GRADUATE SCHOOL OF CHINESE ACADEMY OF AGRICULTURAL SCIENCES
中国农业科学院研究生院

# 茶树MRLK基因序列与功能分析
# Sequence and function analysis of tea MRLK gene

中国农业科学院茶叶研究所

2024级硕士十五班

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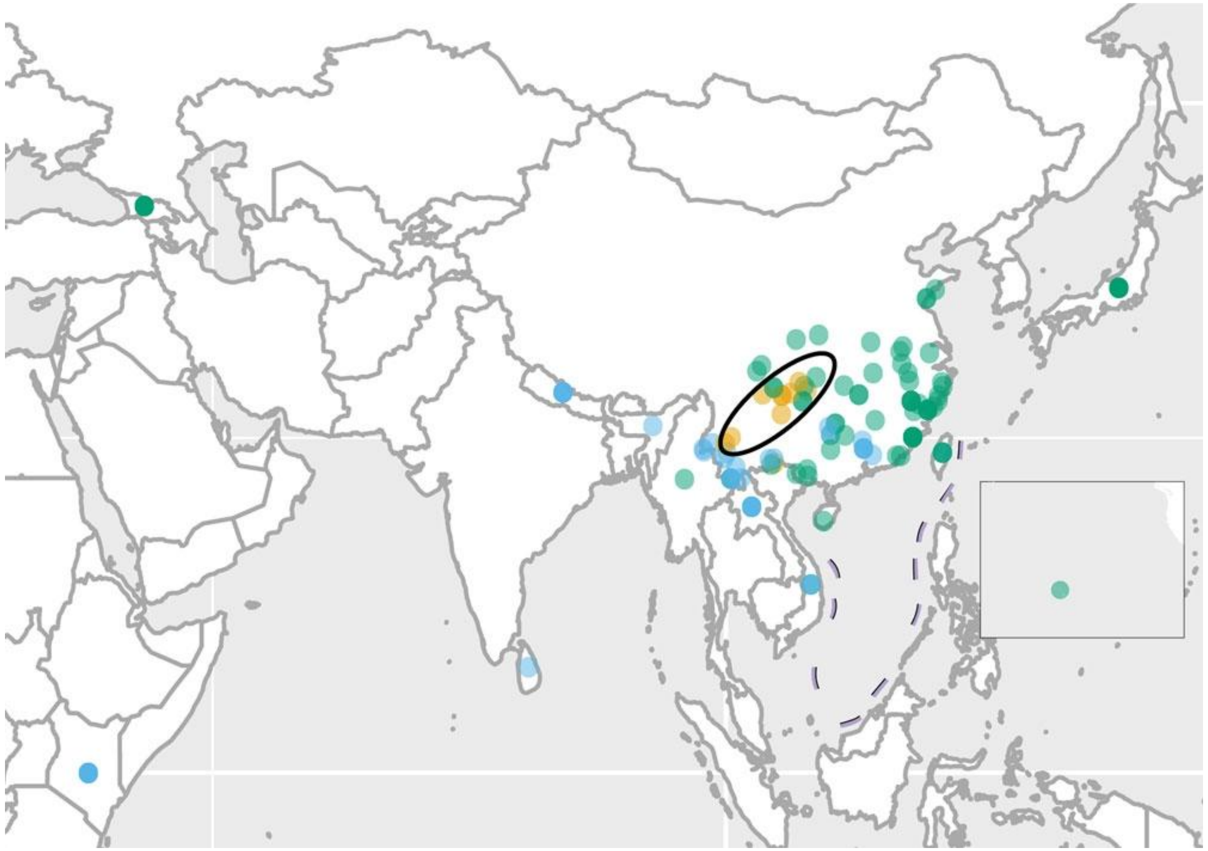
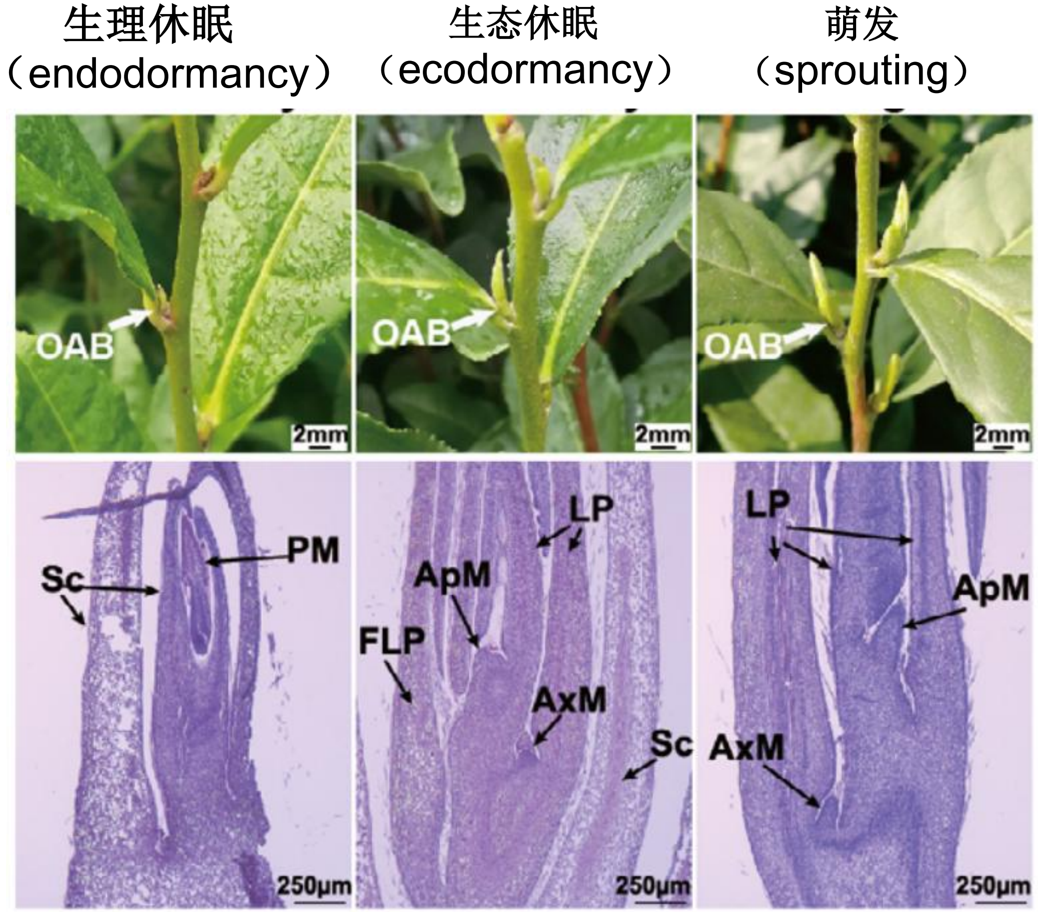
2025年4月

