US Patent & Trademark Office Patent Public Search | Text View

United States Patent

Kind Code

Date of Patent

Inventor(s)

12385046

B2

August 12, 2025

Wang; Yong et al.

Baicalein- and scutellarein-synthesizing microorganism, preparation method and applications thereof

Abstract

Provided are a baicalein- and scutellarein-synthesizing microorganism, a preparation method for same, and applications thereof. By modifying a heterologous metabolic pathway of a host cell per a genetic engineering method, acquired is an engineered strain providing a high yield of baicalein and scutellarein. Also provided is a process for utilizing the engineered strain to produce baicalein and scutellarein.

Inventors: Wang; Yong (Shanghai, CN), Li; Jianhua (Shanghai, CN), Tian;

Chenfei (Shanghai, CN)

Applicant: CAS CENTER FOR EXCELLENCE IN MOLECULAR PLANT

SCIENCES (Shanghai, CN)

Family ID: 1000008747508

Assignee: CAS CENTER FOR EXCELLENCE IN MOLECULAR PLANT

SCIENCES (Shanghai, CN)

Appl. No.: 17/274377

Filed (or PCT

September 06, 2019

Filed):

PCT No.: PCT/CN2019/104658

PCT Pub. No.: WO2020/048523

PCT Pub. Date: March 12, 2020

Prior Publication Data

Document IdentifierUS 20220033827 A1

Publication Date
Feb. 03, 2022

CN 201811043657.0

Publication Classification

Int. Cl.: C12N15/52 (20060101); C07K14/415 (20060101); C12N9/02 (20060101); C12P17/06

Sep. 07, 2018

(20060101)

U.S. Cl.:

CPC **C12N15/52** (20130101); **C07K14/415** (20130101); **C12N9/0042** (20130101);

C12N9/0071 (20130101); C12N9/0073 (20130101); C12P17/06 (20130101);

C12Y106/02004 (20130101); C12Y114/14 (20130101)

Field of Classification Search

CPC: C12N (15/52); C12N (9/0042); C12N (9/0071); C12N (15/70); C12N (15/75); C12N

(15/81); C07K (14/415); C07K (2319/24); C07K (2319/10); C07K (2319/20); C07K (2319/00); C12P (17/06); C12Y (106/02004); C12Y (114/14); C12Y (114/14001); Y02A

(50/30)

References Cited

FOREIGN PATENT DOCUMENTS

Patent No. Application Date Country CPC

106318920 12/2016 CN C12N 9/0071

OTHER PUBLICATIONS

Leonard et al., "Functional expression of a P450 flavonoid hydroxylase for the biosynthesis of plant-specific hydroxylated flavonols in *Escherichia coli*." Metabolic engineering vol. 8,2: 172-81 (available online Dec. 2005); doi: 10.1016/j.ymben.2005.11.001 (Year: 2005). cited by examiner Zhu et al., "Efficient Synthesis of Eriodictyol from L-Tyrosine in *Escherichia coli*," Applied and Environmental Microbiology, Mar. 7, 2014, vol. 80, No. 10, pp. 3072-3080, (on IDS dated Nov. 15, 2022) (Year: 2014). cited by examiner

Leonard et al. 2005. "Investigation of two distinct flavone synthases for plant-specific flavone biosynthesis in *Saccharomyces cerevisiae*". Applied and environmental microbiology, 71(12), 8241-8248. https://doi.org/10.1128/AEM.71.12.8241-8248.2005 (Year: 2005). cited by examiner Zhao et al. 2018. "Two CYP82D Enzymes Function as Flavone Hydroxylases in the Biosynthesis of Root-Specific 4'-Deoxyflavones in Scutellaria baicalensis". Mol. Plant. 11, 135-148 (Year: 2018). cited by examiner

Morrone et al. 2010. "Characterization of the kaurene oxidase CYP701A3, a multifunctional cytochrome P450 from gibberellin biosynthesis." Biochemical Journal 431.3: 337-347 (11 pages total). https://doi.org/10.1042/BJ20100597 (Year: 2010). cited by examiner

Zhu et al. 2014. "Efficient Synthesis of Eriodictyol from L-Tyrosine in *Escherichia coli*," Applied and Environmental Microbiology, Mar. 7, 2014, vol. 80, No. 10, pp. 3072-3080 (Year: 2014). cited by examiner

Biggs et al. 2016. "Overcoming heterologous protein interdependency to optimize P450-mediated Taxol precursor synthesis in *Escherichia coli*". Proc Natl Acad of Sci U.S.A. 113(12), 3209-3214.

https://doi.org/10.1073/pnas.1515826113 (Year: 2016). cited by examiner

Machine translation of the Description of CN106318920A (Tianjin Institute of Industrial Biotechnology, CAS, originally published on Jan. 11, 2017). Translation downloaded from EPO on Apr. 16, 2024, 22 pages total. (Very 2017), cited by examiner.

Apr. 16, 2024. 33 pages total. (Year: 2017). cited by examiner

Artigot et al., "Expression of Flavonoid 6-hydroxylase Candidate Genes in Normal and Mutant Soybean Genotypes for Glycitein Content," Molecular Biology Reports, May 22, 2013, vol. 40, No. 7, pp. 4361-4369. cited by applicant

Biggs et al., "Overcoming heterologous protein interdependency to optimize P450-mediated Taxol precursor synthesis in *Esherichia coli*," Proceedins of National Academy of Sciences of the United States of America, Mar. 22, 2016, vol. 113, No. 12, pp. 3209-3214. cited by applicant

Li et al., "Production of Plant-specific Flavones Baicalein and Scutellarein in an Engineered *E. coli* from Available Phenylalanine and Tyrosine," Metabolic Engineering, Nov. 26, 2018, vol. 52, pp. 124-133. cited by applicant

Mayer et al., "P450 Reductase 2 [*Arabidopsis thaliana*], Accession No. AEE85737.1," NCBI GenBank, Jul. 20, 2017. cited by applicant

NCBI GenBank Accession No. AAA33883.1, Apr. 27, 1993. cited by applicant

NCBI GenBank Accession No. KF765780.1, Jul. 17, 2014. cited by applicant

NCBI GenBank Accession No. KF765781.1, Jul. 17, 2014. cited by applicant

NCBI GenBank Accession No. KF765782.1, Jul. 17, 2014. cited by applicant

NCBI GenBank Accession No. ASW21050.1, Sep. 5, 2017. cited by applicant

NCBI GenBank Accession No. NP_849472.2, Feb. 14, 2019. cited by applicant

NCBI UniProtKB/Swiss-Prot Accession No. Q7XZQ8.1, Dec. 2, 2020. cited by applicant Pandey et al., "Microbial production of natural and non-natural flavonoids: Pathway engineering, directed evolution and systems/synthetic biology", Biotechnology Advances, 2016, vol. 34, pp. 634-662. cited by applicant

Uno et al., "Metabolism of 7-ethoxycoumarin, Safrole, Flavanone and Hydroxyflavanone by Cytochrome P450 2A6 Variants," Biopharmaceutics & Drug Disposition, Dec. 4, 2012, vol. 34, No. 2, pp. 87-97. cited by applicant

Uno et al., "Point Mutation of Cytochrome P450 2A6 (a Polymorphic Variant CYP2A6.25) Confers New Substrate Specificity Towards Flavonoids," Biopharmaceutics & Drug Disposition, Aug. 31, 2015, vol. 36, No. 8, pp. 552-563. cited by applicant

Zhao et al., "Scutellaria Baicalensis Cytochrome P450 CYP82D1.1 mRNA, Complete Cds; Chromoplast, Accession No. MF363006.1," NCBI GenBank, Sep. 5, 2017. cited by applicant Zhao et al., "Two CYP82D Enzymes Function as Flavone Hydroxylases in the Biosynthesis of Root-Specific 4'-Deoxyflavones in Scutellaria Baicalensis," Molecular Plant, Jan. 31, 2018, vol. 11, No. 1, pp. 135-148. cited by applicant

Zhu et al., "Efficient Synthesis of Eriodictyol from L-Tyrosine in *Escherichia coli*," Applied and Environmental Microbiology, Mar. 7, 2014, vol. 80, No. 10, pp. 3072-3080. cited by applicant International Search Report issued in corresponding International Patent Application No. PCT/CN2019/104658, mailed Dec. 2, 2019. cited by applicant

Primary Examiner: McKelvey; Terry A

Assistant Examiner: Moehlman; Andrew T

Attorney, Agent or Firm: Greenberg Traurig, LLP

Background/Summary

CROSS REFERENCE TO RELATED APPLICATIONS

(1) This application is a U.S. National Phase application under 35 U.S.C. 371 of International Application No. PCT/CN2019/104658 filed Sep. 6, 2019, which claims priority to and the benefit of Chinese Patent Application No. 201811043657.0 filed Sep. 7, 2018, the entire disclosure of each of which is incorporated herein by reference.

