID NO (de la solicitud)	NCBI	The Lens	EMBL-EBI	DDJB	Genome Quest
SEC ID NO: 1	gb EDY54343.1 100% de identidad y cobertura				
SEC ID NO: 67	ref WP_042498271.1 100% de identidad y cobertura				
SEC ID NO: 68	ref WP_006127956.1 100% de identidad y cobertura				
SEC ID NO: 145	ref WP_014153759.1 100% de identidad y cobertura				
SEC ID NO: 146	ref WP_015660246.1 100% de identidad y cobertura				
SEC ID NO: 147	emb HE971709.1 100% de identidad y cobertura				
SEC ID NO: 148	ref WP_006379385.1 100% de identidad y cobertura				
SEC ID NO: 150	ref WP_010350151.1 100% de identidad y cobertura				
SEC ID NO: 152	gb EKX63541.1 100% de identidad y cobertura				
SEC ID NO: 154	ref WP_007452659.1 100% de identidad y cobertura				
SEC ID NO: 156	ref WP_014048642.1				

	100% de identidad y cobertura				
SEC ID NO: 158	ref WP_010061898.1 100% de identidad y cobertura				
SEC ID NO: 161	emb FR845719.1 100% de identidad y cobertura				
SEC ID NO: 162	gb EGE41430.1 100% de identidad y cobertura				
SEC ID NO: 164	ref WP_013229519.1 100% de identidad y cobertura				
SEC ID NO: 165	gb CP003777.1 100% de identidad y cobertura				
SEC ID NO: 166	ref WP_014145284.1 100% de identidad y cobertura				
SEC ID NO: 168	ref WP_014135045.1 100% de identidad y cobertura				
SEC ID NO: 169	dbj AP010968.1 100% de identidad y cobertura				

Búsqueda de Secuencias

SEC ID NO: 1

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected:0

Alignments								Download	GenPept	Graphics	Distance tree of results	Multiple alignment	
	Description	Max score	Total score	Query cover	E value	Ident	Accession						
☐	3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sviveus ATCC 29083]	1346	1346	100%	0.0	100%	EDY54343.1						
☐	3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sviveus]	1335	1335	99%	0.0	100%	WP_037900119.1						
☐	3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sviveus]	86.8	86.8	57%	7e-18	43%	WP_007384592.1						
☐	glucose-6-phosphate dehydrogenase assembly protein OpcA [Streptomyces sviveus]	34.0	34.0	5%	0.072	60%	WP_007381232.1						
☐	glucose-6-phosphate dehydrogenase assembly protein OpcA [Streptomyces sviveus]	32.2	32.2	5%	0.24	55%	WP_007385996.1						
☐	oxidoreductase [Streptomyces sviveus ATCC 29083]	31.8	31.8	3%	0.34	69%	EDY60729.2						
☐	hypothetical protein [Streptomyces sviveus]	30.9	30.9	3%	0.60	63%	WP_007385828.1						
☐	conserved hypothetical protein [Streptomyces sviveus ATCC 29083]	29.6	29.6	2%	1.4	80%	EFH28996.1						
☐	UDP-glucose/GDP-mannose dehydrogenase [Streptomyces sviveus]	29.6	29.6	2%	1.6	90%	WP_007385832.1						
☐	hypothetical protein [Streptomyces sviveus]	29.1	29.1	4%	2.1	58%	WP_050789810.1						

Download

GenPept

Graphics

3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sviceus ATCC 29083]
Sequence ID: [gb|EDY54343.1](#) Length: 415 Number of Matches: 1

Range 1: 1 to 415 [GenPept](#) [Graphics](#)

