人参皂苷合成基因鉴定和初步分析

Characterization and Preliminary Analysis of Ginsenoside Synthesis Genes

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RESEARCH CONTENT, PURPOSE AND SIGNIFICANCE

人参（*Panax ginseng C. A. Meyer*）是五加科、人参属多年生草本植物。分布于中国、俄罗斯和朝鲜；在中国分布于辽宁东部、吉林东半部和黑龙江东部，人参主要功用是大补元气、健脾丰晰、宁神益智，用于治疗气虚欲脱、脾气不足、肺气亏虚等症。

人参根据生长环境可分为野山参、林下参、移山参、园参。

人参根据产地可分为吉林参、辽参、高丽参、日本人参（东洋参）等。

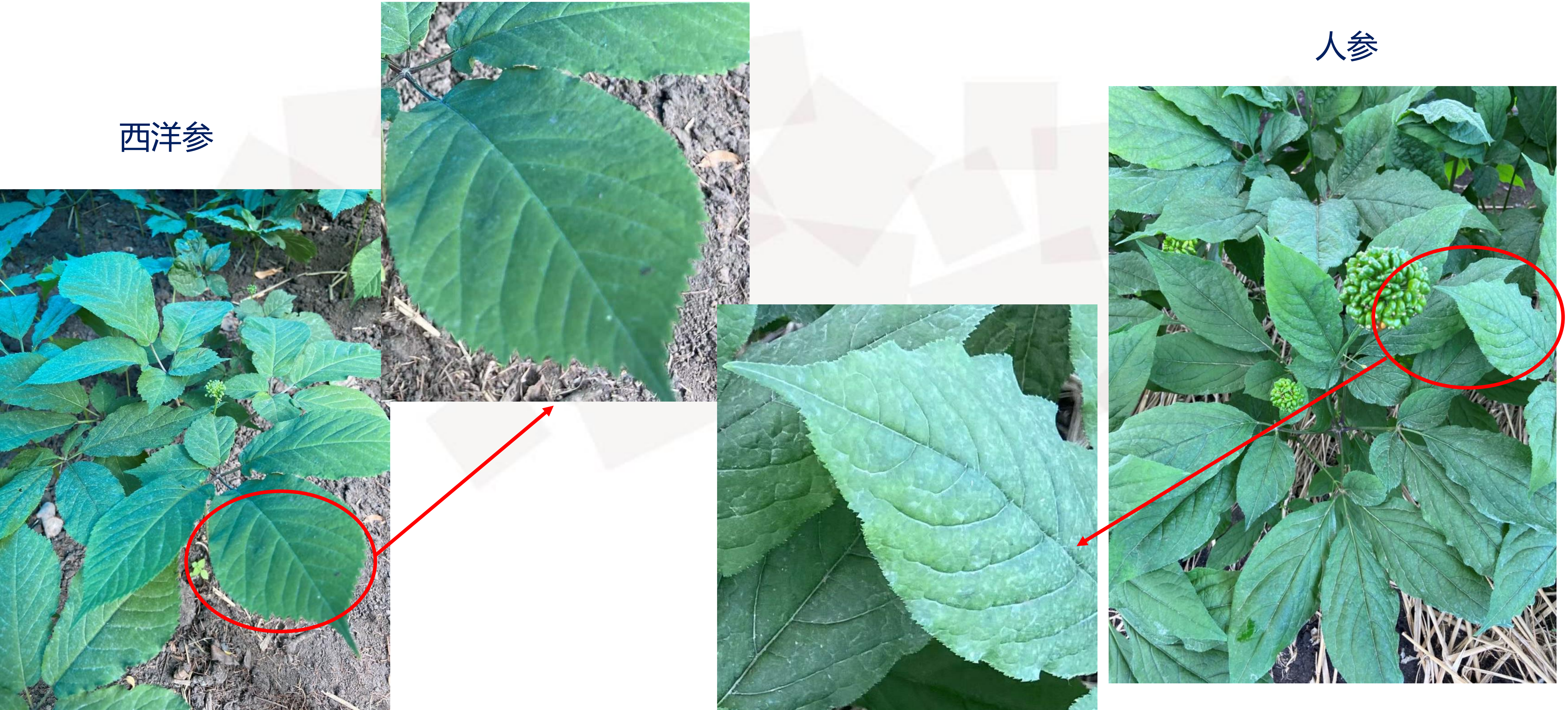
➡ 西洋参（*Panax quiquefolium L.*）同为五加科、人参属多年生草本植物，又名洋参、西参、花旗参，原产北美，我国亦有栽培，主要功效是补肺降火、养胃生津，用于治疗阴虚火旺、喘咳痰血等症。。

➡ 高丽参（*Panax ginseng* ）又称为朝鲜参，是韩国当地种植的人参，被韩国称为高丽参。

野山参、林下参与园参

近缘种区别

西洋参总花梗与叶柄近等长或稍长，小叶片倒卵形，上面脉上几乎无刚毛，边缘的锯齿不规则且较粗大。



Seed

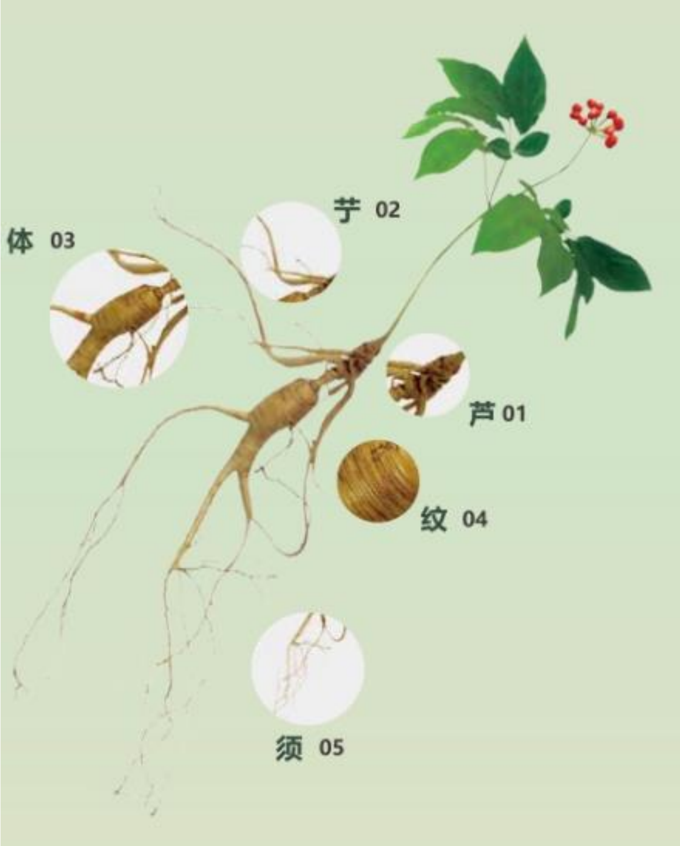
Fruit

人参皂苷

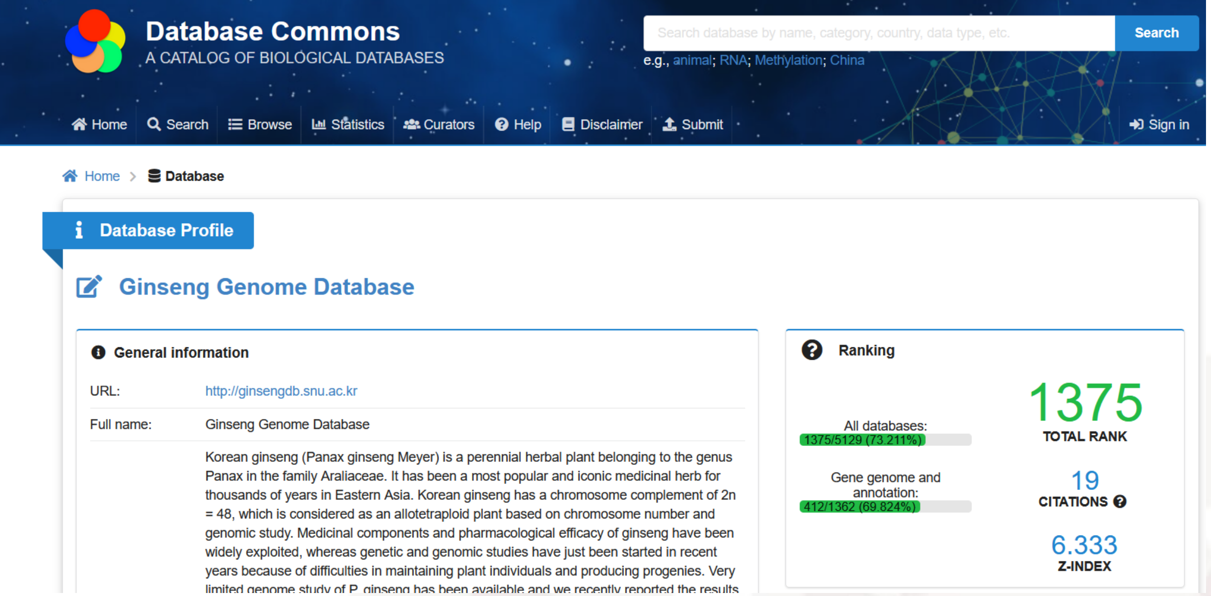
- 人参皂苷（Ginsenoside）是一类固醇类化合物，又称三萜皂苷。主要存在于人参属药材中。
- 人参皂苷作为人参的核心成分具有极大药用价值和经济价值。
- 现代医学研究证明其对中枢神经系统、心血管系统、内分泌系统和免疫系统等均有良好的药理作用。

人参传说

RUN???