(2) The invention relates to the technical fields of synthetic biology and medicine, in particular to a microorganism for synthesizing baicalein and scutellarein, a preparation method and application thereof.

BACKGROUND

FIELD

- (3) Scutellaria baicalensis Georgi is a famous traditional medicine in China, which is a Labiatae plant. Traditional Chinese medicine (TCM) Radix Scutellariae is the dry root of Scutellaria baicalensis Georgi, which has a long medicinal history and can be used for the treatment of wind heat, damp heat and other diseases. Erigerontis Herba is the dry herb of Erigeron breviscapus. It is cold in nature and bitter in taste. It has the functions of anti-inflammatory and analgesic, promoting blood circulation and removing blood stasis, eliminating wind and dampness. Extract of Scutellaria baicalensis Georgi and Erigeron breviscapus have long been widely used in TCM preparations. The main raw materials of Yinhuang tablet, Shuanghuanglian oral liquid and Lanqin oral liquid are extract of Scutellaria baicalensis Georgi. The main active ingredient of Qingkailing is baicalein, which has the effect of anti-inflammatory, prevention and treatment of diarrhea, liver disease and tumor. The common dosage forms of Erigeron breviscapus include Breviscapine tablet and Breviscapine oral liquid, which can be converted to scutellarein and absorbed by an organism. Therefore, baicalein and scutellarein have a certain value in the development of new drugs.

 (4) Baicalein and scutellarein are two important flavonoids (flavones) with similar structures. The molecular formula of baicalein is C.sub.15H.sub.10O.sub.5 with a molecular weight of 270.24,
- molecular formula of baicalein is C.sub.15H.sub.10O.sub.5 with a molecular weight of 270.24, while molecular formula of scutellarein is C.sub.15H.sub.10O.sub.6 with a molecular weight of 286.24. Their structures are shown in FIG. 1.

 (5) Like most natural products from plants, baicalein and scutellarein are mainly prepared by chemical synthesis and organic solvent extraction. Organic solvent extraction extracts ingredient
- chemical synthesis and organic solvent extraction. Organic solvent extraction extracts ingredient from the tissues of *Scutellaria baicalensis* Georgi, *Erigeron breviscapus*, *Scutellaria barbata* and other medicinal plants, which needs a lot of organic solvents and complex separation process. Therefore, the cost of organic solvent extraction is high. In addition, the main problems are that plants grow slow and medicinal resources are destroyed. Although baicalein and scutellarein can also be obtained in large quantities through chemical synthesis, the raw materials in the synthesis process contain cinnamic acid or its derivatives, oxyphenol and other chemical substances, which to some extent limits its application in medicine and food field. In addition, toxic reagents and expensive chemical catalysts are also used in the synthesis process.
- (6) Synthetic biology is a discipline which integrates and assembles standardized biological components based on rational design to build an excellent artificial life system. As soon as synthetic biology was put forward, its ideas and design have a profound impact on the development of industrial microbial technology, which makes microbial technology play a greater role in the development and production of drugs, biofuels and fine chemicals.
- (7) In the art, the synthetic elements of various natural products are assembled to conduct heterologous synthesis in microorganisms. However, the two flavonoids baicalein and scutellarein have not been successfully heterologously synthesized in microorganisms. Therefore, it is urgent to construct a microbial strain capable of heterologous synthesis of baicalein and scutellarein. SUMMARY
- (8) Provided are a baicalein- and scutellarein-synthesizing microorganism, a preparation method for same, and applications thereof.

- (9) The first aspect of the present disclosure provides a method of producing baicalein and scutellarein, comprising: (1) introducing into a host cell genes expressing flavone 6-hydroxylase (F6H) and cytochrome P450 oxidoreductase (CPR), as well as genes for synthesizing chrysin or apigenin; and (2) culturing the host cell in a culture system containing phenylalanine and/or tyrosine to produce baicalein or scutellarein.
- (10) In a preferable example, the genes for synthesizing chrysin or apigenin comprises: genes expressing phenylalanine ammonia-lyase (PAL), 4-coumarate: CoA ligase (4CL), chalcone synthase (CHS), chalcone isomerase (CHI) and flavone synthase I (FNSI). Preferably, when introduced into the host cell, the genes expressing PAL, 4CL, CHS, CHI and FNSI are in the same expression vector.
- (11) In another preferable example, the flavone 6-hydroxylase is derived from *Scutellaria baicalensis*, including its homologues (homologous genes or peptides from other species); the CPR is derived from *Arabidopsis thaliana*, including its homologues.
- (12) In another preferable example, the PAL is derived from *Rhodotorula toruloides*, including its homologues; the 4CL is derived from *Petroselium crispum*, including its homologues; the CHS is derived from *Petunia X hybrida*, including its homologues; the CHI is derived from *Medicago sativa*, including its homologues; and the FNS I is derived from *Petroselium crispum*, including its homologues.
- (13) The another aspect of the present disclosure provides a method of producing baicalein and scutellarein, comprising: (1) introducing into a host cell genes expressing flavone 6-hydroxylase (F6H) and cytochrome P450 oxidoreductase (CPR) to obtain recombinant host cell; and (2) culturing the recombinant host cell in a culture system containing chrysin or apigenin to produce baicalein or scutellarein.
- (14) In another aspect of the disclosure, a method for converting chrysin or apigenin into baicalein or scutellarein is provided: catalyzing chrysin or apigenin by flavone 6-hydroxylase and cytochrome P450 oxidoreductase, thereby adding a hydroxyl group to the structure of chrysin or apigenin to form baicalein or scutellarein.
- (15) In a preferable embodiment, the flavone 6-hydroxylase (F6H) is a mutant flavone 6-hydroxylase with the N-terminal amino acids (1-10) to (20-30) truncated; preferably, it is a mutant flavone 6-hydroxylase with the N-terminal amino acids (2-5) to (22-28) truncated.
- (16) In another preferable embodiment, the flavone 6-hydroxylase is fused with a peptide tag, and the peptide tag is selected from N-terminal 8 amino acid peptide of bovine calf serum 17 hydroxylase (8RP), small ubiquitin-related modifier (Sumo), maltose binding protein (MBP), 2B1 family soluble protein of cytochrome P450 (2B1), or a combination thereof, preferably the peptide tag is maltose binding protein or 2B1 family soluble protein of cytochrome P450, or a combination thereof; preferably, the peptide tag is located at the N-terminal.
- (17) In another preferable embodiment, the cytochrome P450 oxidoreductase (CPR) is a mutant cytochrome P450 oxidoreductase with the N-terminal amino acids (1-20) to (60-85) truncated; preferably, it is a mutant cytochrome P450 oxidoreductase with the N-terminal amino acids (2-10) to (65-80) truncated; more preferably, it is a mutant cytochrome P450 oxidoreductase with the N-terminal amino acids (2-5)-(70-75) truncated.
- (18) In another preferable embodiment, the host cell includes: prokaryotic cell or eukaryotic cell; preferably, the prokaryotic cell includes: *Escherichia coli* cell, *Bacillus subtilis* cell; the eukaryotic cell includes: yeast cell.
- (19) Another aspect of the present disclosure provides a recombinant host cell comprising exogenous genes expressing flavone 6-hydroxylase and cytochrome P450 oxidoreductase.
- (20) In another preferable embodiment, the recombinant host cell also includes exogenous genes for synthesizing chrysin or apigenin.
- (21) In another preferable embodiment, the peptide tag is a single copy or 2-10 copies (such as 3, 4, 5, 6, 8 copies) of tandem sequences.