Next Match

Previous Match

Score	Expect	Identities	Positives	Gaps
1346 bits(3054)	0.0	415/415(100%)	415/415(100%)	0/415(0%)
Query 1	MRGMPALSLPGSKSITARALFLAAAADGVTTLVRPLRSDDTEGFAEGLVRLGYRVGRTPD	60		
Sbjct 1	MRGMPALSLPGSKSITARALFLAAAADGVTTLVRPLRSDDTEGFAEGLVRLGYRVGRTPD	60		
Query 61	TWQVDGRPQGPAVAEADVYCRDGATTARFLPTLAAAGHGTYRFDASPMRRRPLLPLSRA	120		
Sbjct 61	TWQVDGRPQGPAVAEADVYCRDGATTARFLPTLAAAGHGTYRFDASPMRRRPLLPLSRA	120		
Query 121	LRDLGVDLRHEEAEGHHPLTVRAAGVEGGEVTLDAQSSQYLTAALLLGLTRQGLRIRV	180		
Sbjct 121	LRDLGVDLRHEEAEGHHPLTVRAAGVEGGEVTLDAQSSQYLTAALLLGLTRQGLRIRV	180		
Query 181	TDLVSAPYVEITLAMMRAFGVEVAREGDVVFVPPGGYRATTYAIEPDASTASYFFAAAAL	240		
Sbjct 181	TDLVSAPYVEITLAMMRAFGVEVAREGDVVFVPPGGYRATTYAIEPDASTASYFFAAAAL	240		
Query 241	TPGAEVTVPGLGTGALQGD LGFVDVLRMGAEVSVGADATTVRG TGELRGLTANMRDISD	300		
Sbjct 241	TPGAEVTVPGLGTGALQGD LGFVDVLRMGAEVSVGADATTVRG TGELRGLTANMRDISD	300		
Query 301	TMPTLAAIAPFASAPVRIEDVANTRVKECDRLEACAENLRRLGVRVATGPDWIEIHPGPA	360		
Sbjct 301	TMPTLAAIAPFASAPVRIEDVANTRVKECDRLEACAENLRRLGVRVATGPDWIEIHPGPA	360		
Query 361	TGAQVTSYGDHRIVMSFAVTGLRVPGISFDDPGCVRKTFPGFHEAFELRRGIGS	415		
Sbjct 361	TGAQVTSYGDHRIVMSFAVTGLRVPGISFDDPGCVRKTFPGFHEAFELRRGIGS	415		

SEC ID NO: 67

Sequences producing significant alignments:

Select: All None Selected:0

Alignments							Download	GenPept	Graphics	Distance tree of results	Multiple alignment	
	Description	Max score	Total score	Query cover	E value	Ident	Accession					
☐	3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces griseus]	237	237	100%	2e-69	100%	WP_042498271.1					
☐	putative 5-enolpyruvylshikimate-3-phosphate synthase [Streptomyces griseus subsp. griseus NBRC 13350]	237	237	100%	2e-69	100%	BAG18653.1					
☐	3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces griseus]	229	229	100%	2e-66	97%	WP_030704953.1					
☐	3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces griseus]	222	222	100%	5e-64	96%	WP_030715753.1					
☐	3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces griseus]	221	221	100%	1e-63	94%	WP_044375761.1					
☐	MULTISPECIES: 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces]	214	214	100%	3e-61	92%	WP_030344107.1					
☐	MULTISPECIES: 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces]	214	214	100%	3e-61	92%	WP_030197640.1					
☐	3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces griseus]	182	182	100%	4e-50	83%	WP_037676367.1					
☐	3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces griseus]	167	167	97%	8e-45	79%	WP_030754114.1					
☐	cystathionine gamma-synthase [Streptomyces griseus]	34.4	34.4	31%	0.055	63%	WP_030845870.1					

3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces griseus]
Sequence ID: [ref|WP_042498271.1](#) Length: 412 Number of Matches: 1

Range 1: 57 to 128 [GenPept](#) [Graphics](#)

Next Match

Previous Match

Score	Expect	Identities	Positives	Gaps
237 bits(534)	2e-69	72/72(100%)	72/72(100%)	0/72(0%)
Query 1	DRWRVEGRPDGPAAPDADVYCRDGATTARFLPTLVAAAASGTYRFDASAQMRRRPLAPLT	60		
Sbjct 57	DRWRVEGRPDGPAAPDADVYCRDGATTARFLPTLVAAAASGTYRFDASAQMRRRPLAPLT	116		
Query 61	RALTALGVDLRH	72		
Sbjct 117	RALTALGVDLRH	128		

