

Case 3:

**A transgenic plant and the method for producing the same
EpiPlanta Biotech Ltd.**

Claims:

- 1. A transgenic plant in which a nucleic acid molecule encoding an m6A demethylase is introduced, wherein said m6A demethylase has the following two domains:
 - i) N-terminal domain (NTD) having the function of AlkB oxidation demethylase; and**
 - ii) C-terminal domain (CTD).****
- 2. The transgenic plant of claim 1, wherein said m6A demethylase is FTO (fatmass and obesity-associated) protein.**
- 3. The transgenic plant of claim 2, wherein said FTO protein is from vertebrates or marine algae.**

4. The transgenic plant of claim 3, wherein said FTO protein has at least 40% , ..., most preferably 100% identity to any of the **SEQ ID NOs: 1-4**

5. The transgenic plant of any of the claims 1-4, wherein said nucleic acid molecule encoding the m6A demethylase has at least 90%, ..., most preferably 100% identity to any one of **SEQ ID NOs: 5-12**

...

8. A tissue, an organ, a pollen, a seed, a grain or a fruit of the plant of any of the claims 1-7

9. A plant cell...

...

15. A method for producing a transgenic plant...

SEQ ID NOs 1-4 (protein) and 5-12 (nucleic acids) are retrieved from lens.org:

<https://www.lens.org/lens/patent/196-196-347-571-28X/sequences>

Questions:

- 1) What is the technical problem and does the first claim solve it?**
- 2) What is the difference between m6A demethylase, AlkB oxidation demethylase and FTO?**
- 3) Does 40% sequence ID in claim 4 makes sense?**
- 4) How conserved are (the claimed) m6A demethylases?**
- 5) What about the nucleic acid 90% identity in claim 5?**
- 6) Are the sequence searches the right approach to find prior art?**
- 7) Are there some claims which may fall under patentability exceptions, e.g. EPC Art 53 (b)?**
- 8) Is the unity of the claims given?**

Question

1) *What is the technical problem and does the first claim solve it?*

Problem

Low yield of biomass of „agricultural plants“ with state of the art breeding or transgenic approaches

Solution

Claim 1 features a transgenic plant having nucleic acid sequence coding for a m6A demethylase with an N-terminal being an AlkB oxidative demethylase and a C-terminal domain (not mentioning its function).

→ According to the description claim 1 solves the problem by introduction of a AlkB like m6A demethylase. This enzyme is known to remove the methyl group on adenosine in mRNA and has been termed fatmass obesity-associated (FTO) protein.

The applicant refers to Jia et al., Nat Chem Biol, 2011; <https://www.ncbi.nlm.nih.gov/pubmed/22002720>

“FTO belongs to the non-heme Fe^{II}/α-KG-dependent dioxygenase AlkB family proteins”

Uniprot link to the human AlkB (check for prior art): <https://www.uniprot.org/uniprot/Q9C0B1>

Question

2) *What is the difference between m6A demethylase, AlkB oxidation demethylase and FTO?*

M6A demethylases

<https://enzyme.expasy.org/EC/1.14.11.51>

N(6)-methyladenine in **DNA** + 2-oxoglutarate + O(2) \rightleftharpoons adenine in DNA + formaldehyde + succinate + CO(2)

<https://enzyme.expasy.org/EC/1.14.11.53>

N(6)-methyladenosine in **mRNA** + 2-oxoglutarate + O(2) \rightleftharpoons adenosine in mRNA + formaldehyde + succinate + CO(2)

It might be good to check further background citation on **EC 1.14.11.53**

...

Question

3) Does 40% sequence ID in claim 4 makes sense?

Get sequences (do not type it in the form, they are too long and you might introduce mistakes)

[US 2018/0340182 A1](https://www.uspto.gov/patent/publications/US_2018_0340182_A1)

<https://www.lens.org/lens/patent/196-196-347-571-28X/sequences>

To answer this question you have to ask:

4) How conserved are (the claimed) m6A demethylases?