- (22) Another aspect of the present disclosure provides the use of any of the above recombinant host cells in the production of baicalein and scutellarein.
- (23) In one preferable embodiment, for the strain which does not comprise chrysin or apigenin synthesis gene(s) in the cell, the use is to produce baicalein and scutellarein with exogenous chrysin or apigenin as the substrate; for the strain which comprises chrysin or apigenin synthesis gene(s) in the cell, the use is to produce baicalein and scutellarein in the presence of exogenous phenylalanine and/or tyrosine.
- (24) Another aspect of the disclosure provides a method of preparing a host cell for producing baicalein and scutellarein, comprising: introducing genes expressing flavone 6-hydroxylase and cytochrome P450 oxidoreductase into the host cell to obtain a recombinant strain; preferably, the method also comprises: introducing genes for synthesizing chrysin or apigenin.
- (25) In another aspect of the present disclosure, a kit for the production of baicalein and scutellarein is provided, wherein the kit comprises any of the above recombinant host cells.
- (26) In another preferable embodiment, the kit also comprises: culture medium for the host cell, instruction for use, etc.
- (27) In another aspect of the present disclosure, a mutant flavonoid 6-hydroxylase is provided, which corresponds to the wild-type flavonoid 6-hydroxylase (F6H) but the N-terminal amino acids (1-10) to (20-30) are truncated; preferably, the N-terminal amino acids (2-5) to (22-28) are truncated; more preferably, the mutant flavonoid 6-hydroxylase has the amino acid sequence shown in SEQ ID NO: 2.
- (28) In another aspect of the present disclosure, a mutant cytochrome P450 oxidoreductase is provided, which corresponds to the wild-type cytochrome P450 oxidoreductase but the N-terminal amino acids (1-20) to (60-85) are truncated; preferably, the N-terminal amino acids (2-10) to (65-80) are truncated; more preferably, the N-terminal amino acids (2-5) to (70-75) are truncated; preferably, the mutant cytochrome P450 oxidoreductase has the amino acid sequence shown in SEQ ID NO: 8.
- (29) In another aspect of the present disclosure, a fusion polypeptide is provided, which comprises any of the above mutant flavone 6-hydroxylase fused with a peptide tag, the peptide tag is selected from the group consisting of: 8RP, Sumo, MBP, 2B1; preferably is MBP or 2B1.
- (30) In a preferable embodiment, the fusion polypeptide has an amino acid sequence selected from the group consisting of: SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5 or SEQ ID NO: 6.
- (31) In another aspect of the present disclosure, a polynucleotide is provided, which encodes: the mutant flavonoid 6-hydroxylase; or the mutant cytochrome P450 oxidoreductase; or the fusion polypeptide.
- (32) In another aspect of the present disclosure, an expression construct is provided, which comprises: any of the above polynucleotides; or polynucleotides encoding any of the mutant flavonoid 6-hydroxylase or the fusion protein described above, and polynucleotides encoding the mutant cytochrome P450 oxidoreductase described above.
- (33) In another preferable embodiment, the expression construct also comprises promoter and terminator operably linked with the above polynucleotide.
- (34) Another aspect of the disclosure provides the use of the mutant flavonoid 6-hydroxylase or the fusion protein and the mutant cytochrome P450 oxidoreductase in production of baicalein or scutellarein by adding a hydroxyl group to the structure of chrysin or apigenin.
- (35) Other aspects of the disclosure will be apparent to those skilled in the art based on the disclosure herein.

Description

BRIEF DESCRIPTION OF THE DRAWINGS

- (1) FIG. 1. Structural formula of baicalein and scutellarein.
- (2) FIG. **2**. Schematic of biosynthesis pathway of baicalein and scutellarein.
- (3) FIG. **3**. Schematic of plasmid pYH66.
- (4) FIG. **4**. Schematic of plasmid pYH57.
- (5) FIG. **5**. HPLC results of engineering strain BL21(DE3)-pYH57-pYH66 and baicalein standard. i: BL21(DE3)-pETDuet-1-pCDFDuet-1 fermentation broth, as blank control; ii: BL21(DE3)-pYH57-pYH66 fermentation broth added with phenylalanine; baicalein standard.
- (6) FIG. **6**. Mass spectrum results of baicalein produced by engineering strain BL21(DE3)-pYH57-pYH66.
- (7) FIG. **7**. HPLC results of engineering strain BL21(DE3)-pYH57-pYH66 and scutellarein standard. i: BL21(DE3)-pETDuet-1-pCDFDuet-1 fermentation broth, as blank control; ii: BL21(DE3)-pYH57-pYH66 fermentation broth added with tyrosine; iii: scutellarein standard.
- (8) FIG. **8**. Mass spectrum results of scutellarein produced by engineering strain BL21(DE3)-pYH57-pYH66.
- (9) FIG. **9**. Production of baicalein from chrysin catalyzed by SbF6H and AtCPR mutants.
- (10) A. Schematic of the key elements in the constructed plasmid;
- (11) B. The conversion rates of baicalein from chrysin in recombinant *E. coli*;
- (12) C. HPLC results of the catalytic reaction solution of recombinant *E. coli*. Chr: chrysin; Bai: baicalein.

DETAILED DESCRIPTION

- (13) The inventor is committed to the heterologous synthesis of baicalein and scutellarein from microorganisms, and to improving biological production of baicalein and scutellarein. After indepth study, engineering strains with high yield of baicalein and scutellarein is obtained by modifying the heterologous metabolic pathway of host cells through genetic engineering.
- (14) As used herein, "N-terminal amino acids (1-10) to (20-30)" refers to a sequence starting from any amino acid in N-terminal amino acids 1-10 and ending at any amino acid in N-terminal amino acids 20-30.
- (15) As used herein, "N-terminal amino acids (2-5) to (22-28)" refers to a sequence starting from any amino acid in N-terminal amino acids 2-5 and ending at any amino acid in N-terminal amino acids 22-28.
- (16) As used herein, "N-terminal amino acids (1-20) to (60-85)" refers to a sequence starting from any amino acid in N-terminal amino acids 1-20 and ending at any amino acid in N-terminal amino acids 60-85.
- (17) As used herein, "N-terminal amino acids (2-10) to (65-80)" refers to a sequence starting from any amino acid in N-terminal amino acids 2-10 and ending at any amino acid in N-terminal amino acids 65-80.
- (18) As used herein, "N-terminal amino acids (2-5) to (70-75)" refers to a sequence starting from any amino acid in N-terminal amino acids 2-5 and ending at any amino acid in N-terminal amino acids 70-75.
- (19) As used herein, "exogenous" or "heterologous" refers to two or more nucleic acid or protein sequences from different sources.
- (20) As used herein, "operably linked (to)" or "operably connected (to)" is intended to mean a functional spatial arrangement between two or more nucleic acid regions or nucleic acid sequences. For example, a promoter region is "operatively linked" to the nucleic acid sequence of a target gene when the promoter region is placed at a specific position relative to the nucleic acid sequence so that the transcription of the nucleic acid sequence is guided by the promoter region.
- (21) As used herein, the "expression construct" refers to a recombinant DNA molecule that contains the desired nucleic acid coding sequence. An expression construct may contain one or