SEC ID NO: 68

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment							
Description		Max score	Total score	Query cover	E value	Ident	Accession
☐ MULTISPECIES: 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces]		235	235	100%	1e-69	100%	WP_006127956.1
☐ MULTISPECIES: transcriptional regulator [Streptomyces]		28.7	28.7	27%	0.44	60%	WP_010071500.1
☐ conserved hypothetical protein [Streptomyces roseosporus NRRL 15998]		28.7	28.7	27%	0.44	60%	EFE76234.1
☐ acetylxylian esterase [Streptomyces filamentosus]		27.4	27.4	22%	1.1	67%	WP_006127333.1
☐ MULTISPECIES: hypothetical protein [Streptomyces]		27.4	27.4	29%	1.1	52%	WP_024263184.1
☐ hypothetical protein [Streptomyces filamentosus]		27.4	27.4	29%	1.1	52%	WP_006122654.1
☐ hypothetical protein [Streptomyces filamentosus]		26.9	26.9	13%	1.5	80%	WP_010070484.1
☐ conserved hypothetical protein [Streptomyces roseosporus NRRL 15998]		26.9	26.9	13%	1.5	80%	EFE73991.1
☐ ATP utilizing protein [Streptomyces roseosporus NRRL 15998]		26.5	26.5	15%	2.1	73%	EFE79249.1
☐ ATP utilizing protein [Streptomyces filamentosus]		26.5	26.5	15%	2.1	73%	WP_010072932.1

MULTISPECIES: 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces]

Sequence ID: [ref|WP_006127956.1|](#) Length: 426 Number of Matches: 1

[▶ See 2 more title\(s\)](#)

Range 1: 57 to 128 [GenPept](#) [Graphics](#)

[▼ Next Match](#) [▲ Previous Match](#)

Score		Expect	Identities	Positives	Gaps
235 bits(530)		1e-69	72/72(100%)	72/72(100%)	0/72(0%)
Query	1	DRWRVQGRPAGPAATEADVYCRDGATTARFLPTLAAAAASGTYRFDASAQMRRRPLAPLT			60
Sbjct	57	DRWRVQGRPAGPAATEADVYCRDGATTARFLPTLAAAAASGTYRFDASAQMRRRPLAPLT			116
Query	61	RALTALGVDLRH			72
Sbjct	117	RALTALGVDLRH			128

SEC ID NO: 146

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment							
Description		Max score	Total score	Query cover	E value	Ident	Accession
☐ 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces davawensis]		1336	1336	100%	0.0	100%	WP_015660246.1
☐ 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces davawensis]		75.8	75.8	58%	2e-14	42%	WP_015657929.1
☐ hypothetical protein [Streptomyces davawensis]		30.9	30.9	3%	0.60	73%	WP_015662907.1
☐ binding-protein dependent transporter [Streptomyces davawensis]		30.5	30.5	3%	0.81	73%	WP_015657743.1
☐ membrane protein [Streptomyces davawensis]		30.5	30.5	5%	0.83	60%	WP_015656270.1
☐ hybrid non-ribosomal peptide synthase/polyketide synthase [Streptomyces davawensis]		30.5	30.5	5%	0.86	48%	WP_015660593.1
☐ transcriptional regulator [Streptomyces davawensis]		30.0	30.0	8%	1.1	48%	WP_015659763.1
☐ LLM class F420-dependent oxidoreductase [Streptomyces davawensis]		30.0	30.0	2%	1.1	91%	WP_015656765.1
☐ pectate lyase [Streptomyces davawensis]		30.0	30.0	4%	1.1	65%	WP_015661338.1
☐ translation initiation factor IF-2 [Streptomyces davawensis]		29.6	29.6	4%	1.6	62%	WP_015657491.1

3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces davawensis]

Sequence ID: [ref|WP_015660246.1|](#) Length: 410 Number of Matches: 1

► [See 1 more title\(s\)](#)