人参基因组数据库



Ginseng Genome Database

General information

URL:	http://ginsengdb.snu.ac.kr
Full name:	Ginseng Genome Database
	Korean ginseng (Panax ginseng Meyer) is a perennial herbal plant belonging to the genus Panax in the family Araliaceae. It has been a most popular and iconic medicinal herb for thousands of years in Eastern Asia. Korean ginseng has a chromosome complement of 2n = 48, which is considered as an allotetraploid plant based on chromosome number and genomic study. Medicinal components and pharmacological efficacy of ginseng have been widely exploited, whereas genetic and genomic studies have just been started in recent years because of difficulties in maintaining plant individuals and producing progenies. Very limited genome study of P. ginseng has been available and we recently reported the results

Ranking

All databases: 1375/5129 (73.211%)

Gene genome and annotation: 412/1362 (69.824%)

1375 TOTAL RANK

19 CITATIONS

6.333 Z-INDEX

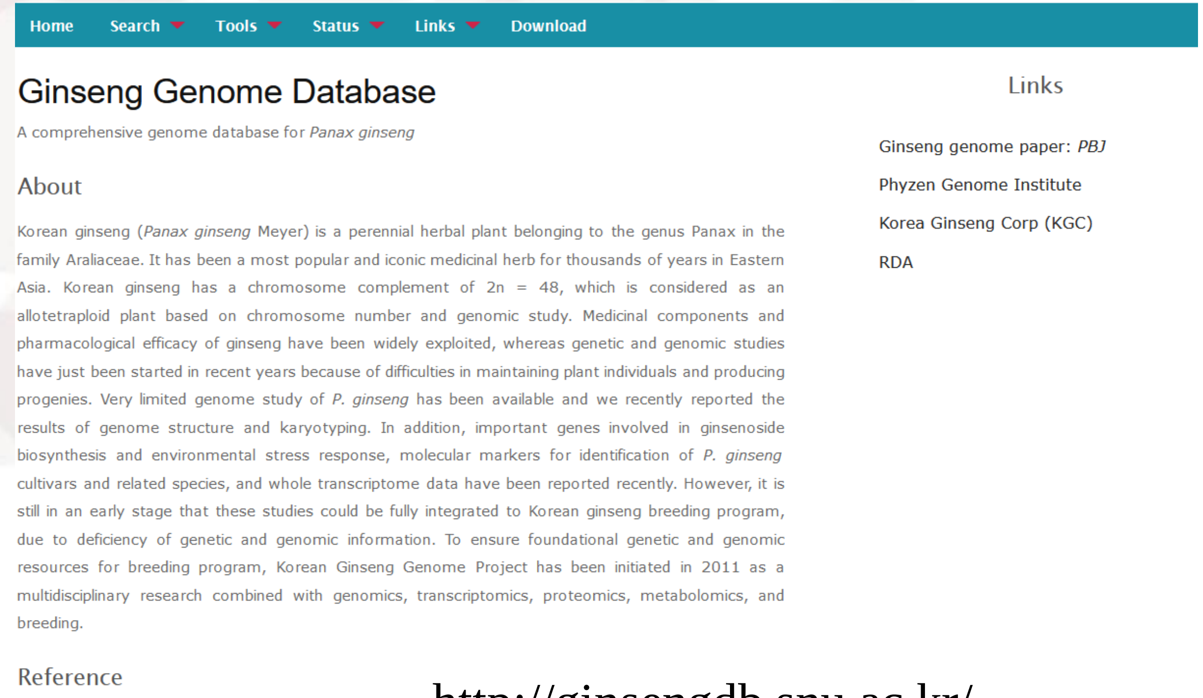
https://ngdc.cncb.ac.cn/databasecommons/search?term=ginseng

ASM2020560v1

Organism name: Panax ginseng (eudicots)
Isolate: WZH-0002
BioSample: SAMN20855168
BioProject: PRJNA752920
Submitter: Fudan university
Date: 2021/10/04
Assembly level: Chromosome
Genome representation: full
RefSeq category: representative genome
GenBank assembly accession: GCA_020205605.1 (latest)
RefSeq assembly accession: n/a
RefSeq assembly and GenBank assembly identical: n/a
WGS Project: JAINUU01
Assembly method: WTDBG2 v. DEC-2020
Expected final version: yes
Genome coverage: 77.0x
Sequencing technology: Oxford Nanopore

IDs: 11059801 [UID] 29228028 [GenBank]

See Genome Information for **Panax ginseng**



Ginseng Genome Database

A comprehensive genome database for *Panax ginseng*

About

Korean ginseng (*Panax ginseng* Meyer) is a perennial herbal plant belonging to the genus Panax in the family Araliaceae. It has been a most popular and iconic medicinal herb for thousands of years in Eastern Asia. Korean ginseng has a chromosome complement of 2n = 48, which is considered as an allotetraploid plant based on chromosome number and genomic study. Medicinal components and pharmacological efficacy of ginseng have been widely exploited, whereas genetic and genomic studies have just been started in recent years because of difficulties in maintaining plant individuals and producing progenies. Very limited genome study of *P. ginseng* has been available and we recently reported the results of genome structure and karyotyping. In addition, important genes involved in ginsenoside biosynthesis and environmental stress response, molecular markers for identification of *P. ginseng* cultivars and related species, and whole transcriptome data have been reported recently. However, it is still in an early stage that these studies could be fully integrated to Korean ginseng breeding program, due to deficiency of genetic and genomic information. To ensure foundational genetic and genomic resources for breeding program, Korean Ginseng Genome Project has been initiated in 2011 as a multidisciplinary research combined with genomics, transcriptomics, proteomics, metabolomics, and breeding.

Reference

Links

- Ginseng genome paper: *PBJ*
- Phyzen Genome Institute
- Korea Ginseng Corp (KGC)
- RDA

http://ginsengdb.snu.ac.kr/

研究背景

RESEARCH BACKGROUNDS

中国农业科学院特产研究所

- 休眠在有利条件下是种子完成萌发的障碍，也给人工栽培和繁殖带来了困难，因此打破种子休眠或者缩短休眠期限对实际生产具有重大的意义。
- 人参种子属种胚发育不完全类型，具有发芽缓慢、休眠的习性。在自然条件下，人参完成两个后熟阶段需要18-20个月的时间。虽然现有的研究方法（层积和激素处理）一定程度上缩短了将人参种子的休眠期限，但工作繁琐且成本较高，且关于人参种子休眠解除分子的机制也知之甚少。
- 研究发现，去除胚乳可以使休眠期较长的种子提前萌发（红豆杉），提高种子发芽率（山茱萸）。