# 研究意义与背景





- 实心点代表茶叶品种的分布。
- 黑色椭圆形内的茶具有最高的核苷酸多态性。

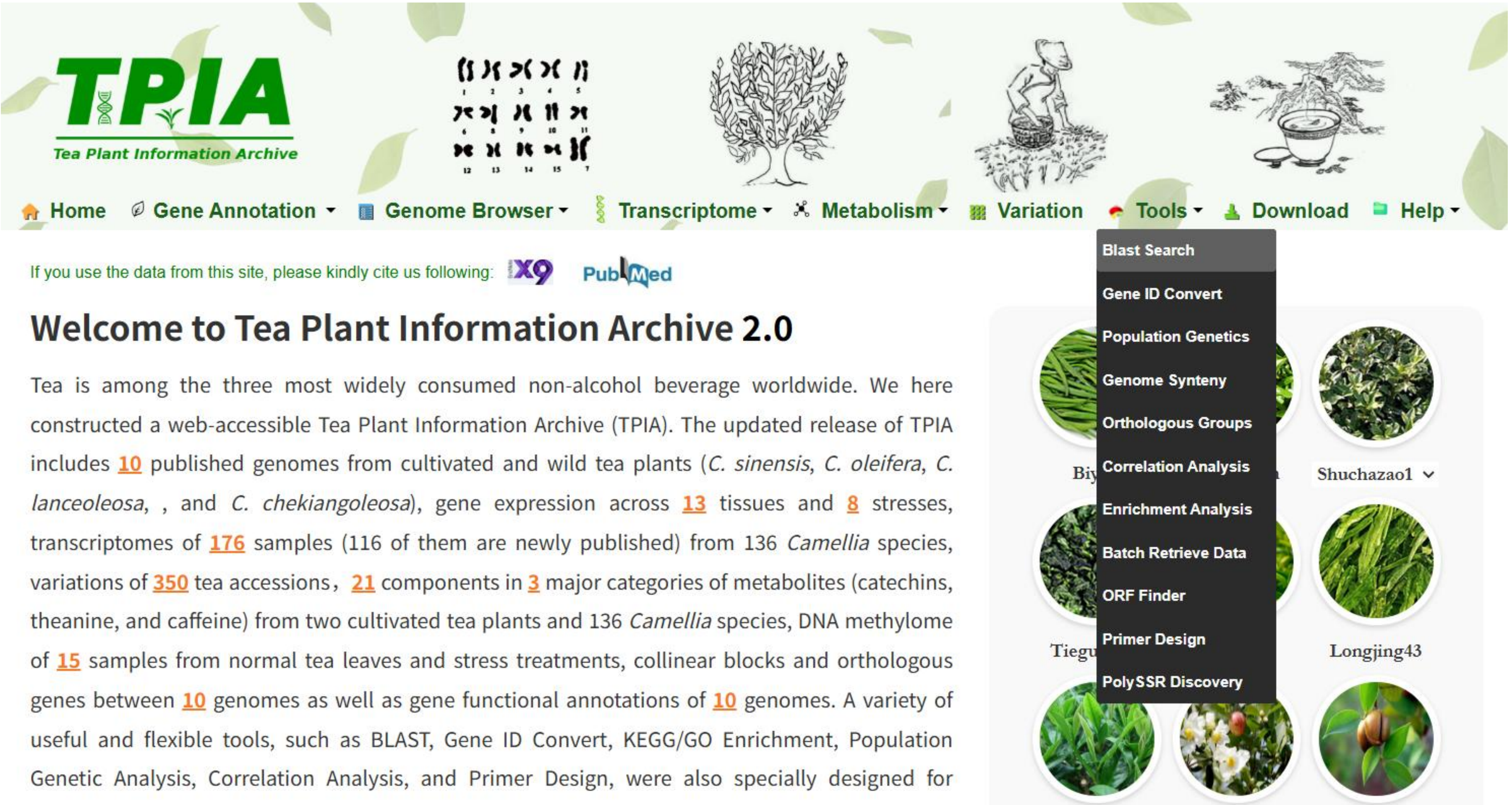
Wang et al. (2020) Nature communications