Range 1: 1 to 410 [GenPept](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
1336 bits(3032)	0.0	410/410(100%)	410/410(100%)	0/410(0%)
Query 1	MPVADIPGSKSITARALFLAAAADGVTTTLVRPLRSDDTEGFAEGLARLGYRVGRTPDSWQ	60		
Sbjct 1	MPVADIPGSKSITARALFLAAAADGVTTTLVRPLRSDDTEGFAEGLARLGYRVGRTPDSWQ	60		
Query 61	VDGRPQGPVAEADVYCRDGATTARFLPTLAAAGHGTYRFDASEQMRRLPLPLTRALRE	120		
Sbjct 61	VDGRPQGPVAEADVYCRDGATTARFLPTLAAAGHGTYRFDASEQMRRLPLPLTRALRE	120		
Query 121	LGVDLRHEERDGHHP LTVRAAGVAGGEVTL DAGQSSQYLTALLLGLPTEKGLRIHVTDL	180		
Sbjct 121	LGVDLRHEERDGHHP LTVRAAGVAGGEVTL DAGQSSQYLTALLLGLPTEKGLRIHVTDL	180		
Query 181	VSVPYIEITLAMMRAFGVEVTREGHDFVVP PGGYRATTYAIEPDASTSSYFFAAAALSGG	240		
Sbjct 181	VSVPYIEITLAMMRAFGVEVTREGHDFVVP PGGYRATTYAIEPDASTSSYFFAAAALSGG	240		
Query 241	EVTVPGLGEGALQGDLGFVDVLR RMGAEEVIGADR TTVRG TGELRGLTVNM RDISDTMPT	300		
Sbjct 241	EVTVPGLGEGALQGDLGFVDVLR RMGAEEVIGADR TTVRG TGELRGLTVNM RDISDTMPT	300		
Query 301	LAAIAPFASGPVRIEDVANTRVKECDRLEACAENLRRLGVRVETGPDWIEIHPGATPTGA	360		
Sbjct 301	LAAIAPFASGPVRIEDVANTRVKECDRLEACAENLRRLGVRVETGPDWIEIHPGATPTGA	360		
Query 361	EIKTYGDHRIVMSFAVTGLRVPGISFDDPGCVRKTFPGFHEEFGALRARL	410		
Sbjct 361	EIKTYGDHRIVMSFAVTGLRVPGISFDDPGCVRKTFPGFHEEFGALRARL	410		

SEC ID NO: 147

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Streptomyces davawensis strain JCM 4913 complete genome	2278	2278	100%	0.0	100%	HE971709.1
☐	Streptomyces glaucescens strain GLA.O, complete genome	1413	1573	99%	0.0	88%	CP009438.1
☐	Streptomyces reticuli genome assembly TUE45, chromosome 1	1232	1232	98%	0.0	85%	LN997842.1
☐	Streptomyces sp. PBH53 genome	1227	1274	98%	0.0	85%	CP011799.1
☐	Streptomyces sp. CdTB01, complete genome	1179	1226	98%	0.0	84%	CP013743.1
☐	Streptomyces incarnatus strain NRRL 8089 sequence	1175	1277	97%	0.0	84%	CP011497.1
☐	Streptomyces griseus subsp. griseus NBRC 13350 DNA, complete genome	974	1019	98%	0.0	81%	AP009493.1
☐	Streptomyces globisporus C-1027, complete genome	968	1014	97%	0.0	81%	CP013738.1
☐	Streptomyces sp. SirexAA-E, complete genome	948	1043	96%	0.0	81%	CP002993.1
☐	Streptomyces sp. PAMC26508, complete genome	941	988	97%	0.0	81%	CP003990.1

SEC ID NO: 172

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Sequence 21418 from patent US 8299318	26.9	26.9	78%	4.4	73%	AFX34323.1
☐	Sequence 67423 from patent US 8344211	26.5	26.5	78%	5.8	75%	AGD62781.1
☐	Sequence 116322 from patent US 7214786	26.1	26.1	78%	8.5	73%	ABT28852.1
☐	unnamed protein product [Mycobacterium avium 104]	26.1	26.1	92%	8.8	69%	CAY03270.1

Búsqueda en PatBase



Username: SIC3@patbase.com
Subaccount: Mario Forero

Menu - Search - History - Session - Folder - Order - Help - Logout

Search 5: TAC=(((GLYPHOSATE~ AND RESISTANCE~ AND GENES~) AND (EPSPS~)))
Results 154