实验背景

发芽情况

激素含量（ABA、GA等）

皂苷含量

转录组

Transcriptome sequencing

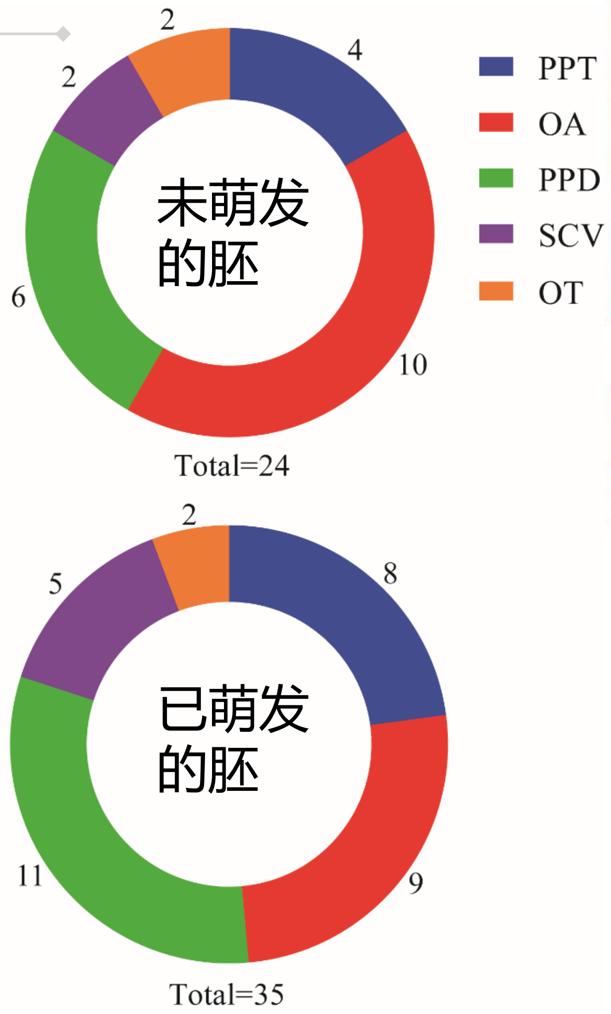
(A)完整种子

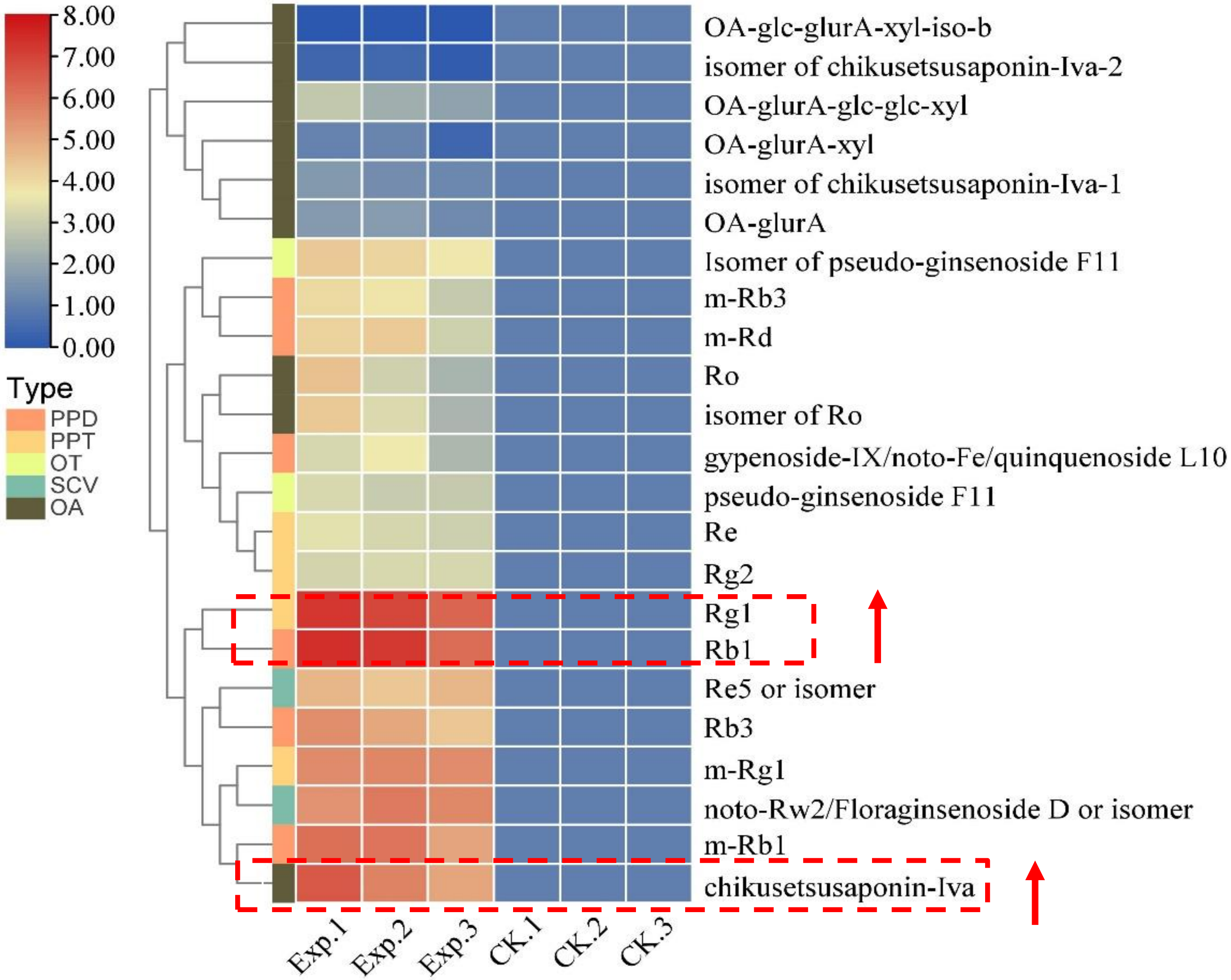
(B)滤纸培养

(C)纯琼脂培养基

(D) MS培养基

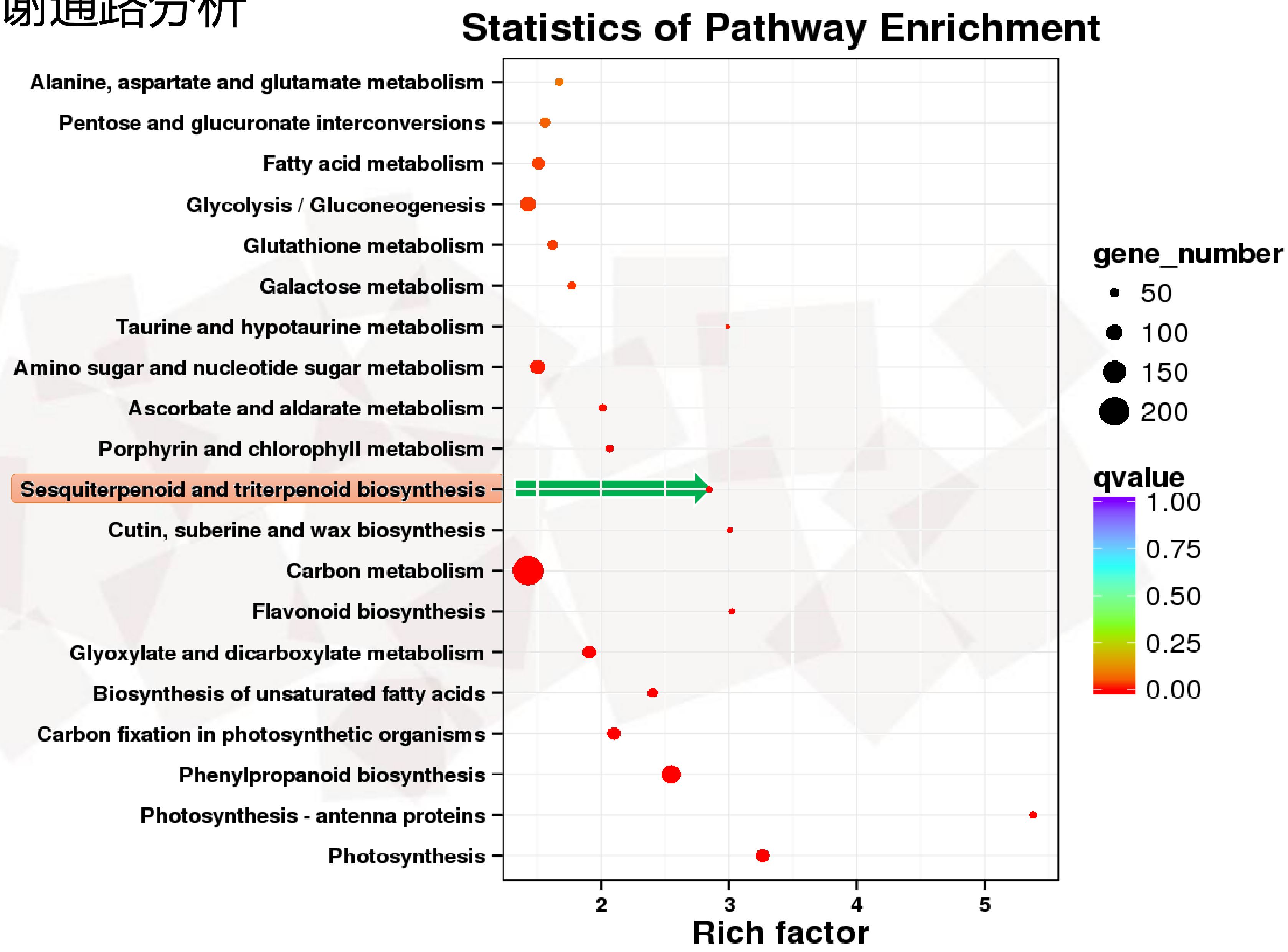
皂苷



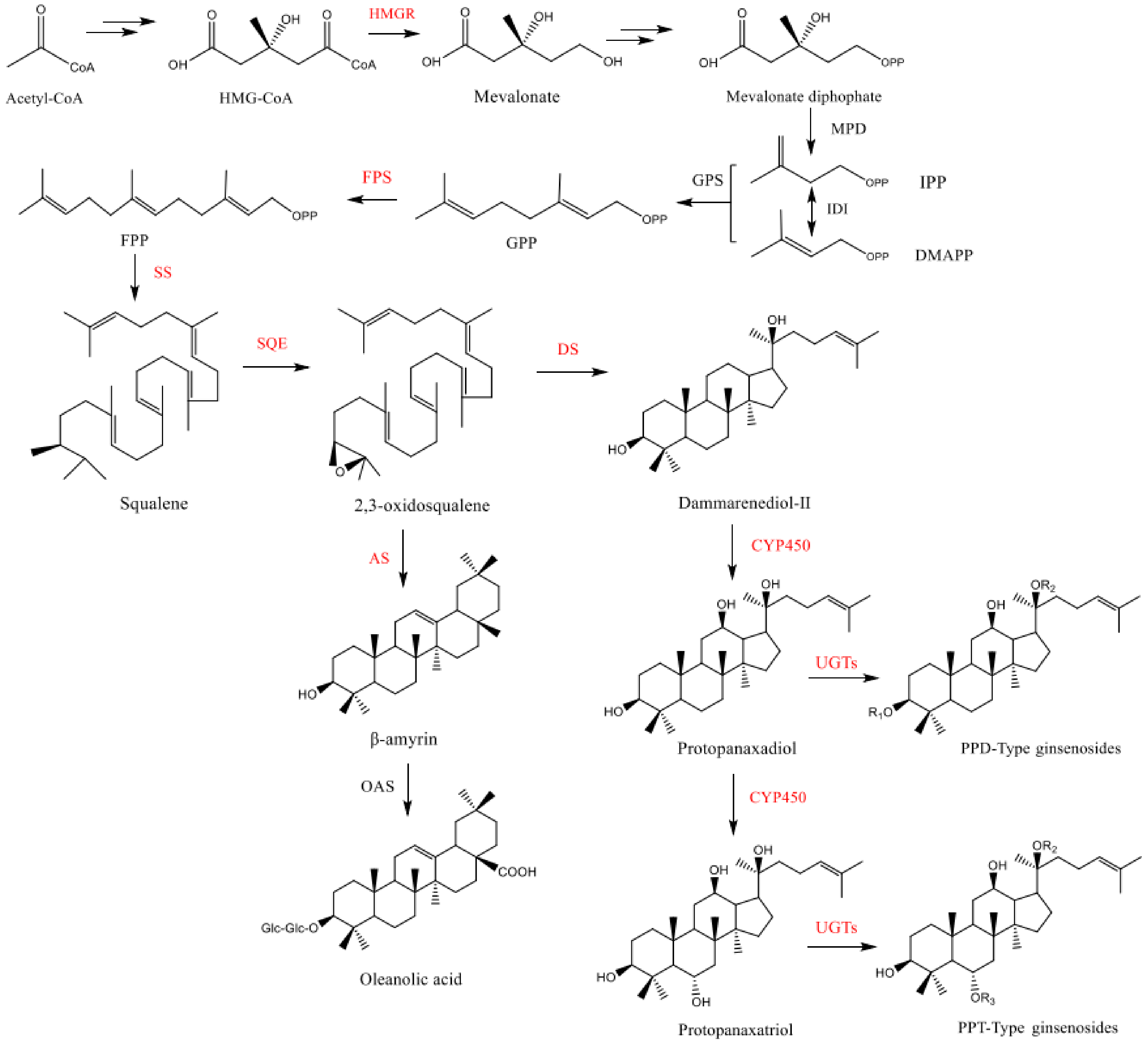


皂苷含量都有不同程度的增加，增加最显著的则是PPD型皂苷的Rb1，增加了131.56倍，其次是PPT型的Rg1，增加了118.83倍，OA型的chikusetsusaponin-Iva增加了60.41倍。