<https://www.ebi.ac.uk/Tools/msa/clustalo/>

CLUSTAL O(1.2.4) multiple sequence alignment

```
US_2018_0340182_A1_1 MKRTPAEEREREAKKLRLLLEELEDTWLPYLTPKDDEFYQQWQLKYPKLILREASSVSEE 60
US_2018_0340182_A1_2 MKRTPAEEREREGAKKLRLLLEELEDTWLPYLTPKDDEFYQQWQLKYPKLILREAGSVPEG 60
US_2018_0340182_A1_3 MKRTPAEEREREAKKLRLLLEELEDTWLPYLTPKDDEFYQQWQLKYPKLILREAASVPEL 60
*****
```

Percent Identity Matrix - created by Clustal2.1 # #

1: US_2018_0340182_A1_1	100.00	88.71	87.72	human
2: US_2018_0340182_A1_2	88.71	100.00	90.10	pig
3: US_2018_0340182_A1_3	87.72	90.10	100.00	cow

> 87% SEQ ID

Question

- 3) Does 40% sequence ID in claim 4 makes sense?
- 4) How conserved are (the claimed) m6A demethylases?

SEQ ID NO: 4 is not of vertebrate origin but marine algae

<https://www.ebi.ac.uk/Tools/msa/clustalo/>

```

US_2018_0340182_A1_4 -----MSPSSSVLEPEDGEPFARVHRAHYRGEFVVDAPSVLPA 37
US_2018_0340182_A1_1 MKRTPAEEREREAKKLRLLEELEDTWLPYLTPKDD-EFYQQWQLKYPKLILREASSVSE 59
US_2018_0340182_A1_2 MKRTPAEEREREGAKKLRLLEELEDTWLPYLTPKDD-EFYQQWQLKYPKLILREAGSVPE 59
US_2018_0340182_A1_3 MKRTPAEEREREAKKLRLLEELEDTWLPYLTPKDD-EFYQQWQLKYPKLILREAASVPE 59
. * *:*. * : : :* ::: . :
```

1:	US_2018_0340182_A1_4	100.00	31.33	30.60	30.60
2:	US_2018_0340182_A1_1	31.33	100.00	88.71	87.72
3:	US_2018_0340182_A1_2	30.60	88.71	100.00	90.10
4:	US_2018_0340182_A1_3	30.60	87.72	90.10	100.00

Question

- 3) Does 40% sequence ID in claim 4 makes sense?
- 4) How conserved are (the claimed) m6A demethylases?

SEQ ID NO: 4 is not of vertebrate origin but marine algae

<https://www.ebi.ac.uk/Tools/msa/clustalo/>

```

US_2018_0340182_A1_4 -----MSPSSSVLEPEDGEPFARVHRAHYRGFVVDAPSVLPA 37
US_2018_0340182_A1_1 MKRTPAEEREREAKKLRLLEELEDTWLPYLTPKDD-EFYQQWQLKYPKLILREASSVSE 59
US_2018_0340182_A1_2 MKRTPAEEREREGAKKLRLLEELEDTWLPYLTPKDD-EFYQQWQLKYPKLILREAGSVPE 59
US_2018_0340182_A1_3 MKRTPAEEREREAKKLRLLEELEDTWLPYLTPKDD-EFYQQWQLKYPKLILREAASVPE 59
. * *:*. * : : :* ::: . :
```

1:	US_2018_0340182_A1_4	100.00	31.33	30.60	30.60
2:	US_2018_0340182_A1_1	31.33	100.00	88.71	87.72
3:	US_2018_0340182_A1_2	30.60	88.71	100.00	90.10
4:	US_2018_0340182_A1_3	30.60	87.72	90.10	100.00

... only **30-31% SEQ ID** algae to human/pig/cow

→ Probably yes, proteins are sometimes quite diverse on the level of sequence identity. However, the function can be highly conserved in some domain.

Question

5) What about the nucleic acid 90% identity in claim 5?

Difficult to predict... Get sequences from: <https://www.lens.org/lens/patent/196-196-347-571-28X/sequences>

There are per each protein two DNA sequences

- one of the natural (SEQ ID NOs: 5,7,9,11)
- one which has been codon optimised (SEQ ID NOs: 6,8,10,12) to enable or enhance expression in a plant (different codon usage).

→ The search using the **natural sequence is expected to give** documents describing the DNA sequence in its original... and might retrieve a **high number of documents...**

→ The search using the **codon optimised DNA** is likely to retrieve at **100% ID only the application...**

Does the sequence search really give you the necessary prior art?

Question

6) Are the sequence searches the right approach to find prior art?

Some considerations:

- If you search with the sequence of one organism, you will probably find a lot of documents describing this sequence in its natural context (protein and DNA).
- The inventive concept in this application is not the sequence per se but rather the fact, that it is introduced in a foreign organism (transgenic plant)
- It might be better to start with a keyword search using the right enzyme names / functions and include the concept of the transgenic plant or patent classes and citations in literature...