Explore search

Edit and resend search

#	Search query	Results	Options
5	TAC=(((GLYPHOSATE~ AND RESISTANCE~ AND GENES~) AND (EPSPS~)))	154	View Browse Hits Optimise more...
4	TAC=(((GLYPHOSATE~ AND RESISTANCE~ AND GENES~) AND (HERBICIDE~ AND RESISTANCE~)))	1230	View Browse Hits Optimise more...
3	TAC=(((EPSPS~ AND POLYNUCLEOTIDE~) AND (GLYPHOSATE~ AND RESISTANCE~)))	74	View Browse Hits Optimise more...
2	TAC=(((EPSPS~ AND CLASS~ IV~) AND (HERBICIDE~ AND RESISTANCE~)))	1	View Browse Hits Optimise more...
1	TAC=(((EPSPS~ AND GENES~) AND (HERBICIDE~ AND RESISTANCE~)))	162	View Browse Hits Optimise more...

Information Shortcuts

Command Reference

- Bibliographic data
- Textual data
- Update commands
- Operators
- Navigation / shortcuts

3) Family number: 11582626 (US6566587B)

Similar • Translate • Full-text • Status • Citations

Title: [EN] MUTATED 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE, GENE CODING FOR SAID PROTEIN AND TRANSFORMED PLANTS CONTAINING SAID GENE

Abstract: Source: US6566587B [EN] The present invention relates to DNA molecules of plant origin encoding a modified 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) enzyme wherein the first EPSPS coding sequence that normally encodes a threonine residue of a mature EPSPS sequence is modified to encode isoleucine of the mature EPSPS sequence, and a second EPSPS coding sequence that normally encodes a proline residue of a mature EPSPS sequence is modified to encode serine of the mature EPSPS sequence, wherein the first and second residues are respectively located at relatively positions 102 and 106 of a mature EPSPS sequence encoded by said DNA molecule; and the production of a transgenic plant resistant or tolerant to a herbicide of the phosphonemethylglycine family, e.g., glyphosate. The mutated enzyme, which substantially maintains the catalytic activity of the wild-type enzyme, allows for increased tolerance or tolerance of the plant to a herbicide of the phosphonemethylglycine family, and allows for the substantially normal growth or development of the plant, its organs, tissues or cells.

Classifications: Classification Explorer

International (IPC 8-9): A01H1/00 A01H5/00 A01M21/04 A01N63/02 C12N15/09 C12N15/29 C12N15/52 C12N15/54 C12N15/82 C12N5/10 C12N9/10 C12N9/12 (Advanced/Invention);

A01H5/00 A01N63/02 C12N15/09 C12N15/54 C12N5/10 C12N9/10 (Advanced/Non-invention);
A01H5/00 A01N63/02 C12N15/09 C12N15/29 C12N15/54 C12N15/82 C12N5/10 C12N9/10 (Core/Invention)

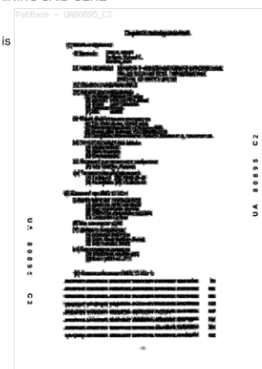
International (IPC 1-7): A01H1/06 A01H4/00 A01H5/00 A01N63/02 C07H21/04 C12N15/09 C12N15/29 C12N15/54 C12N15/82 C12N5/10 C12N9/10
CPC: C12N9/1092 C12N15/8275

European: C12N15/82C8B4 C12N9/10E19 M12N207/00

US: 435/320.1 435/419 47/58.1 47/58.10R 47/58.1R 536/23.6 800/278 800/287 800/300 800/320.1

Family: Family Explorer

Publication number	Publication date	Application number	Application date	Links
AP886 A	20001103	AP19980001195	19960718	
AP9801195 A0	19980331	AP19980001195	19960718	
AT320494 E	20060415	AT19960130564T	19960718	
AT321866 E	20060415	AT19960925812T	19960718	



4) Family number: 33973069 (US2003041357A)

Similar • Translate • Full-text • Status • Citations

Title: [EN] Herbicide resistant plants

Abstract: Source: US2003041357A [EN] The present invention provides inter alia, a polynucleotide comprising at least a first region encoding a first protein capable of conferring on a plant, or tissue comprising it, resistance or tolerance to a first herbicide, and a second region encoding a second protein likewise capable of conferring resistance to a second herbicide, with the provisos (i) that the polynucleotide does not encode a fusion protein comprising only a 5-enol-pyruvyl-3-phosphoshikimate synthetase (EPSPS) and a glutathione S transferase (GST); (ii) that the polynucleotide does not comprise only regions encoding superoxide dismutase (SOD) and glutathione S transferase (GST), and (iii) that the polynucleotide does not comprise only regions encoding GST and phosphinothricin acetyl transferase (PAT).