差异表达基因KEGG代谢通路分析



注：图中每一个圆表示一个KEGG通路，纵坐标表示通路名称，横坐标为富集因子（Enrichment Factor）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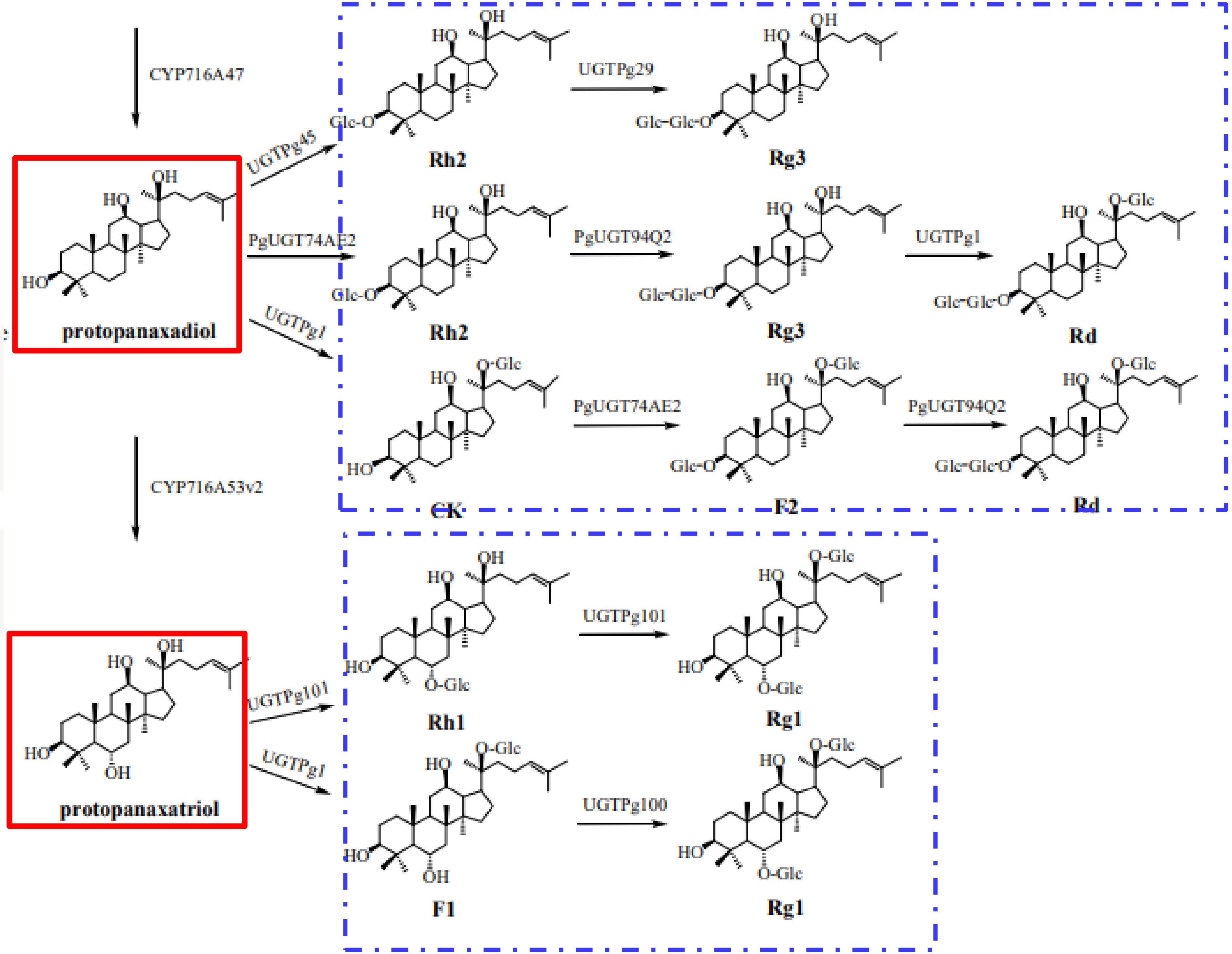
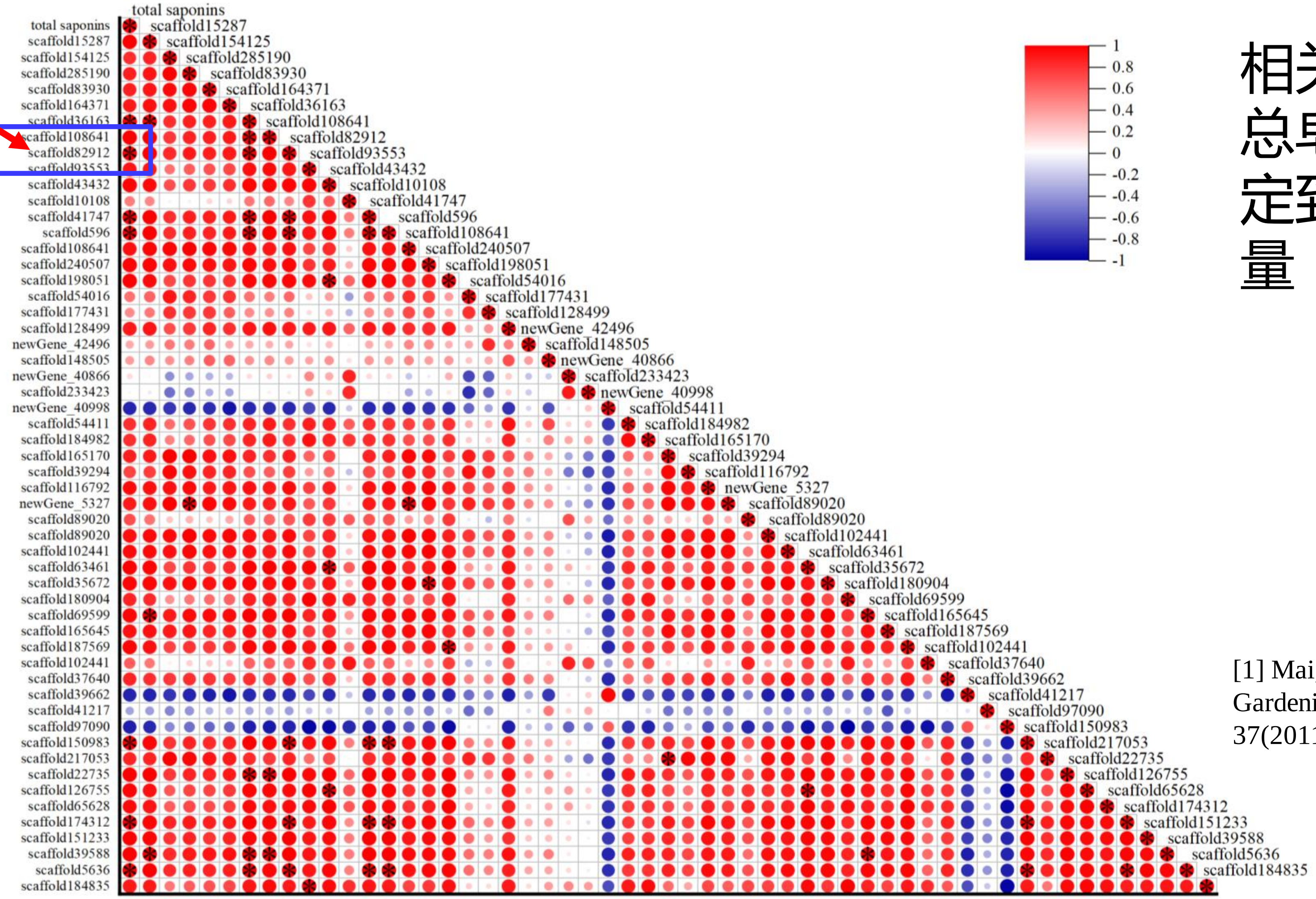
HMG-CoA
HMGR
Mevalonate
Mevalonate diphophate
MPD
IPP
IDI
DMAPP
GPS
GPP
FPS
FPP
SS
Squalene
SQE
2,3-oxidosqualene
DS
Dammarenediol-II
AS
β-amyrin
OAS
Oleanolic acid
CYP450
Protopanaxadiol
UGTs
PPD-Type ginsenosides
CYP450
Protopanaxatriol
UGTs
PPT-Type ginsenosides
CoA
OH
OPP
HO
R1O
OR2
OR3
COOH
Glc-Glc-O

原人参二醇
（PPD）

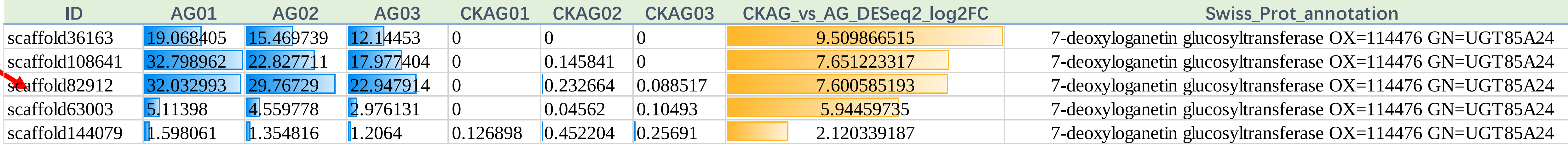
原人参三醇
（PPT）



相关性分析：总皂苷含量与转录组鉴定到的糖基转移酶表达量



[1] Mai, N. , et al. "Iridoid-specific Glucosyltransferase from Gardenia jasminoides ." *Journal of Biological Chemistry* 286. 37(2011):32866-32874.