- 茶腋芽在内休眠、生态休眠和发芽阶段的形态变化和组织切片。

Hao et al. (2024) The Plant Journal

| 影响植物休眠的因素 | |
|---|---|
| 光周期 | 光敏色素A（PHYA）、光敏色素B（PHYB）、生物节律 |
| 温度 | CBF（C-REPEAT BINDING FACTOR）、<br>DREB（DEHYDRATION RESPONSIVE ELEMENT BINDING FACTOR）、<br>光敏色素A（PHYA） |
| 糖 | 葡萄糖、蔗糖含量 |
| 生长素/细胞分裂素 | 细胞周期调控 |
| 独脚金萌发素内酯 | |
| 酶 | |
| 钙离子 | |

- 已知cds序列的基因家族序列获取（Tea Plant Information Archive(TPIA): A comprehensive knowledge database for tea plant.）



If you use the data from this site, please kindly cite us following:

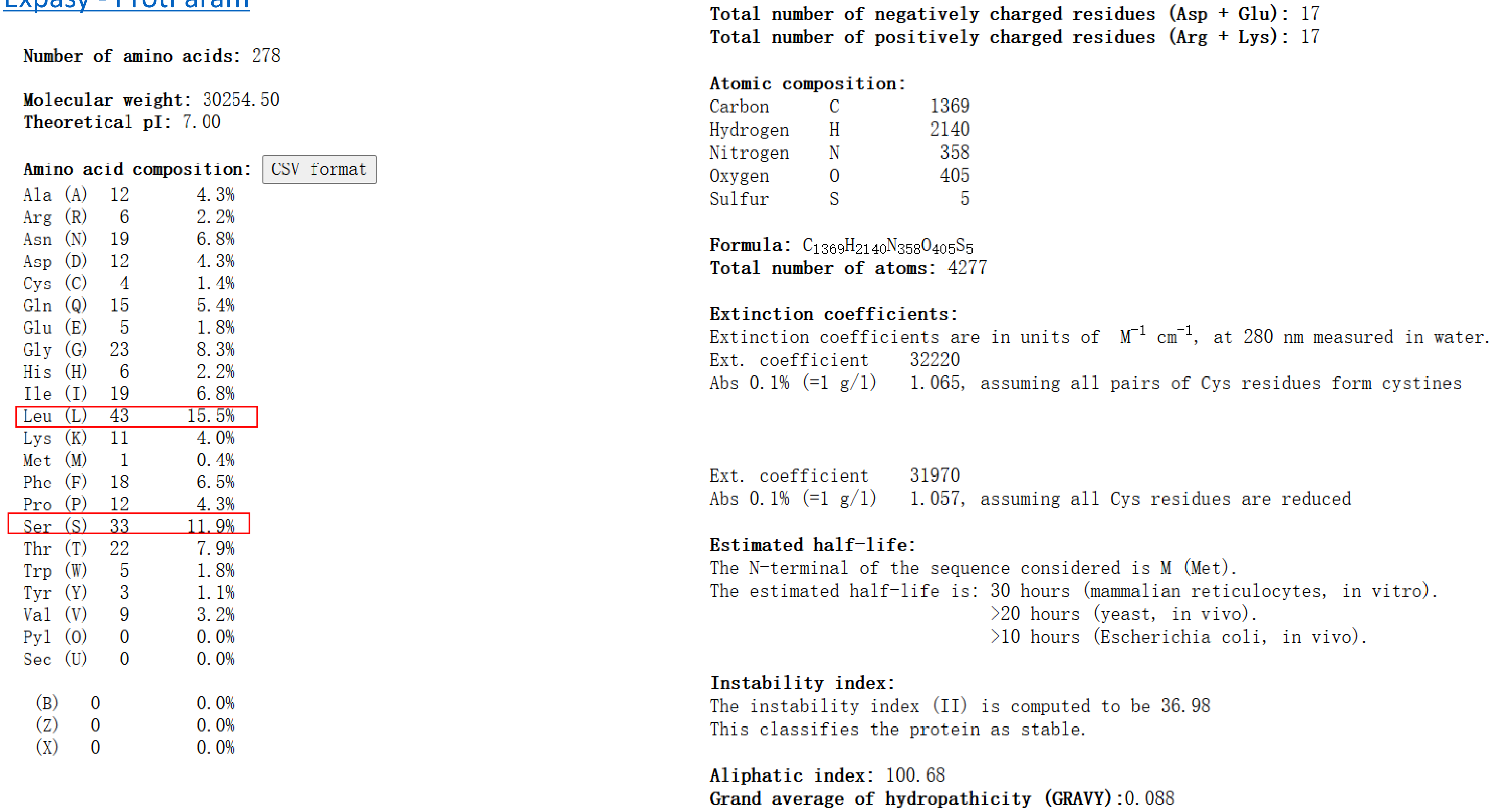
Welcome to Tea Plant Information Archive 2.0