Classifications: Classification Explorer

International (IPC 8-9): A01H1/00 A01H5/00 C07H21/04 C07K14/415 C12N15/09 C12N15/52 C12N15/53 C12N15/54 C12N15/55 C12N15/60 C12N15/82 C12N5/04 C12N5/10 C12N5/14 C12N9/00 C12N9/02 C12N9/06 C12N9/10 C12N9/78 C12N9/88 (Advanced/Invention);

A01H5/00 C12N15/09 C12N15/53 C12N15/52 C12N5/10 (Advanced/Non-invention);
A01H1/00 A01H5/00 C07H21/00 C07K14/415 C12N15/53 C12N15/54 C12N15/55 C12N15/60 C12N15/82 C12N5/04 C12N9/00 C12N9/02 C12N9/06 C12N9/10 C12N9/78 C12N9/88 (Core/Invention)

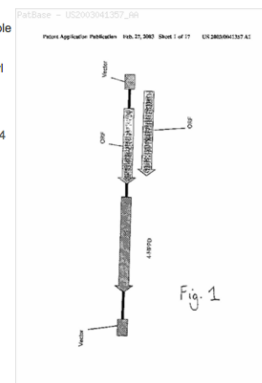
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European: C07K14/415 C12N15/82C8B4 C12N15/82C8B4A C12N15/82C8B4B C12N9/00P C12N9/00P28 C12N9/00P30E C12N9/00P32 C12N9/00P6 C12N9/00P8 C12N9/10C1 C12N9/10E C12N9/10E18 C12N9/10E19 C12N9/78 C12N9/88 C12N9/93 M12N207/00

US: 435/320.1 435/320.100S 435/419 435/419S 435/468 435/468S 536/23.2 536/23.200S 536/23.7 536/23.700S 536/237 800/278 800/278P 800/278S 800/300 800/300P

Family: Family Explorer

Publication number	Publication date	Application number	Application date	Links
AU199747895 A1	19980529	AU19970047895	19971031	
BG103462 A	20000131	BG19990103462	19990603	
BRPI9712695 A	19991019	BR1997P112695	19971031	

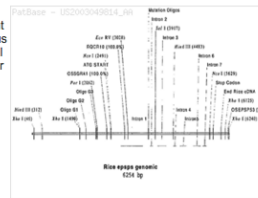


11) Family number: 30909154 (US2003049814A)

Similar • Translate • Full-text • Status • Citations

Title: [EN] Herbicide resistant plants

Abstract: Source: US2003049814A [EN] The present invention provides, inter alia, an isolated polynucleotide comprising a region encoding a chloroplast transit peptide and a glyphosate resistant 5-enolpyruvylshikimate phosphate synthase (EPSPS) 3' of the peptide, the said region being under expression control of a plant operable promoter, with the proviso that the said promoter is not heterologous with respect to the said region, and the chloroplast transit peptide is not heterologous with respect to the said synthase. The polynucleotide may comprise the following components in the 5' to 3' direction of transcription: (i) at least one transcriptional enhancer being that enhancing region which is upstream from the transcriptional start of the sequence from which the enhancer is obtained and which enhancer per se does not function as a promoter either in the sequence in which it is endogenously comprised or when present heterologously as part of a construct; (ii) the promoter from the rice EPSPS gene; (iii) the rice genomic sequence which encodes the rice EPSPS chloroplast transit peptide; (iv) the genomic sequence which encodes the rice EPSPS; (v) a transcriptional terminator, wherein the rice EPSPS coding sequence is modified in that a first position is mutated so that the residue at this position is le rather than Thr and a second position is mutated so that the residue at this position is Ser rather than Pro, the mutations being introduced into EPSPS sequences which comprise the following conserved region GNAGTAMRPLTAAV (SEQ ID NO:41) in the wild type enzyme such that modified sequence reads GNAGIAMSLLTAAV (SEQ ID NO:42).