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scaffold82912	32.032993	29.76729	22.947914	0	0.232664	0.088517	7.600585193	7-deoxyloganetin glucosyltransferase OX=114476 GN=UGT85A24
scaffold63003	5.11398	4.559778	2.976131	0	0.04562	0.10493	5.94459735	7-deoxyloganetin glucosyltransferase OX=114476 GN=UGT85A24
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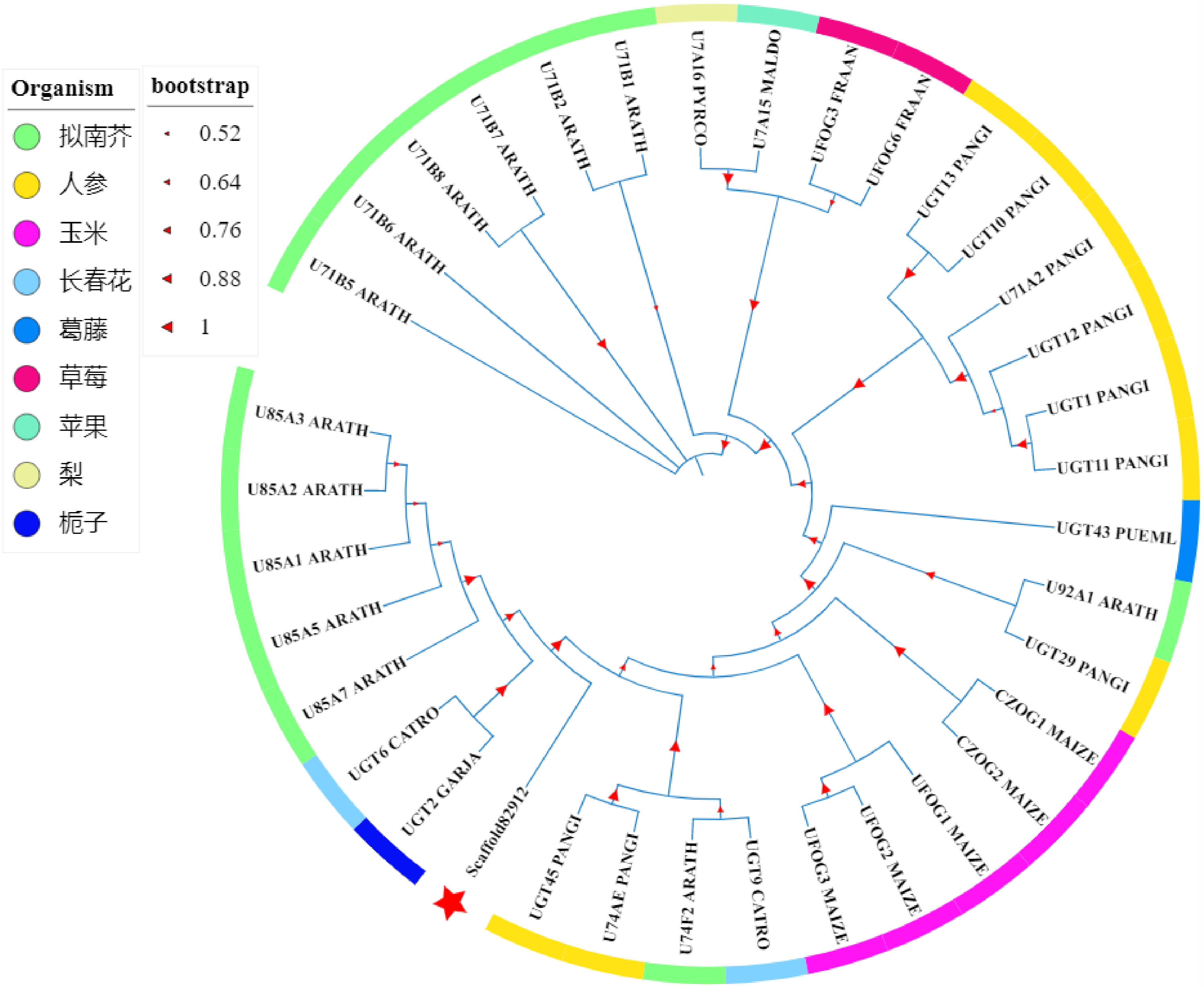
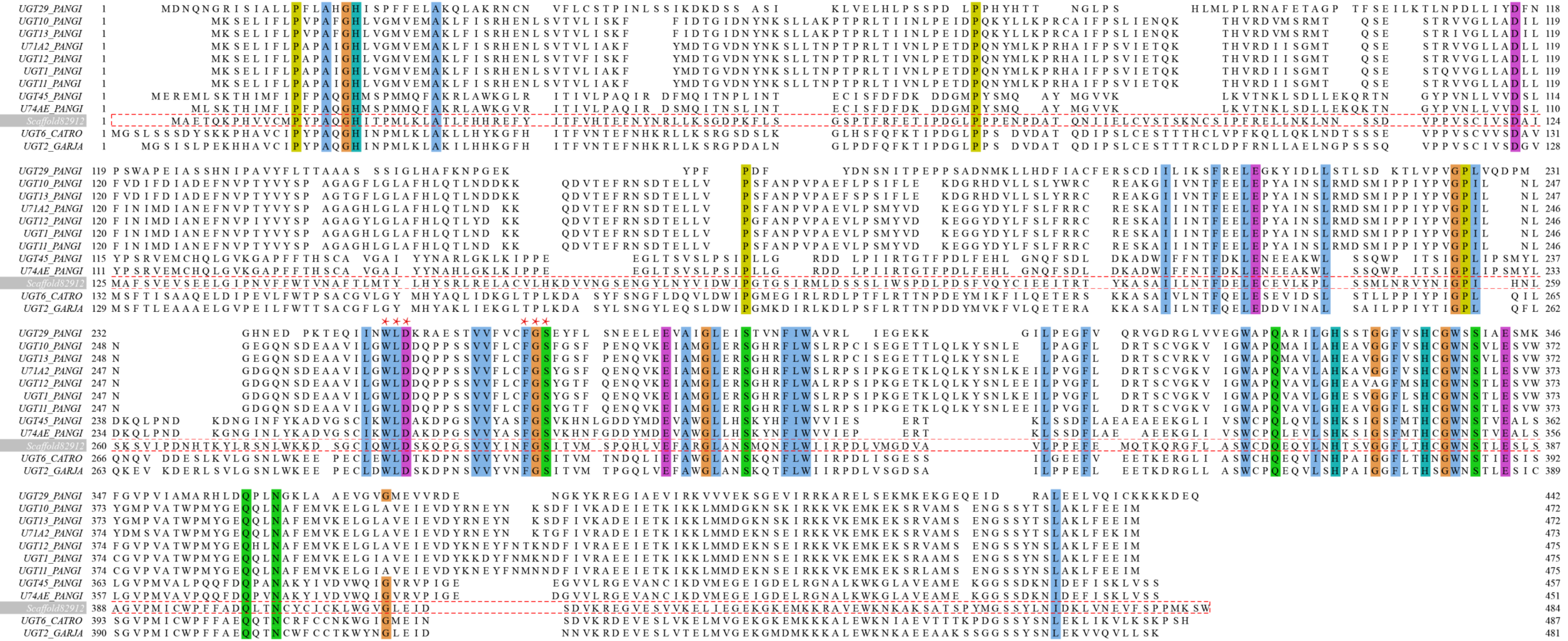


结构域与保守位点



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Scaffold82912 388 AGVPMICWPFFADQLTNCYCICKLWGVGLEID SDVKREGVESVVKELIEGEKGKEMKKRAVEWKNKAKSATSPYMGSSYLNIDKLVNEVFSPPMKSW 484
UGT6_CATRO    393 SGVPMICWPFFAEQQTNCRFCCNKWGIGMEIN SDVKRDEVESLVKELMVGEKGKEMKKKALEWKNIAEVTTTKPDGSSYSNLEKLIKVLKSKPSH 487
UGT2_GARJA    390 SGVPMICWPFFAEQQTNCWFCCTKWYNGLEID NNVKRDEVESLVTELMVGEKGMDMKKKALEWKNKAEEAAKSSGGSSYSNLEKVVQVLLSK 481
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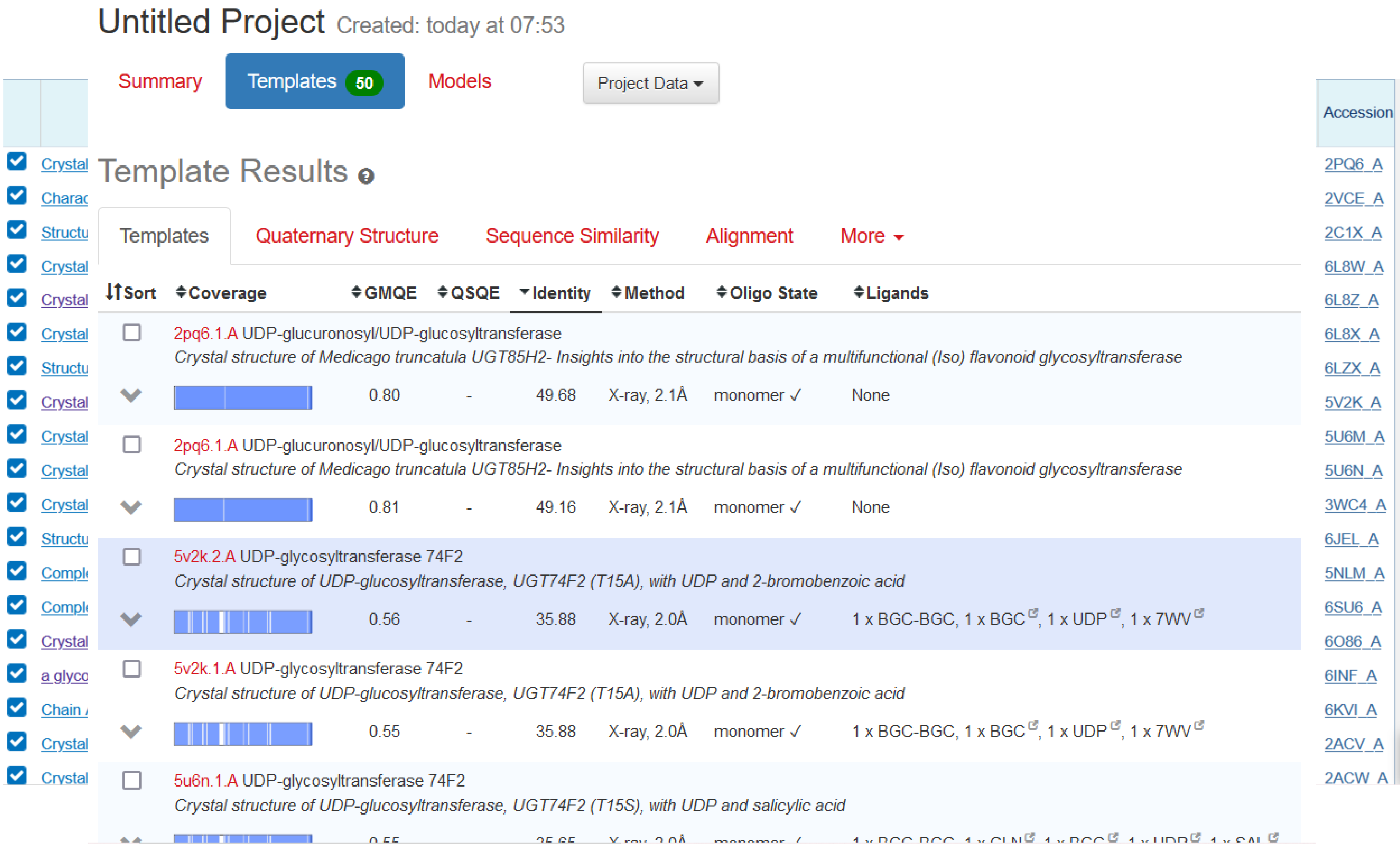