Tea is among the three most widely consumed non-alcohol beverage worldwide. We here constructed a web-accessible Tea Plant Information Archive (TPIA). The updated release of TPIA includes 10 published genomes from cultivated and wild tea plants (*C. sinensis*, *C. oleifera*, *C. lanceoleosa*, , and *C. chekiangoleosa*), gene expression across 13 tissues and 8 stresses, transcriptomes of 176 samples (116 of them are newly published) from 136 *Camellia* species, variations of 350 tea accessions， 21 components in 3 major categories of metabolites (catechins, theanine, and caffeine) from two cultivated tea plants and 136 *Camellia* species, DNA methylome of 15 samples from normal tea leaves and stress treatments, collinear blocks and orthologous genes between 10 genomes as well as gene functional annotations of 10 genomes. A variety of useful and flexible tools, such as BLAST, Gene ID Convert, KEGG/GO Enrichment, Population Genetic Analysis, Correlation Analysis, and Primer Design, were also specially designed for

# 一、蛋白质理化性质和一级结构分析

## 1. 分析蛋白质的 pI、Mw、氨基酸组成、消光系数、稳定系数等

Expasy - ProtParam



**Number of amino acids:** 278

**Molecular weight:** 30254.50
**Theoretical pI:** 7.00

**Amino acid composition:** CSV format

| | | | |
|---|---|---|---|
| Ala | (A) | 12 | 4.3% |
| Arg | (R) | 6 | 2.2% |
| Asn | (N) | 19 | 6.8% |
| Asp | (D) | 12 | 4.3% |
| Cys | (C) | 4 | 1.4% |
| Gln | (Q) | 15 | 5.4% |
| Glu | (E) | 5 | 1.8% |
| Gly | (G) | 23 | 8.3% |
| His | (H) | 6 | 2.2% |
| Ile | (I) | 19 | 6.8% |
| Leu | (L) | 43 | 15.5% |
| Lys | (K) | 11 | 4.0% |
| Met | (M) | 1 | 0.4% |
| Phe | (F) | 18 | 6.5% |
| Pro | (P) | 12 | 4.3% |
| Ser | (S) | 33 | 11.9% |
| Thr | (T) | 22 | 7.9% |
| Trp | (W) | 5 | 1.8% |
| Tyr | (Y) | 3 | 1.1% |
| Val | (V) | 9 | 3.2% |
| Pyl | (O) | 0 | 0.0% |
| Sec | (U) | 0 | 0.0% |
| | | | |
| | (B) | 0 | 0.0% |
| | (Z) | 0 | 0.0% |
| | (X) | 0 | 0.0% |

**Total number of negatively charged residues (Asp + Glu):** 17
**Total number of positively charged residues (Arg + Lys):** 17

**Atomic composition:**

| | | |
|---|---|---|
| Carbon | C | 1369 |
| Hydrogen | H | 2140 |
| Nitrogen | N | 358 |
| Oxygen | O | 405 |
| Sulfur | S | 5 |

**Formula:** $C_{1369}H_{2140}N_{358}O_{405}S_5$
**Total number of atoms:** 4277

**Extinction coefficients:**
Extinction coefficients are in units of $M^{-1}$ $cm^{-1}$, at 280 nm measured in water.
Ext. coefficient 32220
Abs 0.1% (=1 g/l) 1.065, assuming all pairs of Cys residues form cystines

Ext. coefficient 31970
Abs 0.1% (=1 g/l) 1.057, assuming all Cys residues are reduced