→ **Keyword and patent classes (transgenic plants and demethylases...)**

→ **Prior art in scientific journals**

→ **Citation analysis (cited, citing, backward or forward citation)**



Symbol	Classification and description	
<input type="checkbox"/> C12	BIOCHEMISTRY; BEER; SPIRITS; WINE; VINEGAR; MICROBIOLOGY; ENZYMOLOGY; MUTATION OR GENETIC ENGINEERING	i
<input type="checkbox"/> C12N	MICROORGANISMS OR ENZYMES; COMPOSITIONS THEREOF (biocides, pest repellants or attractants, or plant growth regulators, containing microorganisms, viruses, microbial fungi, enzymes, fermentates or substances produced by or extracted from microorganisms or animal material A01N 63/00 ; food compositions A21 , A23 ; medicinal preparations A61K ; chemical aspects of, or use of materials for, bandages, dressings, absorbent pads or surgical articles A61L ; fertilisers C05); PROPAGATING, PRESERVING OR MAINTAINING MICROORGANISMS (preservation of living parts of humans or animals A01N 1/02); MUTATION OR GENETIC ENGINEERING; CULTURE MEDIA (microbiological testing media C12Q)	S D i !
<input checked="" type="checkbox"/> C12N 15/00	Mutation or genetic engineering; DNA or RNA concerning genetic engineering, vectors, e.g. plasmids, or their isolation, preparation or purification; Use of hosts therefor (mutants or genetically engineered microorganisms, <i>per se</i> C12N 1/00 , C12N 5/00 , C12N 7/00 ; new plants <i>per se</i> A01H ; plant reproduction by tissue culture techniques A01H 4/00 ; new animals <i>per se</i> A01K 67/00 ; use of medicinal preparations containing genetic material which is inserted into cells of the living body to treat genetic diseases, gene therapy A61K 48/00)	D
<input checked="" type="checkbox"/> C12N 15/09	• Recombinant DNA-technology	D
<input checked="" type="checkbox"/> C12N 15/63	•• Introduction of foreign genetic material using vectors; Vectors; Use of hosts therefor; Regulation of expression	D
<input checked="" type="checkbox"/> C12N 15/79	••• Vectors or expression systems specially adapted for eukaryotic hosts	D i
<input checked="" type="checkbox"/> C12N 15/82	•••• for plant cells {, e.g. plant artificial chromosomes (PACs)}	D !
<input checked="" type="checkbox"/> C12N 15/8241	••••• {Phenotypically and genetically modified plants via recombinant DNA technology}	
<input checked="" type="checkbox"/> C12N 15/8242	•••••• {with non-agronomic quality (output) traits, e.g. for industrial processing; Value added, non-agronomic traits}	D
<input checked="" type="checkbox"/> C12N 15/8243	••••••• {involving biosynthetic or metabolic pathways, i.e. metabolic engineering, e.g. nicotine, caffeine}	

Symbol	Classification and description
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- C12
- C12N

- ▲ C12N 15/00
- C12N 15/09
- C12N 15/63
- C12N 15/79
- C12N 15/82
- C12N 15/824
- C12N 15/824
- C12N 15/8243

Symbol	Classification and description
--------	--------------------------------

- | | |
|--|---|
| | biosynthesis} |
| <input checked="" type="checkbox"/> C12N 15/8253 | ●●●●●●●● {Methionine or cysteine} |
| <input checked="" type="checkbox"/> C12N 15/8254 | ●●●●●●●● {Tryptophan or lysine} |
| <input checked="" type="checkbox"/> C12N 15/8255 | ●●●●●●●● {involving lignin biosynthesis} |
| <input checked="" type="checkbox"/> C12N 15/8257 | ●●●●●●●● {for the production of primary gene products, e.g. pharmaceutical products, interferon} |
| <input checked="" type="checkbox"/> C12N 15/8258 | ●●●●●●●● {for the production of oral vaccines (antigens) or immunoglobulins} |
| <input checked="" type="checkbox"/> C12N 15/8259 | ●●●●●●●● {Phytoremediation} |
| <input checked="" type="checkbox"/> C12N 15/8261 | ●●●●●●●● {with agronomic (input) traits, e.g. crop yield} |
| | non-agronomic traits} |
| ●●●●●●●● | {involving biosynthetic or metabolic pathways, i.e. metabolic engineering, e.g. nicotine, caffeine} |