Classifications: Classification Explorer

International *epc* s-aj: A01H5/00 A01N57/16 C12N15/09 C12N15/54 C12N15/82 C12N5/10 C12N9/10 C12Q1/04 (Advanced/Invention);

A01H5/00 A01N57/00 C12N15/09 C12N15/54 C12N15/82 C12N5/10 C12N9/10 C12Q1/04 (Core/Invention);

A01H C12N (Subclass/Invention)

International *epc* 1-7j: A01H A01H1/00 A01H5/00 A01N57/16 C07H21/04 C12N C12N15/09 C12N15/54 C12N15/82 C12N5/04 C12N5/10 C12N9/00 C12N9/10 C12N9/16 C12P21/02 C12Q1/04

CPC: C12N9/1092 C12N15/8209 C12N15/8275

European: C12N15/82A8 C12N15/82C8B4A C12N9/10E19 M12N207/00

US: 435/183 435/183P 435/196 435/196S 435/320.1 435/320.100S 435/410 435/410S 435/69.1 435/69.100S 536/23.2 536/23.200S 800/278 800/278P 800/278S 800/320.2 800/320.200S

Family: Family Explorer

Publication number	Publication date	Application number	Application date	Links
AR029628 AA	20030710	AR2000P102085	20000428	
AR029748 AA	20030716	AR2000P102087	20000428	

22) Family number: 32314187 (CN1664095A)

Similar • Translate • Full-text • Status • Citations

Title: [EN] EPSP synthase of variable halomonas high resistance glyphosate and its encoding sequence

Abstract: Source: CN1664095A [EN] The invention discloses a novel 5-enol pyruvyl shikimate3-phosphate (EPSP), the polynucleotide for encoding the EPSP and the method for producing the EPSP through recombination technology. The invention also discloses the use of the polynucleotide for encoding the EPSP.

Classifications: Classification Explorer

International *epc* s-aj: C07K14/195 C07K16/40 C12N15/52 C12N15/64 C12N15/82 C12N5/04 C12N9/00 (Advanced/Invention);

C07K14/195 C07K16/40 C12N15/52 C12N15/64 C12N15/82 C12N5/04 C12N9/00 (Core/Invention)

International *epc* 1-7j: C07K14/195 C07K16/40 C12N15/52 C12N15/64 C12N15/82 C12N5/04 C12N9/00

Family: Family Explorer

Publication number	Publication date	Application number	Application date	Links
CN1289664 C	20061213	CN200410016636	20040301	
CN1664095 A	20050907	CN200410016636	20040301	

Priority: Priority Map

CN200410016636 20040301

Probable Assignee: BIOTECHNOLOGY RES INST CAAS

Assignee(s): (std): BIOTECHNOLOGY RES INST CAAS ; BIOTECHNOLOGY RESEARCH INSTITUTE CAAS

Assignee(s): BIOTECHNOLOGY RESEARCH INST CAAS

Inventor(s): (std): LIN MIN ; LIN MIN LIU ; LIU ZHU ; MIN LIN ; ZHU LIU

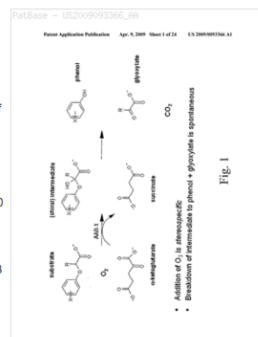
Inventor(s): MIN LIU LIN

25) Family number: 32396701 (US2009093366A)