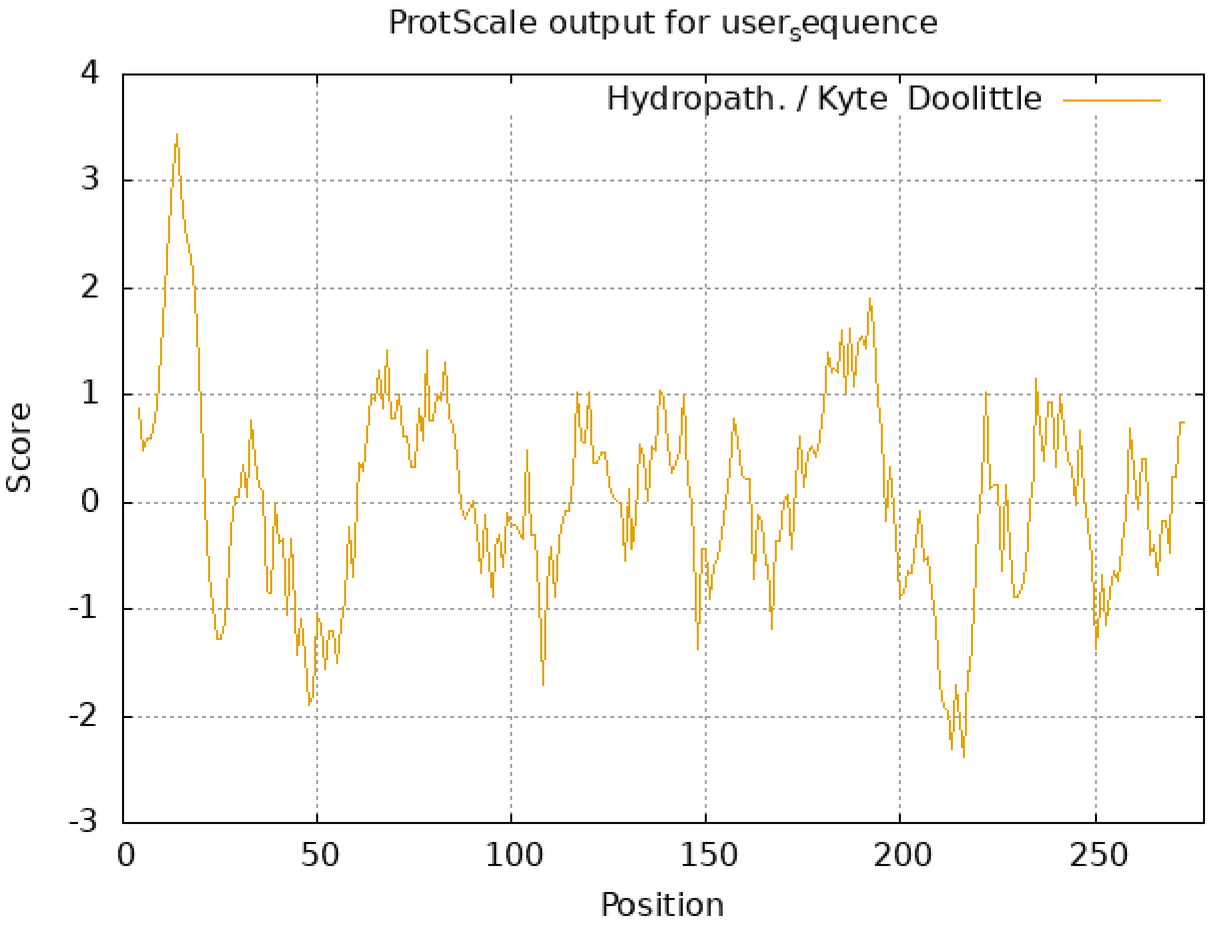
**Estimated half-life:**
The N-terminal of the sequence considered is M (Met).
The estimated half-life is: 30 hours (mammalian reticulocytes, in vitro).
>20 hours (yeast, in vivo).
>10 hours (Escherichia coli, in vivo).

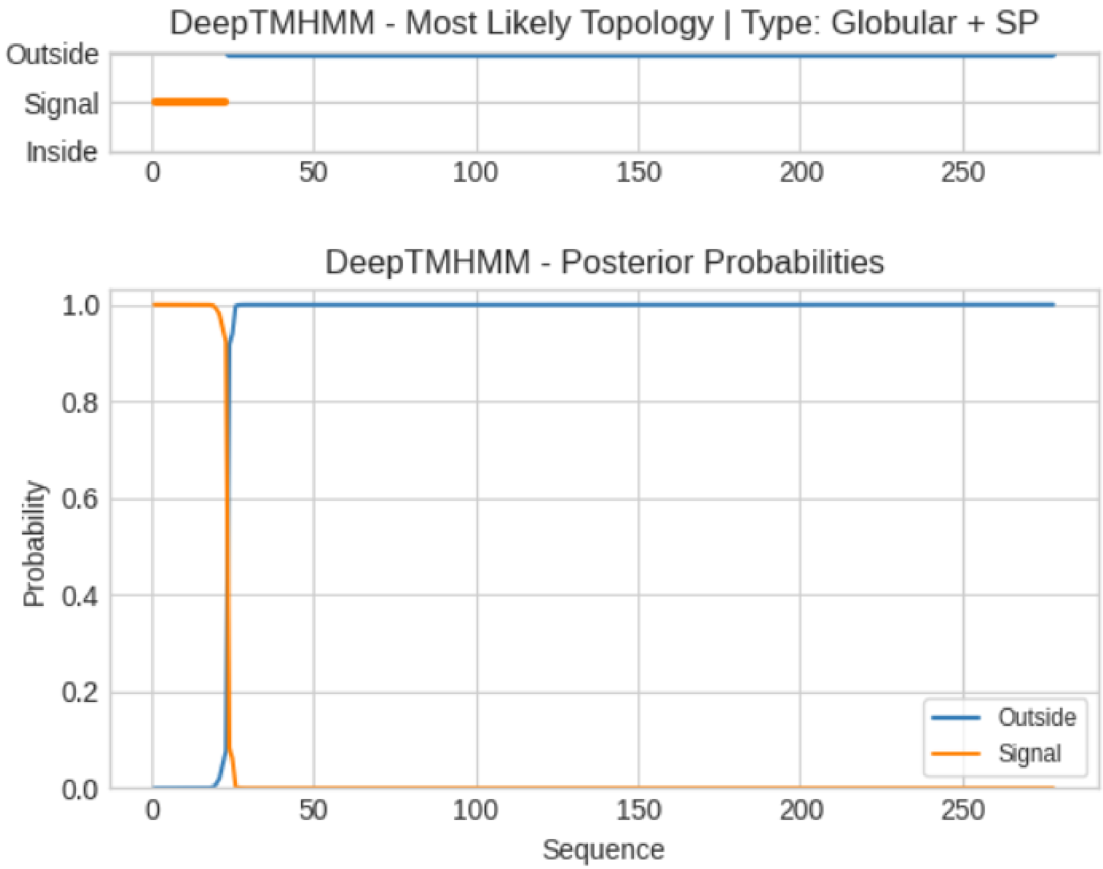
**Instability index:**
The instability index (II) is computed to be 36.98
This classifies the protein as stable.