Sort		Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
☐	2pq6.1.A UDP-glucuronosyl/UDP-glucosyltransferase *Crystal structure of Medicago truncatula UGT85H2- Insights into the structural basis of a multifunctional (Iso) flavonoid glycosyltransferase*		0.80	-	49.68	X-ray, 2.1Å	monomer ✓	None
☐	2pq6.1.A UDP-glucuronosyl/UDP-glucosyltransferase *Crystal structure of Medicago truncatula UGT85H2- Insights into the structural basis of a multifunctional (Iso) flavonoid glycosyltransferase*		0.81	-	49.16	X-ray, 2.1Å	monomer ✓	None
☐	5v2k.2.A UDP-glycosyltransferase 74F2 *Crystal structure of UDP-glucosyltransferase, UGT74F2 (T15A), with UDP and 2-bromobenzoic acid*		0.56	-	35.88	X-ray, 2.0Å	monomer ✓	1 x BGC-BGC, 1 x BGC, 1 x UDP, 1 x 7WV
☐	5v2k.1.A UDP-glycosyltransferase 74F2 *Crystal structure of UDP-glucosyltransferase, UGT74F2 (T15A), with UDP and 2-bromobenzoic acid*		0.55	-	35.88	X-ray, 2.0Å	monomer ✓	1 x BGC-BGC, 1 x BGC, 1 x UDP, 1 x 7WV
☐	5u6n.1.A UDP-glycosyltransferase 74F2 *Crystal structure of UDP-glucosyltransferase, UGT74F2 (T15S), with UDP and salicylic acid*		0.55	-	35.65	X-ray, 2.0Å	monomer ✓	1 x BGC-BGC, 1 x CLN, 1 x BGC, 1 x UDP, 1 x SAL

Accession
2PQ6_A
2VCE_A
2C1X_A
6L8W_A
6L8Z_A
6L8X_A
6LZX_A
5V2K_A
5U6M_A
5U6N_A
3WC4_A
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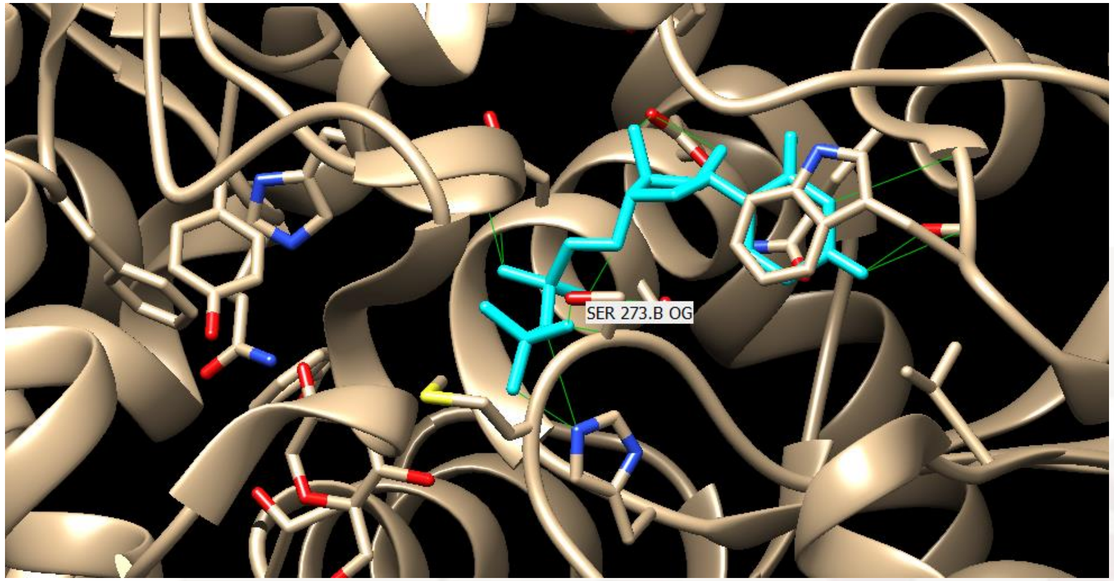
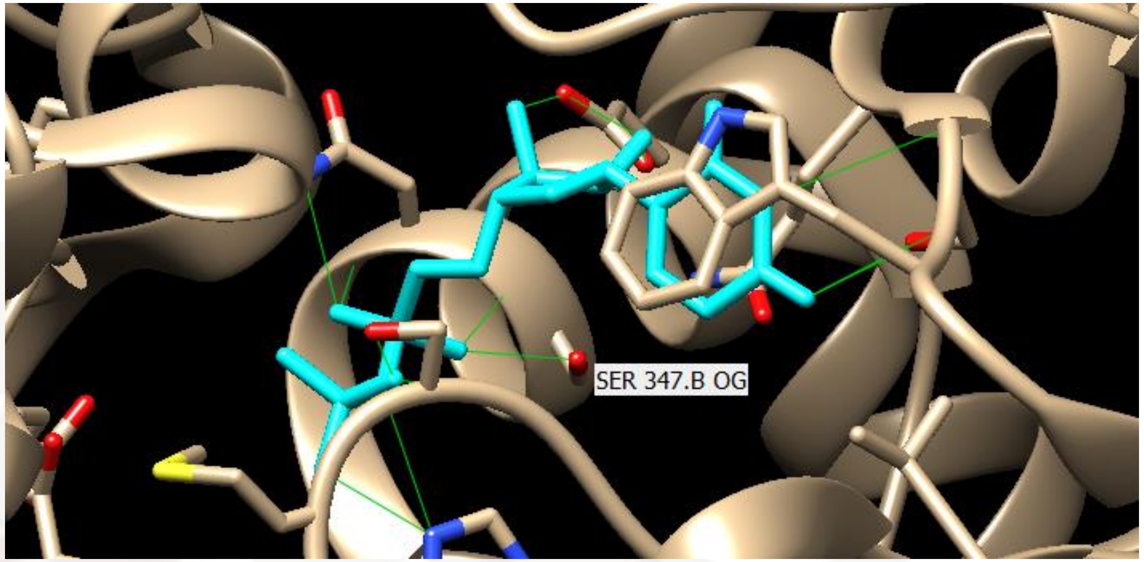
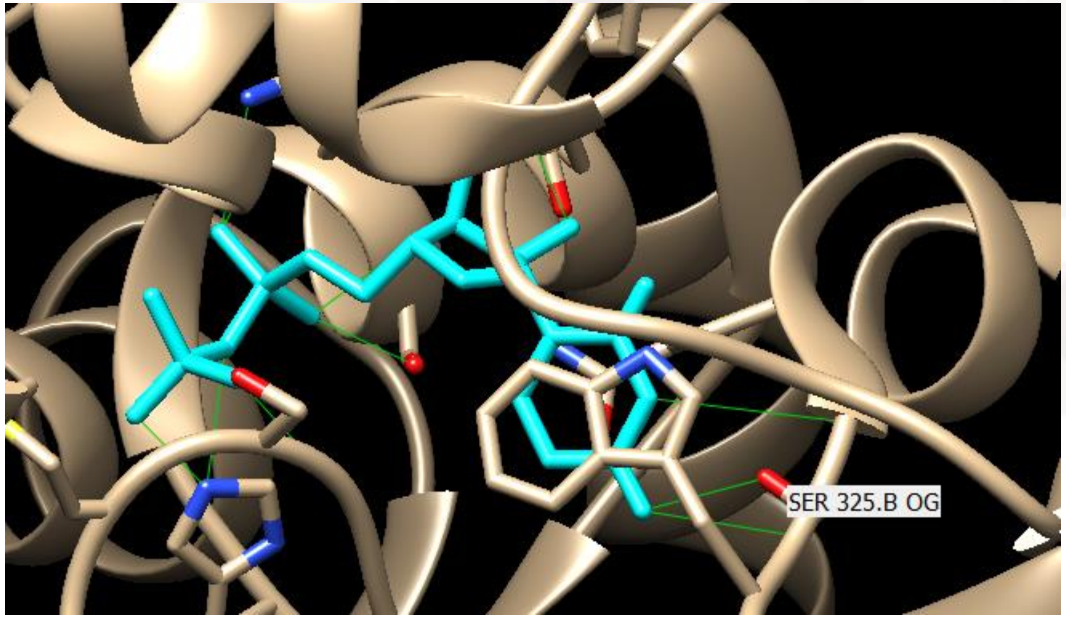
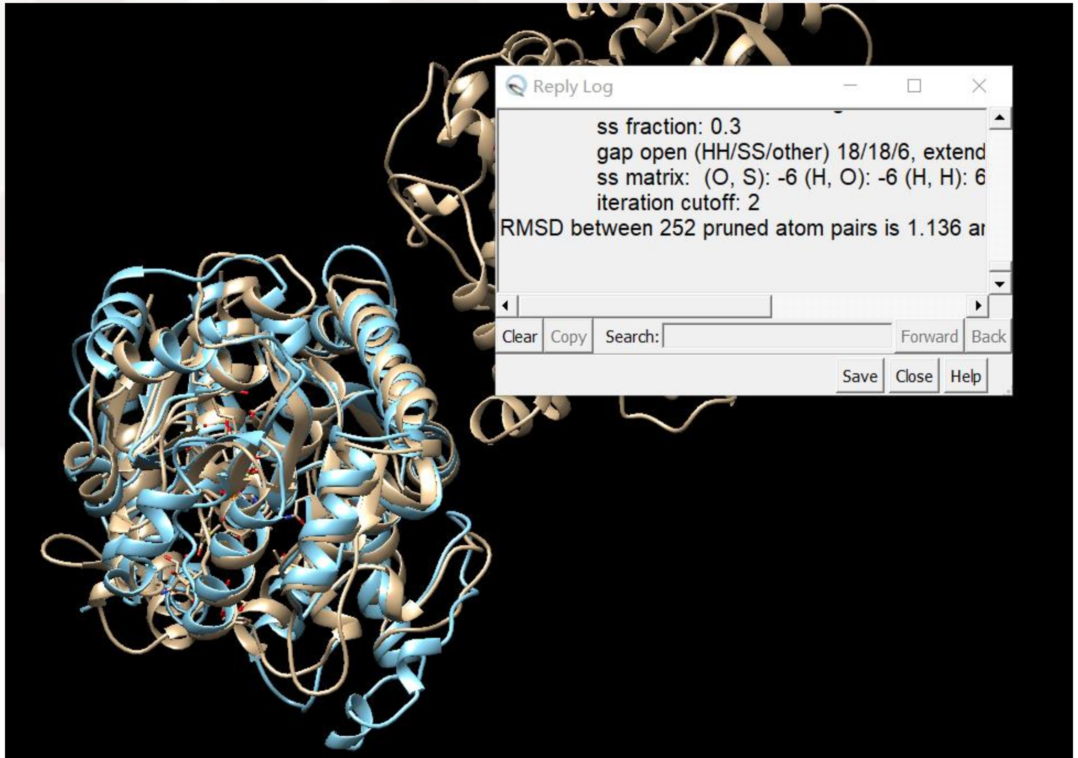
6O86_A
6INF_A
6KVI_A
2ACV_A
2ACW_A