- more gene expression cassettes. The "construct" is usually contained in an expression vector.
- (22) As used herein, the PAL, 4CL, CHS, CHI and FNSI proteins are proteins that constitute the biosynthesis pathway of chrysin or apigenin in the expression system.
- (23) As used herein, the F6H and CPR proteins are the proteins that convert chrysin or apigenin into baicalein or scutellarein in the expression system.
- (24) Wild types of the above proteins or genes have been identified in the art, so they can be available and prepared from the public. As a preferable embodiment of the disclosure, PAL is derived from *Rhodotorula toruloides*, with the sequence shown in GenBank accession number AAA33883.1; 4CL is derived from *Petroselium crispum*, with the sequence shown in GenBank accession number KF765780.1; CHS is derived from *Petunia X hybrida*, with the sequence shown in GenBank accession number KF765781.1; CHI is derived from *Medicago sativa*, with the sequence shown in GenBank accession number KF765782.1; FNS I is derived from *Petroselium crispum*, with the sequence shown in Swiss-Prot accession number Q7XZQ8.1.
- (25) Wild types of F6H and CPR have also been identified in the art. As a preferable embodiment of the disclosure, F6H is derived from *Scutellaria baicalensis*, with the sequence shown in GenBank accession number ASW21050.1. As a preferable embodiment of the disclosure, CPR is derived from *Arabidopsis thaliana*, with the sequence shown in GenBank accession number NP_849472.2.
- (26) The inventor found that when using host cells to produce baicalein and scutellarein, the wild-type F6H can only produce a small amount of products, which cannot achieve large-scale production. Through modification of multiple proteins involved in the reaction and a large number of screening and analysis, optimized modification schemes were obtained, which greatly improved the yield of baicalein and scutellarein of microorganisms, especially prokaryotic expression systems such as *E. coli*.
- (27) Therefore, a preferable embodiment of the present disclosure provides a mutant F6H that corresponds to the wild-type F6H with N-terminal amino acids (1-10) to (20-30) truncated; preferably, it is a mutant F6H with N-terminal amino acids (2-5) to (22-28) truncated; more preferably, it is a mutant F6H with N-terminal amino acids 2 to 25 truncated.
- (28) In a preferable embodiment of the disclosure, a fusion protein containing F6H or mutant F6H is provided, which includes F6H or any mutant F6H, and a peptide tag fused therewith, wherein the peptide tag is selected from the group consisting of 8RP, Sumo, MBP, 2B1, or a combination of them; preferably is MBP or 2B1. The peptide tag and the F6H or mutant F6H may or may not contain a linker peptide, and the linker peptide does not affect their biological activities.
- (29) In a preferable embodiment of the present disclosure, a mutant CPR is provided, which corresponds to the wild-type CPR with N-terminal amino acids (1-20) to (60-85) truncated; preferably, it is a mutant CPR with N-terminal amino acids (2-10) to (65-80) truncated; more preferably, it is a mutant CPR with N-terminal amino acids (2-5) to (70-75) truncated.
- (30) In addition to the above preferable proteins (including the above wild-type proteins and mutant proteins), the disclosure also includes their bioactive fragments, derivatives and analogues. Their fragments, derivatives or analogues may comprise deletion, insertion and/or substitution of several (usually 1-50, more preferably 1-20, yet more preferably 1-10, 1-5, 1-3, or 1-2) amino acids, as well as addition or deletion of one or more (for example, less than 100, 80, 50, 20, more preferably less than 10, yet more preferably less than 5) amino acids at C-terminal and/or N-terminal. For example, substitution with amino acids of comparable or similar properties usually does not change protein function in the art. As another example, addition of deletion of one or more amino acids to the C-terminus and/or N-terminus usually does not change the function of a protein either. However, for further variation of the above mutant protein, the N-terminal was truncated as
- (31) In addition to the above preferable proteins (including the above wild-type proteins and mutant proteins), the disclosure also includes their analogues. The differences between analogs and the

described above.

original protein may be the difference in amino acid sequences, and may also be the difference in the forms of modifications that will not affect the sequence, or both. These proteins include natural or induced genetic variants. Induced variants can be obtained by a variety of techniques, such as generating random mutagenesis by irradiation or exposure to mutagens, and can also be obtained by directed mutagenesis or other known molecular biology techniques. Analogs mentioned herein also include analogs with residue(s) different from natural L-amino acid (e.g., D-amino acids), as well as analogs with a non-naturally occurred or synthetic amino acid (such as β , γ -amino acids). It should be understood that the proteins of the present disclosure are not limited to the representative proteins described above.

- (32) In addition to the above preferable proteins (including the above wild-type proteins and mutant proteins), the disclosure also includes the protein with high homology (for example, having 70% or higher, preferable 80% or higher, more preferable 90% or higher (such as 95%, 98% or 99%) homology with the sequence of the particular described protein) and having the same function as the corresponding protein.
- (33) The disclosure describes proteins or genes from specific species. It should be understood that although the proteins or genes obtained from a specific species are preferably studied in the present disclosure, other proteins or genes obtained from other species and having high homology (such as having more than 60%, such as 70%, 80%, 85%, 90%, 95%, or even 98% sequence identity) with the proteins or genes also fall within the scope of the present disclosure.
- (34) The disclosure also provides a polynucleotide sequence encoding the protein of the disclosure or a conserved variant thereof. The polynucleotide sequences herein can be in the form of DNA or RNA. Forms of DNA include cDNA, genomic DNA or artificially synthesized DNA. DNA can be single-stranded or double-stranded. The DNA may be coding strand or non-coding strand. The polynucleotide encoding the mutant mature protein of the disclosure includes: the coding sequence only encoding the mature protein; the coding sequence encoding the mature protein and a various additional coding sequence; the coding sequence encoding the mature protein (and an optional additional coding sequence) and a noncoding sequence.
- (35) The disclosure also includes the codon-optimized polynucleotide sequence of the gene sequence, for example, the codon-optimized according to the codon bias of the host cell.
- (36) In the disclosure, an engineering strain with high yield of baicalein and scutellarein is also constructed, which includes exogenous genes expressing F6H (especially the mutant F6H or fusion protein) and CPR (especially the mutant CPR or fusion protein). Baicalein or scutellarein can be produced by culturing the recombinant strain and adding chrysin or apigenin into the culture system.
- (37) In the disclosure, another engineering strain with high yield of baicalein and scutellarein is constructed, which includes exogenous genes expressing F6H (especially the mutant F6H or fusion protein) and CPR (especially the mutant CPR or fusion protein), as well as genes for synthesizing chrysin or apigenin. The genes for synthesizing chrysin or apigenin comprise genes expressing PAL, 4CL, CHS, CHI and FNSI proteins.
- (38) By use of the strain according to the disclosure, which has great stability, large-scale cultivation and production of baicalein or scutellarein in a bioreactor can be realized. The yield of baicalein or scutellarein of the optimized strain of the disclosure is very high.
- (39) In the disclosure, more economical and convenient manufacture of baicalein or scutellarein can be conducted by production of baicalein or scutellarein from *E. coli*.
- (40) The disclosure also provides a kit for producing baicalein or scutellarein engineering strains. In addition, it can also include culture medium for *E. coli*, separation or detection reagent for baicalein or scutellarein, instruction for use, etc.
- (41) The disclosure is further illustrated by the specific examples described below. It should be understood that these examples are merely illustrative, and do not limit the scope of the present disclosure. The experimental methods without specifying the specific conditions in the following