Similar • Translate • Full-text • Status • Citations

Title: [EN] NOVEL HERBICIDE RESISTANCE GENES

Abstract: Source: US2009093366A [EN] The subject invention provides novel plants that are not only resistant to 2,4-D and other phenoxy auxin herbicides, but also to aryloxyphenoxypropionate herbicides. Heretofore, there was no expectation or suggestion that a plant with both of these advantageous properties could be produced by the introduction of a single gene. The subject invention also includes plants that produce one or more enzymes of the subject invention alone or "stacked" together with another herbicide resistance gene, preferably a glyphosate resistance gene, so as to provide broader and more robust weed control, increased treatment flexibility, and improved herbicide resistance management options. More specifically, preferred enzymes and genes for use according to the subject invention are referred to herein as AAD (aryloxyalkanoate dioxygenase) genes and proteins. No alpha-ketoglutarate-dependent dioxygenase enzyme has previously been reported to have the ability to degrade herbicides of different chemical classes and modes of action. This highly novel discovery is the basis of significant herbicide tolerant crop trait opportunities as well as development of selectable marker technology. The subject invention also includes related methods of controlling weeds. The subject invention enables novel combinations of herbicides to be used in new ways. Furthermore, the subject invention provides novel methods of preventing the formation of, and controlling, weeds that are resistant (or naturally more tolerant) to one or more herbicides such as glyphosate.



Classifications: Classification Explorer

International *epc* s-aj: A01H1/00 A01H5/00 A01N25/00 A01N25/32 A01N37/00 A01N37/34 A01N39/02 A01N39/04 A01N43/40 A01N43/50 A01N43/60 A01N47/34 A01N47/36 A01N57/20 A01P13/00 A01P13/02 C07H21/04 C12N15/09 C12N15/51 C12N15/52 C12N15/53 C12N15/82 C12N15/84 C12N5/10 C12N9/00 C12N9/02 C12N9/04 C12Q1/68 G01N33/53 (Advanced/Invention);

A01H5/00 C12N15/00 (Core/Invention);

A01H C12N (Subclass/Invention)

International *epc* 1-7j: A01H1/00 A01H5/00 C12N5/10

CPC: C12N15/8274 C12N9/0069 C12N9/0071 C12N15/8209 C12N15/8241 C12N15/8286 C12N15/8282 C12N15/8271 C12N15/8261 C12N15/8247 C12N15/8283

C12N15/8249 C12N15/8273 C12N15/8255

European: C12N15/82A8 C12N15/82C8B4 C12N9/00P28 C12N9/00P30

US: 435/412 435/412S 435/414 435/414S 435/415 435/415S 435/419 435/419S 435/6 435/6.12 435/6.120S 435/6S 436/501 436/501S 504/142 504/206 504/317

504/317S 504/323 504/323S 504/329 504/329S 536/23.2 536/23.200S 800/288 800/298 800/300 800/300S

Family: Family Explorer

26) Family number: 33000630 (US2006225147A)

Similar • Translate • Full-text • Status • Citations

Title: [EN] GLYPHOSATE-RESISTANT PLANTS

Abstract: Source: US2006225147A [EN] This invention relates to glyphosate-resistant transgenic plants and methods of making the same. In a preferred embodiment, a DNA fragment which comprises an EPSPS 5' regulatory sequence and a glyphosate-resistant EPSPS coding sequence is introduced into regenerable plant cells. The encoded EPSPS has a chloroplast transit peptide. The DNA fragment does not contain a non-EPSPS enhancer. Cells are selected for stable transformation, and the selected cells can be used to regenerate glyphosate-resistant transgenic plants. The DNA fragment used for transformation preferably comprises a modified plant genomic sequence, such as SEQ ID NO: 2, SEQ ID NO:4 or SEQ ID NO: 6. In one embodiment, two DNA fragments of this invention are stably transformed into a plant to confer glyphosate-resistance.

Classifications: Classification Explorer

International *epc* s-aj: A01H1/00 A01H5/00 C12N15/82 C12N5/04 (Advanced/Invention);

A01H1/00 A01H5/00 C12N15/82 C12N5/04 (Core/Invention)

CPC: C12N15/8275

European: C12N15/82C8B4A

US: 435/415 435/419 435/468 800/278 800/300 800/312

Family: Family Explorer

Publication number	Publication date	Application number	Application date	Links
US2006225147 AA	20061005	US20060409909	20060424	
US7045684 BA	20060516	US20020223241	20020819	
US7626077 BB	20091201	US20060409909	20060424	
USRE41943 E	20101116	US20090633520	20091208	