5U6S









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        gap open (HH/SS/other) 18/18/6, extend
        ss matrix:  (O, S): -6 (H, O): -6 (H, H): 6
        iteration cutoff: 2
RMSD between 252 pruned atom pairs is 1.136 ar
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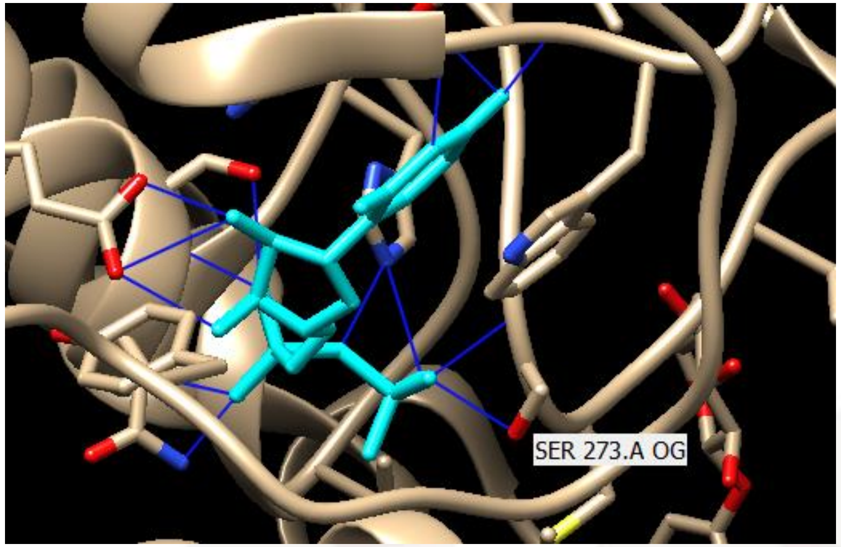
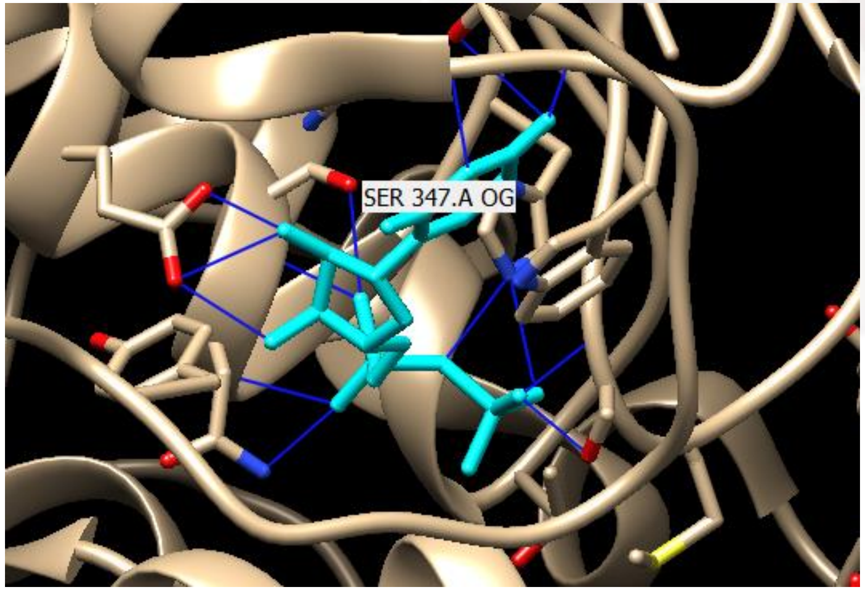
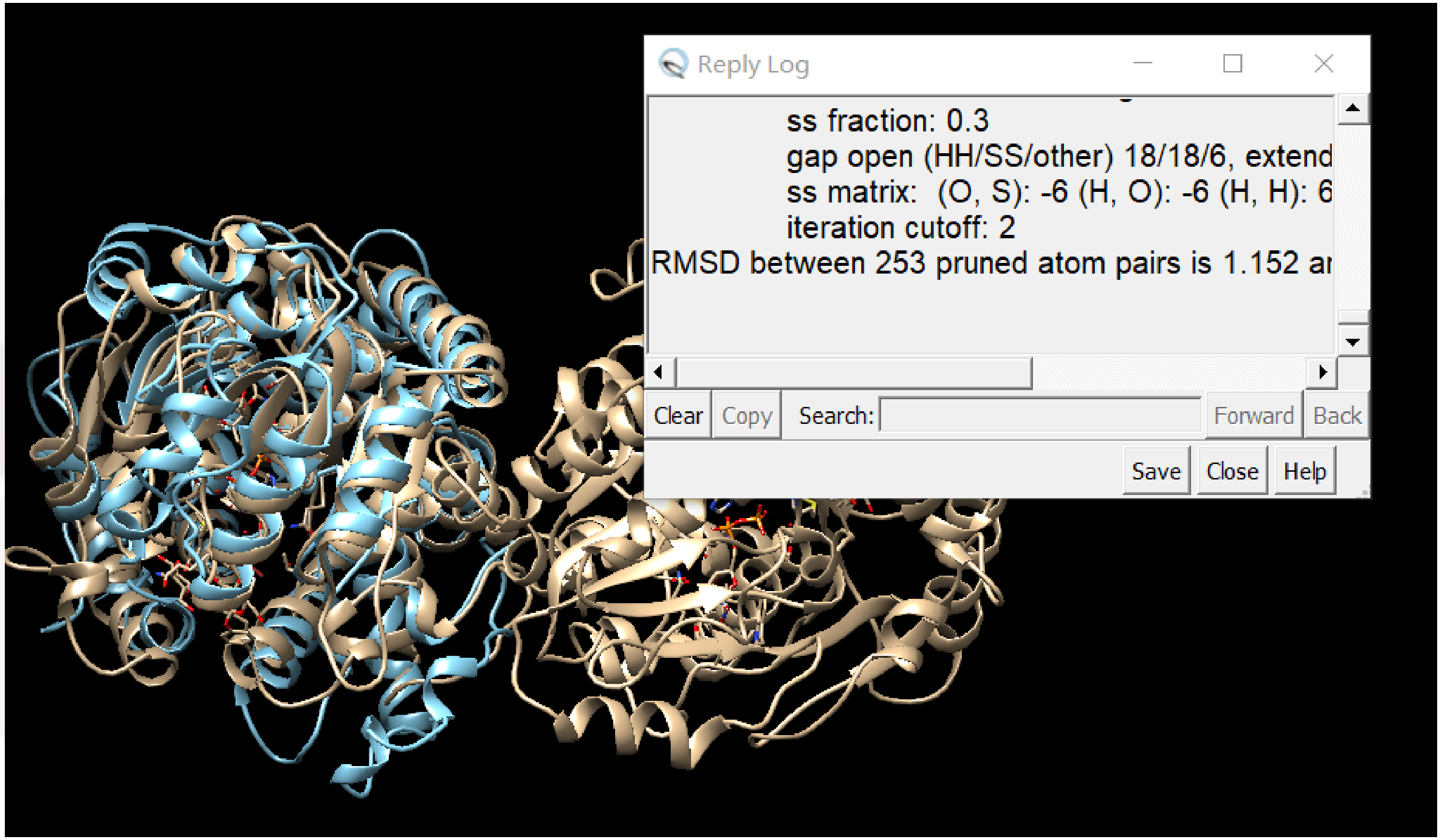
5V2K







```
        ss fraction: 0.3
        gap open (HH/SS/other) 18/18/6, extend
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        iteration cutoff: 2
RMSD between 253 pruned atom pairs is 1.152 ar
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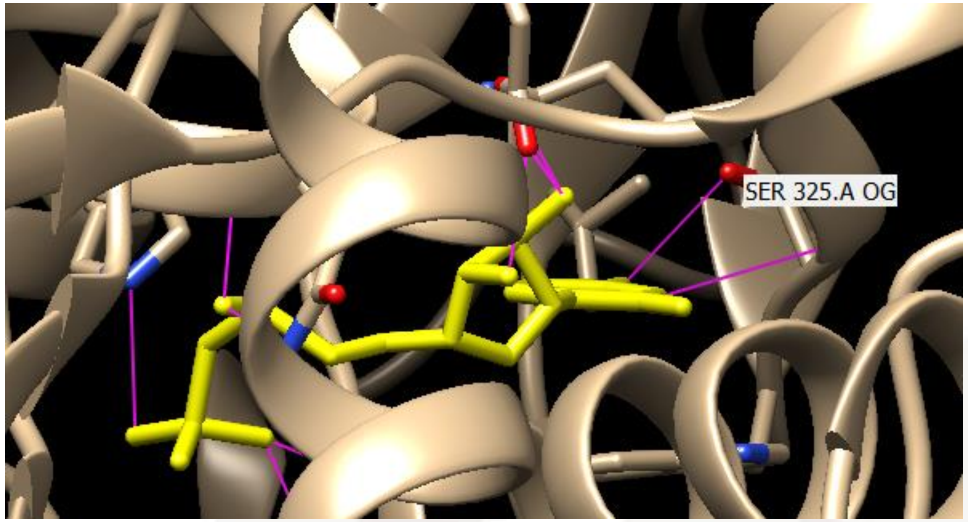
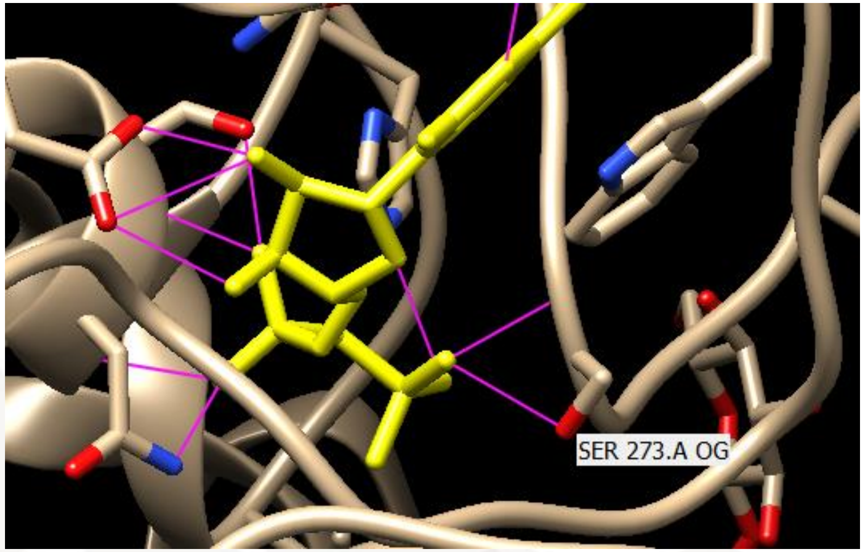
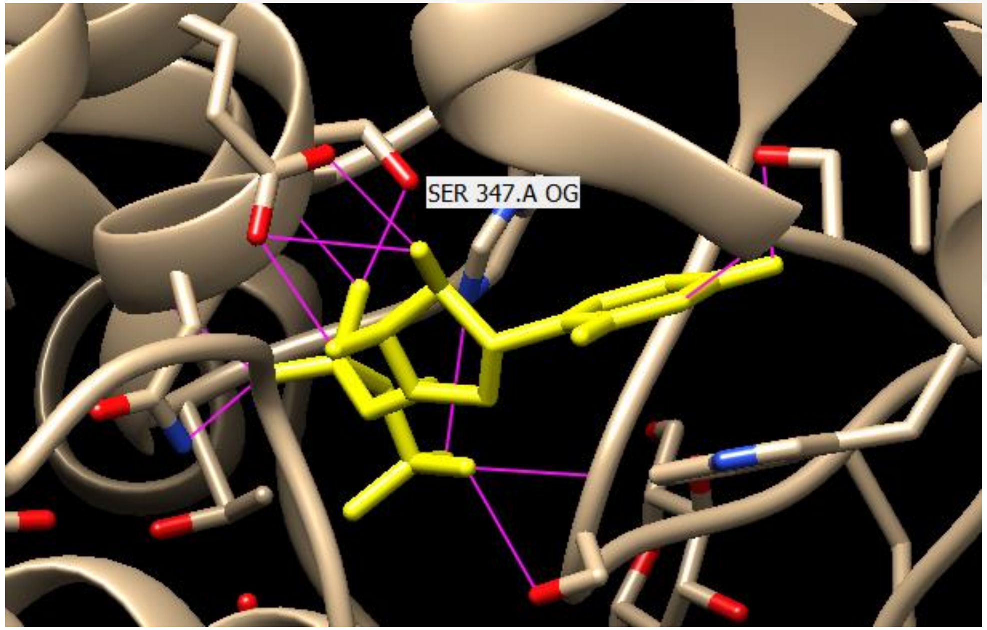
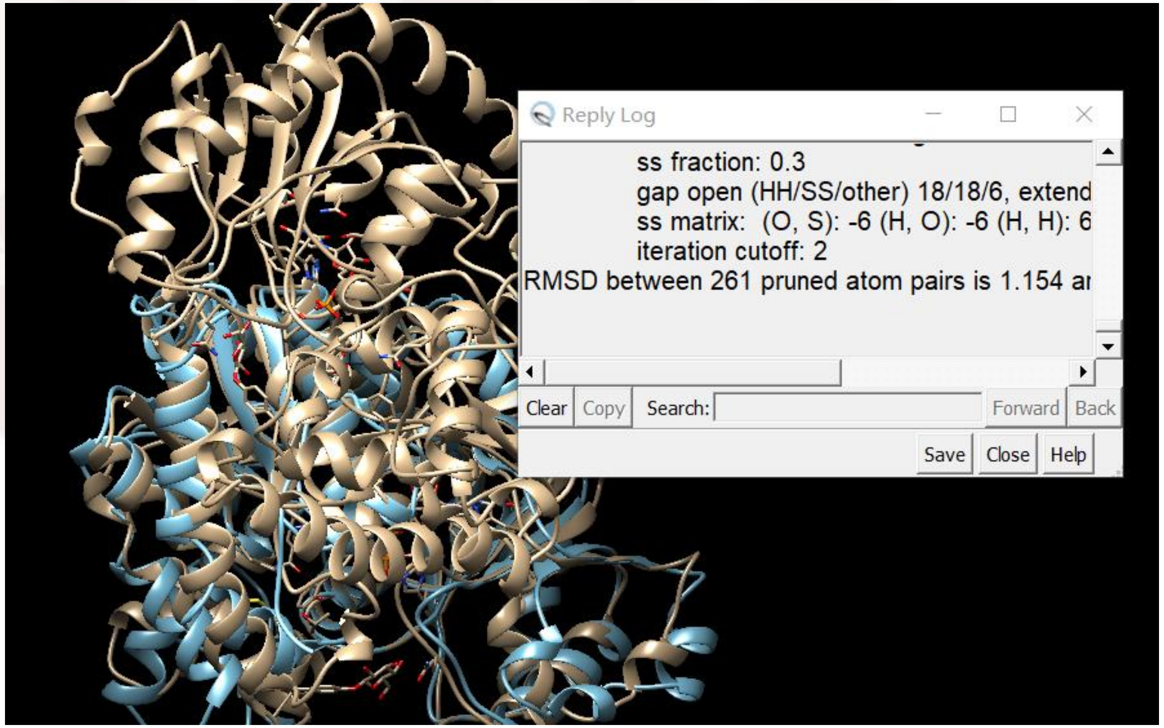
5U6M