- examples generally used the conventional conditions, such as those described in J. Sambrook, Molecular Cloning: A Laboratory Manual (3rd ed. Science Press, 2002) or followed the manufacturer's recommendation.
- (42) Experimental Materials
- (43) AxyPrep Total RNA Miniprep Kit, PCR Gel Extraction Kit, Plasmid Extraction Kit are from Axygen; PrimeScript RT reagent Kit with gDNA Eraser (Perfect Real Time), PrimeSTAR Max DNA Polymerase are from Takara, and restriction enzymes are from NEB.
- (44) *E. coli* DH10B was used for gene cloning, *E. coli* BL21 (DE3) was used for protein expression and baicalein and scutellarein production. pET28a, pEDDuet-1 and pCDFDuet-1 vectors were used for assembling of genes in metabolic pathway.
- (45) Baicalein and scutellarein standards were purchased from Shanghai Yuanye Biotechnology Co., Ltd. Other reagents are analytical grade reagent or chromatographic grade reagent, purchased from Sinopharm Chemical Reagent Co., Ltd.
- (46) PCR was conducted on Arktik Thermal Cycler (Thermo Fisher Scientific); ZXGP-A2050 Incubator and ZWY-211G Constant Temperature Oscillator were used for culture; high-speed freezing Centrifuge 5418R and Centrifuge 5418 (Eppendorf) were used for centrifugation. Vacuum concentration was performed with Concentrator Plus (Eppendorf); OD.sub.600 was detected using UV-1200 Ultraviolet/Visible Spectrophotometer (Shanghai Mapada Instrument Co., Ltd.). Rotary evaporation system consists of IKA RV 10 Digital Rotary Evaporator (IKA), MZ 2C NT Chemical Diaphragm Pump and CVC3000 vacuum controller (Vacuubrand). Dionex UltiMate 3000 Liquid Chromatography System (Thermo Fisher Scientific) was used for HPLC.
- (47) Liquid phase detection conditions: A phase: 0.1% formic acid solution, B phase: acetonitrile; separation conditions: 0-20 min, 20% B phase-55% B phase, 20-22 min, 55% B phase-100% B phase, 22-27 min, 100% B phase-20% B phase, 27-35 min, 100% B phase-20% B phase, 35-40 min, 20% B phase; detection wavelength: 340 nm, column temperature: 30° C. The chromatographic column was Thermo syncronis C18 RP column (250 mm*4.6 mm, 5 μ m). Example 1. Polypeptide and its Sequence Optimization
- (48) 1. Optimization of F6H Polypeptide Sequence
- (49) The sequence of *Scutellaria baicalensis* F6H (SbF6H, 517aa, Genbank access No. ASW21050.1) is:
- (50) TABLE-US-00001

MELSSVIYGAIALLSLFYCYLHFSKPKKSSLNAPPEAGGARFITGHLHLM DGRSASDKLPHINLGLLADQHGPIFTIRLGVHRAVVVSSWELAKEIFTTH DTAVMARPRLIADDYLSYDGASLGFSPYGPYWREIRKLVTTELLSARRIE LQRATRVREITQFTGELYKLWEEKKDGSGRVLVDMKQWLGNLSLNLVSRM VVGKRFYGGDDSETTKRWRGVMREFFQLIGQFIPGDGLPFLRWLDLGGFE KRTRDTAYELDKIIAMWLAEYRKREYSGDDKEQCFMALMLSLVQANPTLQ LHYDADTIIKATCQVLISAASDTTTVILIWVISLLLNNADVLKKVQEELD EQVGRERRVEESDISNLPYLQAVVKETMRLYPPAPFAGVRAFSEDCTVGG YHIQKGTFLIVNLWKLHRDPRVWSDDALEFKPQRFFDKKVEVKGQDFELM PFGGGRRMCPGSNLGMHMVHFVLANILQAFDITTGSTVDMTESVGLTNMK ATPLDAILTPRLSPTLY*

- (51) Modification 1: the modified F6H mutant trF6H was constituted by removing the amino acids 2-25 of SEQ ID NO: 1 and adding two amino acids MA to the N-terminal. The sequence of trF6H is as follows (SEQ ID NO: 2):
- (52) TABLE-US-00002

MAMPKKSSLNAPPEAGGARFITGHLHLMDGRSASDKLPHINLGLLADQHG PIFTIRLGVHRAVVVSSWELAKEIFTTHDTAVMARPRLIADDYLSYDGAS LGFSPYGPYWREIRKLVTTELLSARRIELQRATRVREITQFTGELYKLWE EKKDGSGRVLVDMKQWLGNLSLNLVSRMVVGKRFYGGDDSETTKRWRGVM REFFQLIGQFIPGDGLPFLRWLDLGGFEKRTRDTAYELDKIIAMWLAEYR KREYSGDDKEQCFMALMLSLVQANPTLQLHYDADTIIKATCQVLISAASD TTTVILIWVISLLLNNADVLKKVQEELDEQVGRERRVEESDISNLPYLQA VVKETMRLYPPAPFAGVRAFSEDCTVGGYHIQKGTFLIVNLWKLHRDPRV WSDDALEFKPQRFFDKKVEVKGQDFELMPFGGGRRMCPGSNLGMHMVHFV LANILQAFDITTGSTVDMTESVGLTNMKATPLDAILTPRLSPTLY*

- (53) Modification 2: the modified F6H mutant 8RPtrF6H was constituted by removing the amino acids 2-25 of SEQ ID NO: 1 and adding amino acids of 8RP to the N-terminal. The sequence of 8RPtrF6H is as follows (SEQ ID NO: 3):
- (54) TABLE-US-00003

MALLLAVFMPKKSSLNAPPEAGGARFITGHLHLMDGRSASDKLPHINLGL
LADQHGPIFTIRLGVHRAVVVSSWELAKEIFTTHDTAVMARPRLIADDYL
SYDGASLGFSPYGPYWREIRKLVTTELLSARRIELQRATRVREITQFTGE
LYKLWEEKKDGSGRVLVDMKQWLGNLSLNLVSRMVVGKRFYGGDDSETTK
RWRGVMREFFQLIGQFIPGDGLPFLRWLDLGGFEKRTRDTAYELDKIIAM
WLAEYRKREYSGDDKEQCFMALMLSLVQANPTLQLHYDADTIIKATCQVL
ISAASDTTTVILIWVISLLLNNADVLKKVQEELDEQVGRERRVEESDISN
LPYLQAVVKETMRLYPPAPFAGVRAFSEDCTVGGYHIQKGTFLIVNLWKL
HRDPRVWSDDALEFKPQRFFDKKVEVKGQDFELMPFGGGRRMCPGSNLGM
HMVHFVLANILQAFDITTGSTVDMTESVGLTNMKATPLDAILTPRLSPTL Y*

- (55) Modification 3: the modified F6H mutant SumotrF6H was constituted by removing the amino acids 2-25 of SEQ ID NO: 1 and adding amino acids of Sumo to the N-terminal. The sequence of SumotrF6H is as follows (SEQ ID NO: 4):
- (56) TABLE-US-00004

MADSEVNQEAKPEVKPEVKPETHINLKVSDGSSEIFFKIKKTTPLRRLME
AFAKRQGKEMDSLRFLYDGIRIQADQTPEDLDMEDNDIIEAHREQIGGMP
KKSSLNAPPEAGGARFITGHLHLMDGRSASDKLPHINLGLLADQHGPIFT
IRLGVHRAVVVSSWELAKEIFTTHDTAVMARPRLIADDYLSYDGASLGFS
PYGPYWREIRKLVTTELLSARRIELQRATRVREITQFTGELYKLWEEKKD
GSGRVLVDMKQWLGNLSLNLVSRMVVGKRFYGGDDSETTKRWRGVMREFF
QLIGQFIPGDGLPFLRWLDLGGFEKRTRDTAYELDKIIAMWLAEYRKREY
SGDDKEQCFMALMLSLVQANPTLQLHYDADTIIKATCQVLISAASDTTTV
ILIWVISLLLNNADVLKKVQEELDEQVGRERRVEESDISNLPYLQAVVKE
TMRLYPPAPFAGVRAFSEDCTVGGYHIQKGTFLIVNLWKLHRDPRVWSDD
ALEFKPQRFFDKKVEVKGQDFELMPFGGGRRMCPGSNLGMHMVHFVLANI
LQAFDITTGSTVDMTESVGLTNMKATPLDAILTPRLSPTLY*

- (57) Modification 4: the modified F6H mutant MBPtrF6H was constituted by removing the amino acids 2-25 of SEQ ID NO: 1 and adding amino acids of MBP to the N-terminal. The sequence of MBPtrF6H is as follows (SEQ ID NO: 5):
- (58) TABLE-US-00005

MAKIEEGKLVIWINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFP
QVAATGDGPDIIFWAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTWDAVR
YNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPALDKELKAKGKSALM
FNLQEPYFTWPLIAADGGYAFKYENGKYDIKDVGVDNAGAKAGLTFLVDL
IKNKHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVTVLP
TFKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKP
LGAVALKSYEEELVKDPRIAATMENAQKGEIMPNIPQMSAFWYAVRTAVI
NAASGRQTVDEALKDAQTMPKKSSLNAPPEAGGARFITGHLHLMDGRSAS
DKLPHINLGLLADQHGPIFTIRLGVHRAVVVSSWELAKEIFTTHDTAVMA
RPRLIADDYLSYDGASLGFSPYGPYVVREIRKLVTTELLSARRIELQRAT

RVREITQFTGELYKLWEEKKDGSGRVLVDMKQWLGNLSLNLVSRMVVGKR FYGGDDSETTKRWRGVMREFFQLIGQFIPGDGLPFLRWLDLGGFEKRTRD TAYELDKIIAMWLAEYRKREYSGDDKEQCFMALMLSLVQANPTLQLHYDA DTIIKATCQVLISAASDTTTVILIWVISLLLNNADVLKKVQEELDEQVGR ERRVEESDISNLPYLQAVVKETMRLYPPAPFAGVRAFSEDCTVGGYHIQK GTFLIVNLWKLHRDPRVWSDDALEFKPQRFFDKKVEVKGQDFELMPFGGG RRMCPGSNLGMHMVHFVLANILQAFDITTGSTVDMTESVGLTNMKATPLD AILTPRLSPTLY*

- (59) Modification 5: the modified F6H mutant 2B1trF6H was constituted by removing the amino acids 2-25 of SEQ ID NO: 1 and adding amino acids of 2B1 to the N-terminal. The sequence of 2B 1trF6H is as follows (SEO ID NO: 6):
- (60) TABLE-US-00006

MAKKTSKGKLPPGPSMPKKSSLNAPPEAGGARFITGHLHLMDGRSASDK
LPHINLGLLADQHGPIFTIRLGVHRAVVVSSWELAKEIFTTHDTAVMARP
RLIADDYLSYDGASLGFSPYGPYVVREIRKLVTTELLSARRIELQRATRV
REITQFTGELYKLWEEKKDGSGRVLVDMKQWLGNLSLNLVSRMVVGKRFY
GGDDSETTKRWRGVMREFFQLIGQFIPGDGLPFLRWLDLGGFEKRTRDTA
YELDKIIAMWLAEYRKREYSGDDKEQCFMALMLSLVQANPTLQLHYDADT
IIKATCQVLISAASDTTTVILIWVISLLLNNADVLKKVQEELDEQVGRER
RVEESDISNLPYLQAVVKETMRLYPPAPFAGVRAFSEDCTVGGYHIQKGT
FLIVNLWKLHRDPRVWSDDALEFKPQRFFDKKVEVKGQDFELMPFGGGRR
MCPGSNLGMHMVHFVLANILQAFDITTGSTVDMTESVGLTNMKATPLDAI LTPRLSPTLY*
2. Modification of CPR

- (61) The sequence of *Arabidopsis thaliana* CPR (AtCPR, 712aa, Genebank access No. NP_849472.2) is as follows (SEQ ID NO: 7):
- (62) TABLE-US-00007

MSSSSSSTSMIDLMAAIIKGEPVIVSDPANASAYESVAAELSSMLIENR
QFAMIVTTSIAVLIGCIVMLVWRRSGSGNSKRVEPLKPLVIKPREEEIDD
GRKKVTIFFGTQTGTAEGFAKALGEEAKARYEKTRFKIVDLDDYAADDDE
YEEKLKKEDVAFFFLATYGDGEPTDNAARFYKWFTEGNDRGEWLKNLKYG
VFGLGNRQYEHFNKVAKVVDDILVEQGAQRLVQVGLGDDDQCIEDDFTAW
REALWPELDTILREEGDTAVATPYTAAVLEYRVSIHDSEDAKFNDINMAN
GNGYTVFDAQHPYKANVAVKRELHTPESDRSCIHLEFDIAGSGLTYETGD
HVGVLCDNLSETVDEALRLLDMSPDTYFSLHAEKEDGTPISSSLPPPFPP
CNLRTALTRYACLLSSPKKSALVALAAHASDPTEAERLKHLASPAGKVDE
YSKWVVESQRSLLEVMAEFPSAKPPLGVFFAGVAPRLQPRFYSISSSPKI
AETRIHVTCALVYEKMPTGRIHKGVCSTWMKNAVPYEKSENCSSAPIFVR
QSNFKLPSDSKVPIIMIGPGTGLAPFRGFLQERLALVESGVELGPSVLFF
GCRNRRMDFIYEEELQRFVESGALAELSVAFSREGPTKEYVQHKMMDKAS
DIWNMISQGAYLYVCGDAKGMARDVHRSLHTIAQEQGSMDSTKAEGFVKN
LQTSGRYLRDVW*

(63) The modified AtCPR mutant trAtCPR was constituted by removing the amino acids 2-72 of SEQ ID NO: 7. The sequence of trAtCPR is as follows (SEQ ID NO: 8): (64) TABLE-US-00008

MRRSGSGNSKRVEPLKPLVIKPREEEIDDGRKKVTIFFGTQTGTAEGFAK ALGEEAKARYEKTRFKIVDLDDYAADDDEYEEKLKKEDVAFFFLATYGDG EPTDNAARFYKWFTEGNDRGEWLKNLKYGVFGLGNRQYEHFNKVAKVVDD ILVEQGAQRLVQVGLGDDDQCIEDDFTAWREALWPELDTILREEGDTAVA TPYTAAVLEYRVSIHDSEDAKFNDINMANGNGYTVFDAQHPYKANVAVKR ELHTPESDRSCIHLEFDIAGSGLTYETGDHVGVLCDNLSETVDEALRLLD

MSPDTYFSLHAEKEDGTPISSSLPPPFPPCNLRTALTRYACLLSSPKKSA LVALAAHASDPTEAERLKHLASPAGKVDEYSKWVVESQRSLLEVMAEFPS AKPPLGVFFAGVAPRLQPRFYSISSSPKIAETRIHVTCALVYEKMPTGRI HKGVCSTWMKNAVPYEKSENCSSAPIFVRQSNFKLPSDSKVPIIMIGPGT GLAPFRGFLQERLALVESGVELGPSVLFFGCRNRRMDFIYEEELQRFVES GALAELSVAFSREGPTKEYVQHKMMDKASDIWNMISQGAYLYVCGDAKGM ARDVHRSLHTIAQEQGSMDSTKAEGFVKNLQTSGRYLRDVW*