Definitions

Glossary of terms

In this place, the following terms or expressions are used with the meaning indicated:

Input trait influences the input required for growth and development of the plant or its parts

- [Can I start a new search using the classifications listed?](#)
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Selected classifications

C12N15/8261 /low







C12N9/0071 /low

Clear

Find patents

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m6A demethylases
EC 1.14.11.53

Symbol	Classification and description	
<input type="checkbox"/> C12N	MICROORGANISMS OR ENZYMES; COMPOSITIONS THEREOF (biocides, pest repellants or attractants, or plant growth regulators, containing microorganisms, viruses, microbial fungi, enzymes, fermentates or substances produced by or extracted from microorganisms or animal material A01N 63/00 ; food compositions A21 , A23 ; medicinal preparations A61K ; chemical aspects of, or use of materials for, bandages, dressings, absorbent pads or surgical articles A61L ; fertilisers C05); PROPAGATING, PRESERVING OR MAINTAINING MICROORGANISMS (preservation of living parts of humans or animals A01N 1/02); MUTATION OR GENETIC ENGINEERING; CULTURE MEDIA (microbiological testing media C12Q)	   
<input type="checkbox"/> C12N 9/00	Enzymes; Proenzymes; Compositions thereof (preparations containing enzymes for cleaning teeth A61K 8/66 , A61Q 11/00 ; medicinal preparations containing enzymes or proenzymes A61K 38/43 ; enzyme containing detergent compositions C11D ; {enzymes with nucleic acid structure, e.g. ribozymes, C12N 15/113 }); Processes for preparing, activating, inhibiting, separating or purifying enzymes (preparation of malt C12C 1/00)	 
<input type="checkbox"/> C12N 9/0004	• {Oxidoreductases (1.)}	
<input checked="" type="checkbox"/> C12N 9/0071	•• {acting on paired donors with incorporation of molecular oxygen (1.14)}	
<input checked="" type="checkbox"/> C12N 9/0073	••• {with NADH or NADPH as one donor, and incorporation of one atom of oxygen 1.14.13}	
<input checked="" type="checkbox"/> C12N 9/0075	•••• {Nitric-oxide synthase (1.14.13.39)}	
<input checked="" type="checkbox"/> C12N 9/0077	••• {with a reduced iron-sulfur protein as one donor (1.14.15)}	
<input checked="" type="checkbox"/> C12N 9/0079	•••• {Steroid 11 beta monooxygenase (P-450 protein)(1.14.15.4)}	
<input checked="" type="checkbox"/> C12N 9/0081	•••• {Cholesterol monooxygenase (cytochrome P 450sc)(1.14.15.6)}	
<input checked="" type="checkbox"/> C12N 9/0083	••• {Miscellaneous (1.14.99)}	

2 results found in the Worldwide database for:
demethyl* or FTO or AikB or M6A in the title or abstract AND **C12N15/8261/low** and **C12N9/0071** as the Cooperative Patent Classification

Sort by Sort order

1. **A transgenic plant cell and a method for producing the transgenic plant**


★	Inventor: JIA GUIFANG HE CHUAN	Applicant: EPIPLANTA BIOTECH LTD	CPC: <u>A01H4/008</u> C12N15/8261 (+2)	IPC: A01H5/00 C12N15/53 C12N15/82	Publication info: CN108949806 (A) 2018-12-07	Priority date: 2017-05-24
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2. **SOYBEAN TRANSGENIC EVENT MON87708 AND USE METHODS THEREOF**

★	Inventor: RONALD J BRINKER WEN C BURNS (+5)	Applicant: MONSANTO TECHNOLOGY LLC	CPC: <u>A23D9/00</u> <u>A23L11/03</u> <u>C12N15/8274</u> (+3)	IPC: A01H1/00 C12N1/15 C12N1/21 (+2)	Publication info: JP2015077134 (A) 2015-04-23 JP5985588 (B2) 2016-09-06	Priority date: 2009-09-17
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2 results found in the Worldwide database for:
demethyl* or ETO or AlkB or M6A in the title or abstract AND **C12N15/8261/low** and **C12N9/0071** as the Cooperative Patent

Abstract of JP2015077134 (A)

Translate this text into 

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PROBLEM TO BE SOLVED: To provide transgenic soybean plants exhibiting commercially acceptable tolerance to applications of dicamba herbicide. **SOLUTION:** The invention provides a transgenic soybean event MON87708 transformed to have dicamba monooxygenase (DMO), an enzyme cloned from *Stenotrophomonas maltophilia* commonly found in soil rhizosphere. Dicamba monooxygenase catalyzes deactivation of dicamba to a non-herbicidal compound, 3,5-dichlorosalicylic acid, via O-**demethylation** reaction. Also provided are polynucleotide specific for the event MON87708, as well as plants, plant cells, seeds, plant parts and commodity products comprising polynucleotides specific for event MON87708.