**Aliphatic index:** 100.68
**Grand average of hydropathicity (GRAVY)**:0.088

2. 分析蛋白质的亲水性和疏水性 [Expasy - ProtScale]

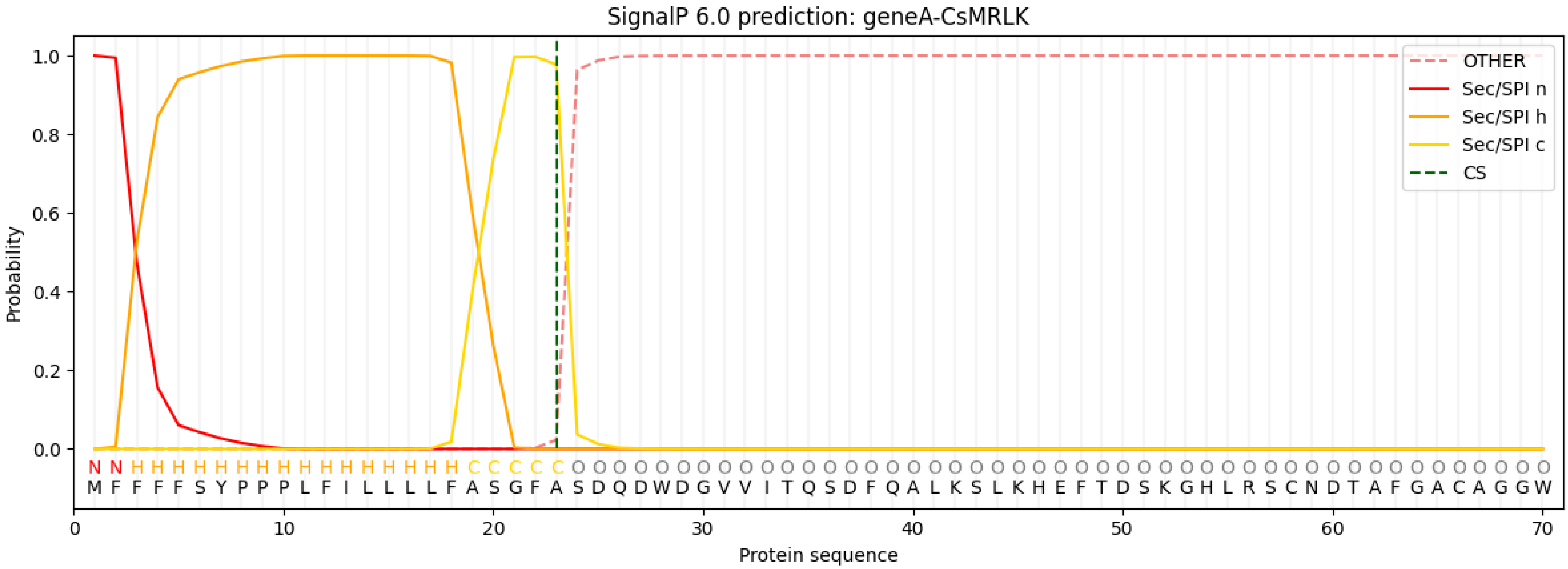
3. 分析蛋白质的跨膜区和信号肽
[TMHMM 2.0 - DTU Health Tech - Bioinformatic Services]





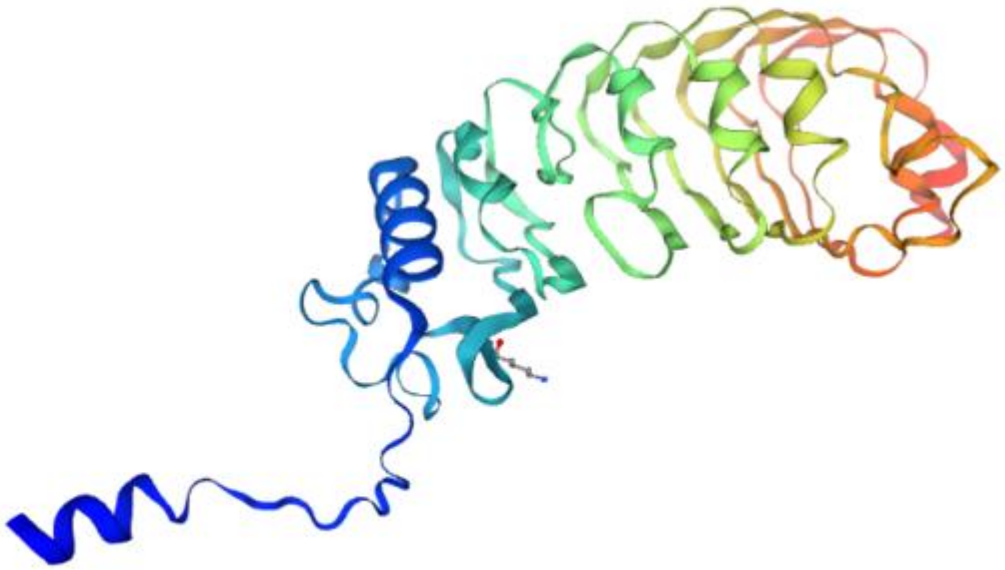
## 4. 信号肽预测 SignalP

[SignalP 6.0 - DTU Health Tech - Bioinformatic Services]