Example 2. Construction of Recombinant Plasmid Containing Novel F6H Mutant

- (65) Based on pETDuet-1, plasmid pYH45 was constituted by linking AtCPR into NdeI and XhoI sites by one-step cloning method.
- (66) Based on pETDuet-1, plasmid pYH46 was constituted by linking trAtCPR into NdeI and XhoI sites by one-step cloning method.
- (67) Furthermore, pUC19-F6H was constituted by linking the codon optimized coding sequence of F6H (synthesized by GenScript) into pUC19. PCR was conducted using F6H-F/R as primers and pUC19-F6H as templates. The PCR system was 50 μ L (Primestar Max Premix, 25 μ L; final concentration 0.2-0.3 μ M of the two primers; pUC19-F6H, 0.2 μ L; the remaining volume was supplemented with sterilized distilled water). PCR reaction procedure is: pre-denaturation at 98° C. for 2 min, denaturation at 98° C. for 10 s, annealing at 55° C. for 15 s, extension at 72° C. for 20 s, 25 cycles. The amplified fragment of about 1.5 kb was detected by agarose electrophoresis, purified and digested with Nco I and BamH I. The digested fragment was ligated into pYH46 digested by the same enzymes, and the ligated product was transformed into competent cells of *E. coli* DH10B. The plasmid was extracted. The recombinant plasmid pYH59 was verified by double digestion (on restriction sites introduced during plasmid construction) and gene sequencing. Similarly, the digested fragment was ligated into pYH45 to obtain the recombinant plasmid pYH59.
- (68) PCR was conducted using trF6H-F/F6H-R as primers and pUC19-trF6H as templates. Plasmid pYH58 was obtained by ligating the amplified fragment into NdeI and BamH I of pYH46 by one-step cloning method.
- (69) PCR was conducted using 8RP-trF6H-F/F6H-R as primers and pUC19-trF6H as templates. Plasmid pYH60 was obtained by ligating the amplified fragment into NdeI and BamH I of pYH46 by one-step cloning method.
- (70) DNA fragment containing Sumo sequence was amplified using pETSumo (Invitrogen) as templates and Sumo-F/Sumo-trF6H-R as primers. DNA fragment containing trF6H was amplified using pUC19-trF6H as templates and Sumo-trF6H-F/F6H-R as primers. PCR amplification was conducted using Sumo-F/F6H-R as primers and the above two DNA fragments as templates. Plasmid pYH61 was obtained by ligating the amplified fragment into NdeI and BamH I of pYH46 by one-step cloning method.
- (71) DNA fragments containing MBP sequence was amplified using pMAL-c5x (Invitrogen) as templates and MBP-F/MBP-trF6H-R as primers. DNA fragments containing trF6H was amplified using pUC19-trF6H as templates and MBP-trF6H-F/F6H-R as primers. Then PCR amplification was conducted using MBP-F/F6H-R as primers and the above two DNA fragments as templates. Plasmid pYH62 was obtained by ligating the amplified fragment into NdeI and BamH I of pYH46 by one-step cloning method.
- (72) PCR was conducted using 2B1-F/F6H-R as primers and pUC19-trF6H as templates. Plasmid pYH63 was obtained by ligating the amplified fragment into NdeI and BamH I of pYH46 by one-step cloning method.
- (73) PCR was conducted using trF6H-F/F6H-R as primers and pUC19-trF6H as templates. Plasmid pYH64 was obtained by ligating the amplified fragment into NdeI and BamH I of pYH45 by one-step cloning method.
- (74) DNA fragments containing MBP sequence was amplified using pMAL-c5x as templates and

- MBP-F/MBP-trF6H-R as primers. DNA fragments containing trF6H was amplified using pUC19-trF6H as templates and MBP-trF6H-F/F6H-R as primers. Then PCR amplification was conducted using MBP-F/F6H-R as primers and the above two DNA fragments as templates. Plasmid pYH65 was obtained by ligating the amplified fragment into NdeI and BamH I of pYH45 by one-step cloning method.
- (75) PCR was conducted using 2B1-F/F6H-R as primers and pUC19-2B1trF6H as templates. Plasmid pYH66 was obtained by ligating the amplified fragment into NdeI and BamH I of pYH45 by one-step cloning method. Schematic of plasmid pYH66 is shown in FIG. 3.
- (76) The primers used in the above constructions are shown in Table 1. Schematic of the key elements in the constructed plasmid is shown in FIG. **9**A.
- (77) TABLE-US-00009 TABLE 1 Primers Sequences F6H-F TATACCATGGAACTGAGCAGTGTGA (SEQ ID NO: 9) F6H-R CTCGAATTC<u>GGATCC</u>ACTAGTTTAATATAAAGTCGG (SEQ ID NO: 10) trF6H-F CTTTAAGAAGGAGATATACCATGGCGATGCCGAAGAAAAGCTC (SEQ ID 11) 8RP-trF6H-F CTTTAAGAAGGAGATATACCATGGCTCTGTTATTAGCAGTTTTTAT GCCGAAGAAAGCTCTT (SEQ ID NO: 12) MBP-F CTTTAAGAAGGAGATATACCATGGCTAAAATCGAAGAAG (SEQ ID NO: 13) MBPtrF6H-F CTGAAAGACGCGCAGACTATGCCGAAGAAAAGCTC (SEQ ID NO: 14) MBP-trF6H-R GAGCTTTTCTTCGGCATAGTCTGCGCGTCTTTCAG (SEQ ID NO: 15) 2B1-F CTTTAAGAAGGAGATATACCATGGCTAAGAAAACGAGCTCTAAA GGGAAGCTCCCACCAGGACCTAGCATGCCGAAGAAAAGCTCTT (SEQ ID NO: 16) Sumo-F CTTTAAGAAGGAGATATACCATGGCGGACTCAGAAGTCAATCTT (SEQ ID 17) Sumo-trF6H-F GAGAACAGATTGGTGGTATGCCGAAGAAAAGCTCTT (SEQ ID NO: 18) Sumo-trF6H-R AAGAGCTTTTCTTCGGCATACCACCAATCTGTTCTC ID NO: 19)
- Example 3. Construction of Recombinant Plasmids Expressing PAL, 4CL, CHS, CHI and FNSI (78) *Rhodotorula toruloides* PAL (GenBankAccess No. AAA33883.1), *Petroselium crispum* 4CL (GenBank Access No. KF765780.1), *Petunia* X hybrid CHS (GenBankAccess No. KF765781.1), *Medicago sativa* CHI gene (GenBankAccess No. KF765782.1), *Petroselium crispum* FNS I gene (Swiss-ProtAccess No. Q7XZQ8.1) were synthesized by GenScript and constructed into pET28a, forming plasmids pET28-PAL, pET28-4CL, pET28-CHS, pET28a-CHI, and pET28a-FNSI, respectively.
- (79) The primers in Table 2 were synthesized. PCR amplification was conducted using pET28-4CL as templates and 4CL-F-NcoI/4CL-R-BamHI as primers. pYH40 was constructed by ligation of the amplified products with NcoI/BamHI digested pCDFDuet-1.
- (80) PCR amplification was conducted using pET28-CHS as templates and CHS-F-NdeI/CHS-R-XhoI as primers. pYH50 was constructed by ligation of the amplified products with NdeI/XhoI digested pYH40.
- (81) PCR amplification was conducted using pET28a-CHI as templates and T7CHI-F-XhoI/CHI-R-AvrII as primers. Then pYH51 was constructed by ligation of the amplified products with pYH50.
- (82) PCR amplification was conducted using pET28-PAL as templates and T7PAL-F-BamH I/PAL-R-Hind III as primers. The amplified products were digested by BamH I and Hind III, and ligated with pYH51 digested by the same enzymes to form plasmid pYH55.
- (83) PCR amplification was conducted using pET28a-FNSI as templates and FNSI-HindIII-F/FNSI-NotI-R as primers. The amplified products were digested by Hind III and Not I, and ligated with pYH55 digested by the same enzymes to form plasmid pYH57. Schematic of plasmid pYH57 is shown in FIG. 4.
- (84) TABLE-US-00010 TABLE 2 Primers Sequences 4CL-F-NcoI TATACCATGGGTGACTGCGTTGCCCCG (SEQ ID NO: 20) 4CL-R-BamHI

CGGGATCCTTACTTCGGCAGGTCGCCGCTC (SEQ ID NO: 21) T7PAL-F-BamHI CGGGATCCCTTATGCGACTCCTGCATTAG (SEQ ID NO: 22) PAL-R-HindIII GCCCAAGCTTTTATGCCAGCATCTTC (SEQ ID NO: 23) CHS-F-NdeI AGATATACATATGGTTACGGTGGAAGAATAC (SEQ ID NO: 24) CHS-R-XhoI CCGCTCGAGTTAGGTAGCCACACTATGCAG (SEQ ID NO: 25) T7CHI-F-XhoI CCGCTCGAGCTAGAAATAATTTTGTTTAAC (SEQ ID NO: 26) CHI-R-AvrII GAGCCTAGGTTAGCTACCGATTTTAAAG (SEQ ID NO: 27) FNSI-HindIII-F GAAGATGCTGGCATAAAAGCTTCGATCCCGCGAAATTA (SEQ ID NO: 28) FNSI-NotI-R CGACTTAAGCATTATGCGGCCGCCTACGCCAGGTTTTC (SEQ ID NO: 29) Example 4. Construction and Functional Verification of Baicalein and Scutellarein Synthesizing Strains