2. SOYBEAN TRANSGENIC EVENT MON87708 AND USE METHODS THEREOF

<p>★ Inventor: RONALD J BRINKER WEN C BURNS (+5)</p>	<p>Applicant: MONSANTO TECHNOLOGY LLC</p>	<p>CPC: <u>A23D9/00</u> <u>A23L11/03</u> <u>C12N15/8274</u> (+3)</p>	<p>IPC: A01H1/00 C12N1/15 C12N1/21 (+2)</p>	<p>Publication info: JP2015077134 (A) 2015-04-23 JP5985588 (B2) 2016-09-06</p>	<p>Priority date: 2009-09-17</p>
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Format: Abstract ▼

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Nature. 2009 Apr 16;458(7240):894-8. doi: 10.1038/nature07848. Epub 2009 Feb 22.

Inactivation of the Fto gene protects from obesity.

Fischer J¹, Koch L, Emmerling C, Vierkotten J, Peters T, Brüning JC, Rüther U.

[+ Author information](#)

Abstract

Several independent, genome-wide association studies have identified a strong correlation between body mass index and polymorphisms in the human FTO gene. Common variants in the first intron define a risk allele predisposing to obesity, with homozygotes for the risk allele weighing approximately 3 kilograms more than homozygotes for the low risk allele. Nevertheless, the functional role of FTO in energy homeostasis remains elusive. Here we show that the loss of Fto in mice leads to postnatal growth retardation and a significant reduction in adipose tissue and lean body mass. The leanness of Fto-deficient mice develops as a consequence of increased energy expenditure and systemic sympathetic activation, despite decreased spontaneous locomotor activity and relative hyperphagia. Taken together, these experiments provide, to our knowledge, the first direct demonstration that Fto is functionally involved in energy homeostasis by the control of energy expenditure.

Comment in

FTO effect on energy demand versus food intake. [Nature. 2010]

PMID: 19234441 DOI: [10.1038/nature07848](https://doi.org/10.1038/nature07848)

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[Regulation of Fto/Ftm gene expression in mice and humans.](#) [Am J Physiol Regul Integr Comp...]

[Review The 'Fat Mass and Obesity Related' \(FTO\) gene: Mechanisms](#) [Curr Obes Rep. 2015]

[Review FTO and obesity: mechanisms of association.](#) [Curr Diab Rep. 2014]

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Format: Abstract

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Mol Cell. 2018 Sep 20;71(6):973-985. e5. doi: 10.1016/j.molcel.2018.08.011. Epub 2018 Sep 6.

Differential m⁶A, m⁶A_m, and m¹A Demethylation Mediated by FTO in the Cell Nucleus and Cytoplasm.

Wei J¹, Liu F¹, Lu Z², Fei Q¹, Ai Y¹, He PC¹, Shi H¹, Cui X¹, Su R³, Klungland A⁴, Jia G⁵, Chen J³, He C⁶.

Author information

Abstract

FTO, the first RNA demethylase discovered, mediates the demethylation of internal N⁶-methyladenosine (m⁶A) and N⁶, 2-O-dimethyladenosine (m⁶A_m) at the +1 position from the 5' cap in mRNA. Here we demonstrate that the cellular distribution of FTO is distinct among different cell lines, affecting the access of FTO to different RNA substrates. We find that FTO binds multiple RNA species, including mRNA, snRNA, and tRNA, and can demethylate internal m⁶A and cap m⁶A_m in mRNA, internal m⁶A in U6 RNA, internal and cap m⁶A_m in snRNAs, and N¹-methyladenosine (m¹A) in tRNA. FTO-mediated demethylation has a greater effect on the transcript levels of mRNAs possessing internal m⁶A than the ones with cap m⁶A_m in the tested cells. We also show that FTO can directly repress translation by catalyzing m¹A tRNA demethylation. Collectively, FTO-mediated RNA demethylation occurs to m⁶A and m⁶A_m in mRNA and snRNA as well as m¹A in tRNA.