- 起始部分有较高概率属于信号肽 **N** 端。

# 二、蛋白质三级结构预测



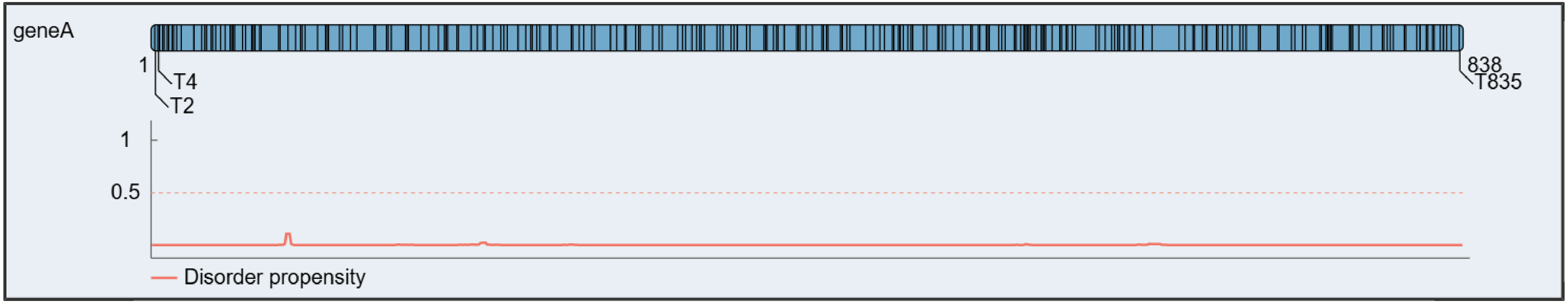
同源建模「SWISS-MODEL」

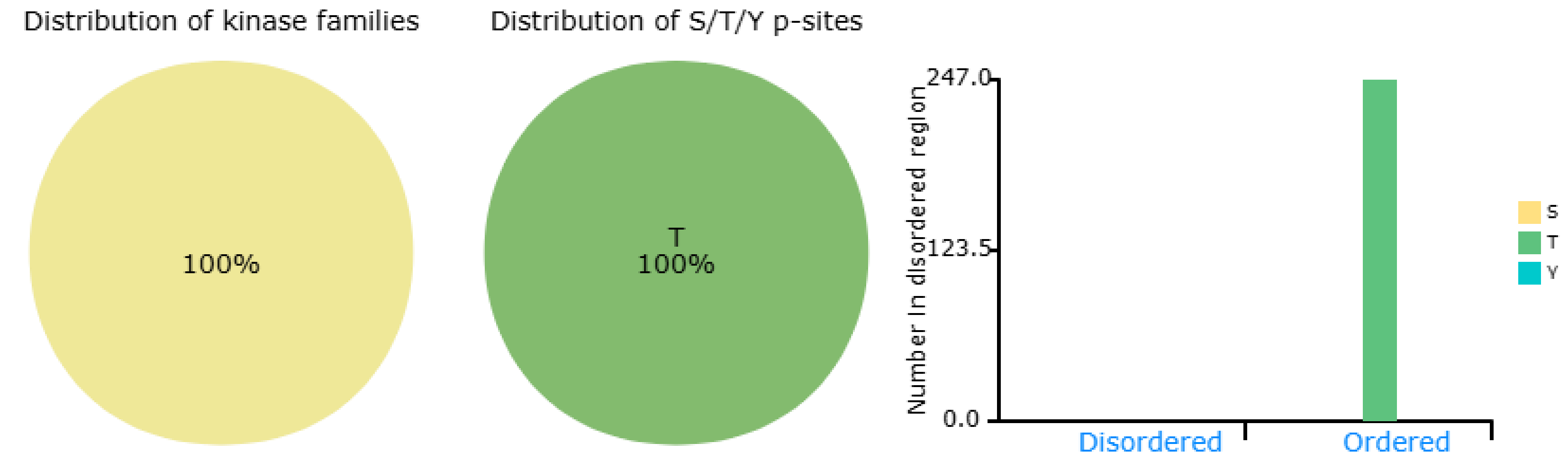
| | Logo ? | E-value ? | Sites ? | Width ? | More ? | Submit/Download ? |
|---|---|---|---|---|---|---|
| 1. | QDWDGVVITQSDFQALKSLKHEFTDSRGHLRSWNDTGYGACSGGWVGIKC | 3.4e-347 | 9 | 50 | ↧ | ⇢ |
| 2. | KGQVIALQLPWRGLSGRISEKIGQLQALRKLSLHDNALTGVIPNSLGSLP | 1.1e-284 | 9 | 50 | ↧ | ⇢ |
| 3. | IPPSISGCPVLRTLNLNNNKLTGTIPSSLANSTKLYRINLSFNSISGSIP | 1.2e-177 | 7 | 50 | ↧ | ⇢ |
| 4. | IMGKSTYGTVYKATLEDGNHVAVKRLREKVAKGRKEFEIEVVELGKIRHP | 4.8e-196 | 6 | 50 | ↧ | ⇢ |
| 5. | FDPSSFVGNSQLCGYITSTPCPSPPPQTLPSPPPSSSNHRDRKLNTKDII | 5.9e-177 | 6 | 50 | ↧ | ⇢ |
| 6. | CSVLLCCLIRKKAAKRNNGKKTGQAVSGRGEKGVPVVGGEIESGGETGGK | 6.9e-170 | 6 | 50 | ↧ | ⇢ |
| 7. | NILALRAYYLGPKGEKLLVFDYMPNGSLATFLHARGPDTLVTWPTRMNIA | 1.9e-179 | 6 | 50 | ↧ | ⇢ |
| 8. | PATIGNISSITQLDFSNNNFTGKIPTSLSNLPNLTHFNVSYNNLSGSVPY | 8.1e-161 | 6 | 50 | ↧ | ⇢ |
| 9. | MNQSHTYPLQFRHFTQKWISVRCSSSSHTHLLLFILLLLFA | 1.1e-149 | 6 | 41 | ↧ | ⇢ |
| 10. | IVKEDWTNEVFDVELMRDASNSGDGLLQTLKLALHCVDPSPAARPEAQQV | 2.2e-147 | 5 | 50 | ↧ | ⇢ |