- (85) The biosynthesis process of baicalein and scutellarein is shown in FIG. 1.
- (86) The engineering strain BL21(DE3)-pYH57-pYH66 was obtained by co-transformation of the recombinant plasmids pYH66 and pYH57 into *E. coli* BL21 (DE3) competent cells.
- (87) The cells were cultured in LB solid medium (containing 80 μ g/ml spectinomycin, 100 μ g/ml ampicillin) overnight at 37° C. Single colony was transferred to a 2 mL LB liquid medium (containing 80 μ g/ml spectinomycin, and 100 μ g/ml ampicillin) and incubated overnight. The bacterial fluid was transferred to a new 10 ml MOPS liquid medium with antibiotics and incubated at 37° C. and 250 r/min until OD.sub.600 reached 0.5-0.6. The culture was cooled down to 16° C. in a water bath. Then inducer IPTG was added at a final concentration of 1 mM, and different concentrations of sterilized phenylalanine or tyrosine was added. The mixture was placed at 22° C. for low temperature induction, and cultured for 48 h at 220 r/min. The BL21 (DE3) recombinant strain containing empty plasmid pETDuet-1 and pCDFDuet-1 without foreign gene(s) was used as blank control, and the culture procedure was the same as above.
- (88) At the same time, the recombinant plasmids listed in Table 2 were transformed into *E. coli* and cultured to detect the production of their products.
- (89) After culture, the expression of compounds in each recombinant strain harboring recombinant plasmid was detected, which are shown in Table 3.
- (90) TABLE-US-00011 TABLE 3 Plasmids Features Uses pYH40 expressing 4CL Synthesis of pinocembrin and pYH50 expressing 4CL and CHS proteins naringenin pYH51 expressing 4CL, CHS and CHI proteins pYH55 expressing PAL, and CHI proteins pYH57 expressing PAL, 4CL, CHS, CHI and FNSI Synthesis chrysin from proteins phenylalanine Synthesis of apigenin from of tyrosine pYH58 expressing trF6H and trCPR proteins Synthesis of baicalein pYH59 expressing F6H and CPR proteins chrysin pYH60 expressing 8RPF6H and trCPR proteins Synthesis of scutellarein from pYH61 expressing SumotrF6H trCPR proteins apigenin pYH62 expressing MBPtrF6H and trCPR proteins pYH63 expressing 2B1trF6H and trCPR proteins pYH64 expressing trF6H and CPR proteins pYH65 expressing MBPtrF6H and CPR proteins pYH66 expressing 2B1trF6H and CPR proteins
- (91) It was verified that each recombinant strain of the disclosure can successfully synthesize the target compound.
- (92) HPLC results of engineering strain BL21(DE3)-pYH57-pYH66 and baicalein standard are shown in FIG. **5**. Mass spectrum results of baicalein produced by engineering strain BL21(DE3)-pYH57-pYH66 are shown in FIG. **6**.
- (93) HPLC results of engineering strain BL21(DE3)-pYH57-pYH66 and scutellarein standard are shown in FIG. **7**. Mass spectrum results of scutellarein produced by engineering strain BL21(DE3)-pYH57-pYH66 are shown in FIG. **8**.
- Example 5: Production with Chrysin as Substrate
- (94) Six recombinant plasmids (pYH58 to pYH66) were transformed into competent cells of *E. coli*

BL21 (DE3) to obtain the engineering strains BL21(DE3)-pYH58 to BL21(DE3)-pYH66, respectively.

- (95) The cells were cultured in LB solid medium (containing 100 µg/ml ampicillin) overnight at 37° C. Single colony was transferred to a 2 mL LB liquid medium (containing 100 µg/ml ampicillin) and incubated overnight. The bacterial fluid was transferred to a new 20 ml MOPS liquid medium with antibiotics and incubated at 37° C. and 250 r/min until OD.sub.600 reached 0.5-0.6. The culture was cooled down to 16° C. in a water bath. Then inducer IPTG was added at a final concentration of 1 mM. The mixture was cultured for 12 h at 22° C. and 220 r/min. After centrifugation at 6000 rpm, 4° C. for 10 min, the supernatant was removed, and the bacteria were collected and re-suspended in a reaction buffer (50 mM Tris-HCl, pH 7.4, 0.1% Trixton) until OD.sub.600 reached 30.5 µL chrysin (25 mM) and 2.5 µL NADPH (100 mM) were added to 1 mL of the suspension of the recombinant bacteria, and the reaction was continued at 37° C. for 8 hours. After completion of the reaction, the solution was extracted for 3 times by 10 µL HCl (6 M) and 1 mL ethyl acetate. The organic phase was concentrated, and the resulting residue was dissolved with 200 µL methanol, wherein 10 µL was used for HPLC analysis.
- (96) The conversion rates of baicalein from chrysin in each recombinant *E. coli* were shown in FIG. **9**B.
- (97) HPLC results of the catalytic reaction solution of each recombinant *E. coli* were shown in FIG. **9**C.
- (98) Each reference provided herein is incorporated by reference to the same extent as if each reference was individually incorporated by reference. In addition, it should be understood that based on the above teaching content of the disclosure, those skilled in the art can practice various changes or modifications to the disclosure, and these equivalent forms also fall within the scope of the appended claims.

Claims

- 1. A method of producing baicalein and scutellarein, comprising: (1) introducing genes expressing flavone 6-hydroxylase and cytochrome P450 oxidoreductase into a host cell to obtain a recombinant strain, wherein said flavone 6-hydroxylase is a mutant flavone 6-hydroxylase with the N-terminal amino acids 2 to 25 truncated and fused with a peptide tag, said peptide tag is a 2B1 family soluble protein of cytochrome P450, and said host cell is a *Escherichia coli* cell; (2) culturing the recombinant host cell in a culture system containing chrysin or apigenin to produce baicalein or scutellarein.
- 2. A method of producing baicalein and scutellarein, comprising: (1) introducing genes expressing flavone 6-hydroxylase and cytochrome P450 oxidoreductase, as well as genes for synthesizing chrysin or apigenin, into a host cell, wherein said flavone 6-hydroxylase is a mutant flavone 6-hydroxylase with the N-terminal amino acids 2 to 25 truncated and fused with a peptide tag, said peptide tag is a 2B1 family soluble protein of cytochrome P450, and said host cell is a *Escherichia coli* cell; (2) culturing the host cell in a culture system containing phenylalanine and/or tyrosine to produce baicalein or scutellarein.
- 3. The method according to claim 2, wherein, the genes for synthesizing chrysin or apigenin comprises: genes expressing phenylalanine ammonia-lyase, 4-coumarate: CoA ligase, chalcone synthase, chalcone isomerase and flavone synthase I.
- 4. The method according to claim 3, wherein, when introduced into the host cell, the genes expressing phenylalanine ammonia-lyase, 4-coumarate: CoA ligase, chalcone synthase, chalcone isomerase and flavone synthase I are in the same expression vector.
- 5. The method according to claim 2, wherein, the cytochrome P450 oxidoreductase is a full-length or mutant cytochrome P450 oxidoreductase with the N-terminal amino acids (1-20) to (60-85) truncated.

- 6. The method according to claim 2, wherein, the cytochrome P450 oxidoreductase is a full-length or mutant cytochrome P450 oxidoreductase with the N-terminal amino acids (2-10) to (65-80) truncated.
- 7. The method according to claim 2, wherein, the cytochrome P450 oxidoreductase is a full-length or mutant cytochrome P450 oxidoreductase with the N-terminal amino acids (2-5) to (70-75) truncated.