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KEYWORDS: FTO; cap m(6)A(m); cytoplasmic demethylation; m(6)A; nuclear m(6)A demethylation; snRNA demethylation; tRNA m(1)A demethylation; translation regulation

PMID: 30197295 PMCID: PMC6151148 [Available on 2019-09-20] DOI: 10.1016/j.molcel.2018.08.011

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FTO controls reversible m⁶A_m RNA methylation during snRNA I [Nat Chem Biol. 2019]

Structural insights into FTO's catalytic mechanism for t [Proc Natl Acad Sci U S A. 2019]

Reversible methylation of m⁶A_m ir [Nature. 2017]

Review FTO, m⁶A_m, and the hypothesis of reversible [FEBS Lett. 2018]

Review Novel positioning from obesity to cancer: FTO, an m⁶A [J Cancer Res Clin Oncol. 2019]

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Patent Summary **Cites 17 Works** Cites 11 patents Family Info Sequences Legal Info Notes 0

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📄 N(6)-Methyladenosine RNA Modification Regulates Shoot Stem Cell Fate in Arabidopsis. 📞 028-449-453-963-958

Lisha Shen, Zhe Liang, Xiaofeng Gu, Ying Chen, Zhi Wei Norman Teo, Xingliang Hou, Weiling Maggie Cai, Peter C. Dedon, Lu Liu, Hao Yu 📖 View this article via PubMed

Developmental Cell, Issue: 2, Volume: 38, Pages: 186-200. | Jul 7, 2016 🌐 View this article via Crossref

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📄 Mammalian WTAP is a regulatory subunit of the RNA N6-methyladenosine methyltransferase 📞 066-078-489-133-41X

Xiao-Li Ping, Bao Fa Sun, Lu Wang, Wen Shao Xiao, Xin Yang, Wen-Jia Wang, Samir Adhikari, Yue Shi, Ying Lv, Yu-Sheng Chen, Xu Zhao, Ang Li, Ying Yang, Ujwal Dahal, Xiao-Min Lou, Xi Liu, Jun Huang, Weiping Yuan, Xiaofan Zhu, Tao Cheng, Yong-Liang Zhao, Xinquan Wang, Jannie M. Rendtlew Danielsen, Feng Liu, Yun-Gui Yang 📖 View this article via PubMed

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EUROPEAN SEARCH REPORT

Application Number
EP 18 17 1487

DOCUMENTS CONSIDERED TO BE RELEVANT					
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (IPC)		
X	<p>GUAN-ZHENG LUO ET AL: "Unique features of the m6A methylome in Arabidopsis thaliana", NATURE COMMUNICATIONS, vol. 5, no. 1, 28 November 2014 (2014-11-28), XP55486590, DOI: 10.1038/ncomms6630</p> <p>* abstract *</p> <p>* page 2, column 1, paragraph 3 *</p> <p>* page 4, column 2, paragraph 1 *</p> <p>* page 4, column 2, paragraph 3 *</p> <p>* page 5, column 2 *</p> <p>* page 7, column 1, paragraph 2 *</p> <p>-----</p>	1-16	INV. C12N15/82		
X	<p>XIAO WANG ET AL: "N6-methyladenosine-dependent regulation of messenger RNA stability", NATURE, vol. 505, no. 7481, 27 November 2013 (2013-11-27), pages 117-120, XP55487166, GB ISSN: 0028-0836, DOI: 10.1038/nature12730</p> <p>* the whole document *</p> <p>-----</p>	1-16	<table border="1"> <tr> <td>TECHNICAL FIELDS SEARCHED (IPC)</td> </tr> <tr> <td>C12N</td> </tr> </table>	TECHNICAL FIELDS SEARCHED (IPC)	C12N
TECHNICAL FIELDS SEARCHED (IPC)					
C12N					
A	<p>SCHRAGA SCHWARTZ ET AL: "Perturbation of m6A Writers Reveals Two Distinct Classes</p>	1-6			

Questions:

- 1) *What is the technical problem and does the first claim solve it?*
- 2) *What is the difference between m6A demethylase, AlkB oxidation demethylase and FTO?*
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- 6) *Are the sequence searches the right approach to find prior art?*
- 7) ***Are there some claims which may fall under patentability exceptions, e.g. EPC Art 53 (b)?***
- 8) ***Is the unity of the claims given?***

...Discussion...