```
        ss fraction: 0.3
        gap open (HH/SS/other) 18/18/6, extend
        ss matrix:  (O, S): -6 (H, O): -6 (H, H): 6
        iteration cutoff: 2
RMSD between 261 pruned atom pairs is 1.154 ar
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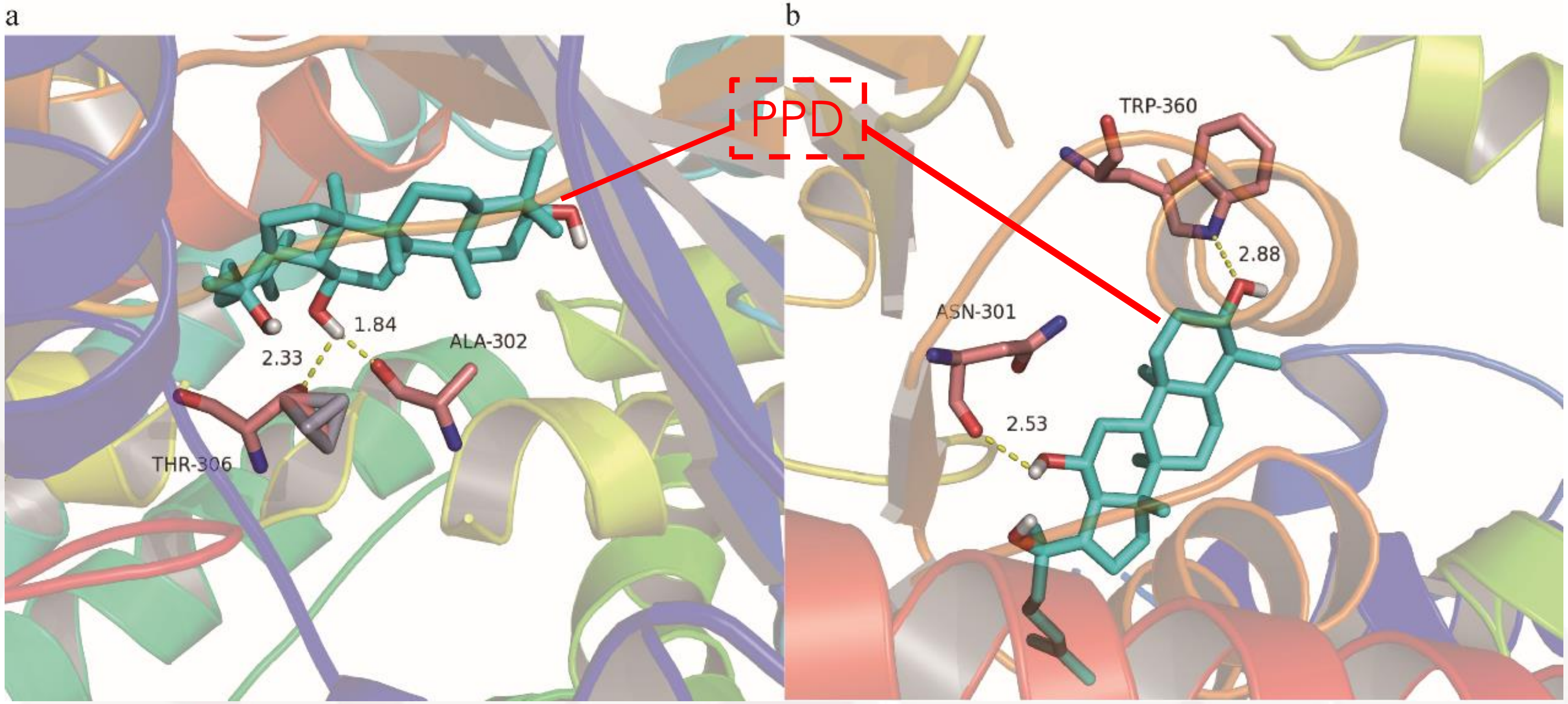
分子对接分析



蛋白名称	结合能（kcal·mol^{-1}）	氢键键长（Å）	残基
CYP71D313	-7.5	2.33	THR-306
		1.84	ALA-302
UGT85A24	-9.2	2.88	TRP-360
		2.53	ASN-301

小结

人参皂苷可能在种子萌发过程中发挥重要的作用。UGT85A24最可能催化PPD型人参皂苷的糖基化

。

感谢各位的聆听

THANKS