**Stopped because requested number of motifs (10) found.**

# 三、蛋白质的翻译后修饰（Post-Translational Modifications，PTMs）位点预测

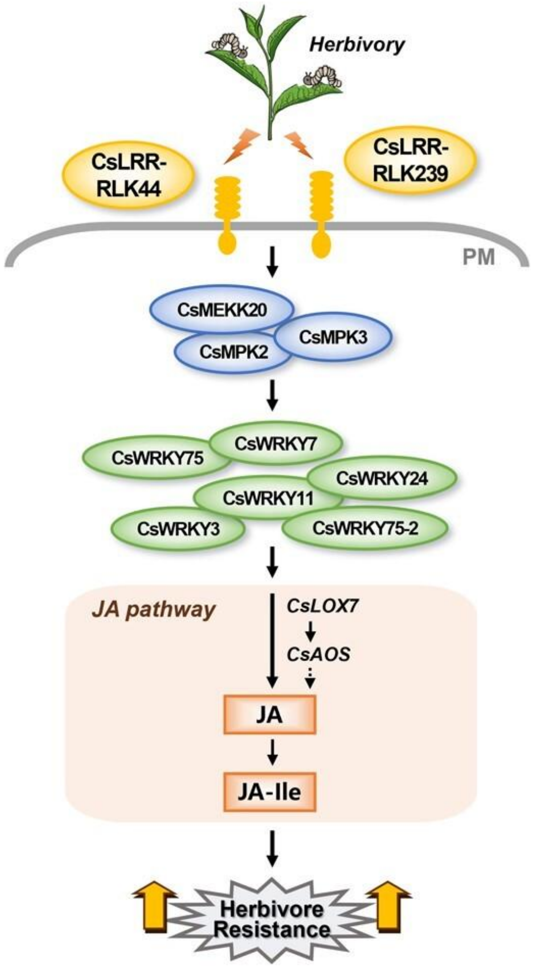
GPS 6.0 - Kinase-specific Phosphorylation Site Prediction

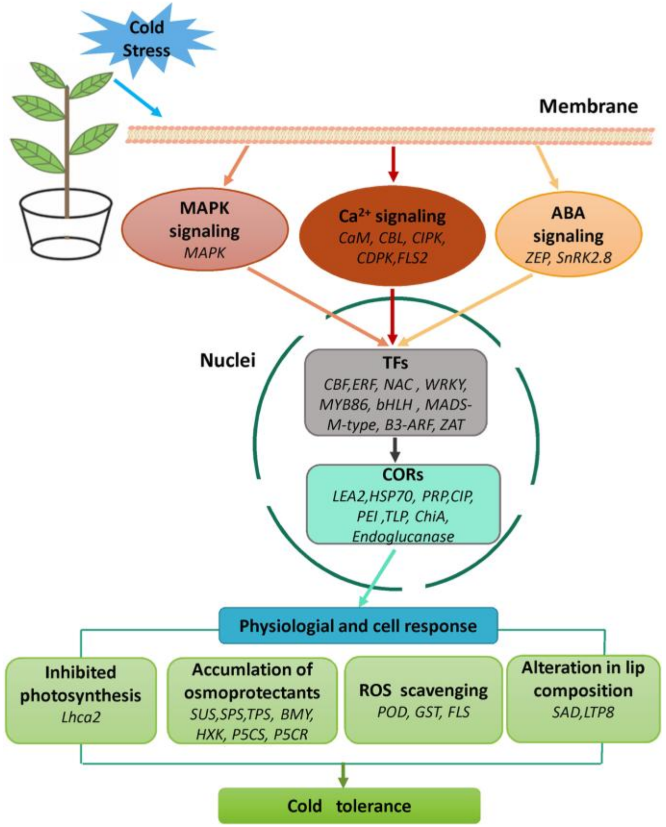



Distribution of kinase families

Distribution of S/T/Y p-sites

# 研究展望

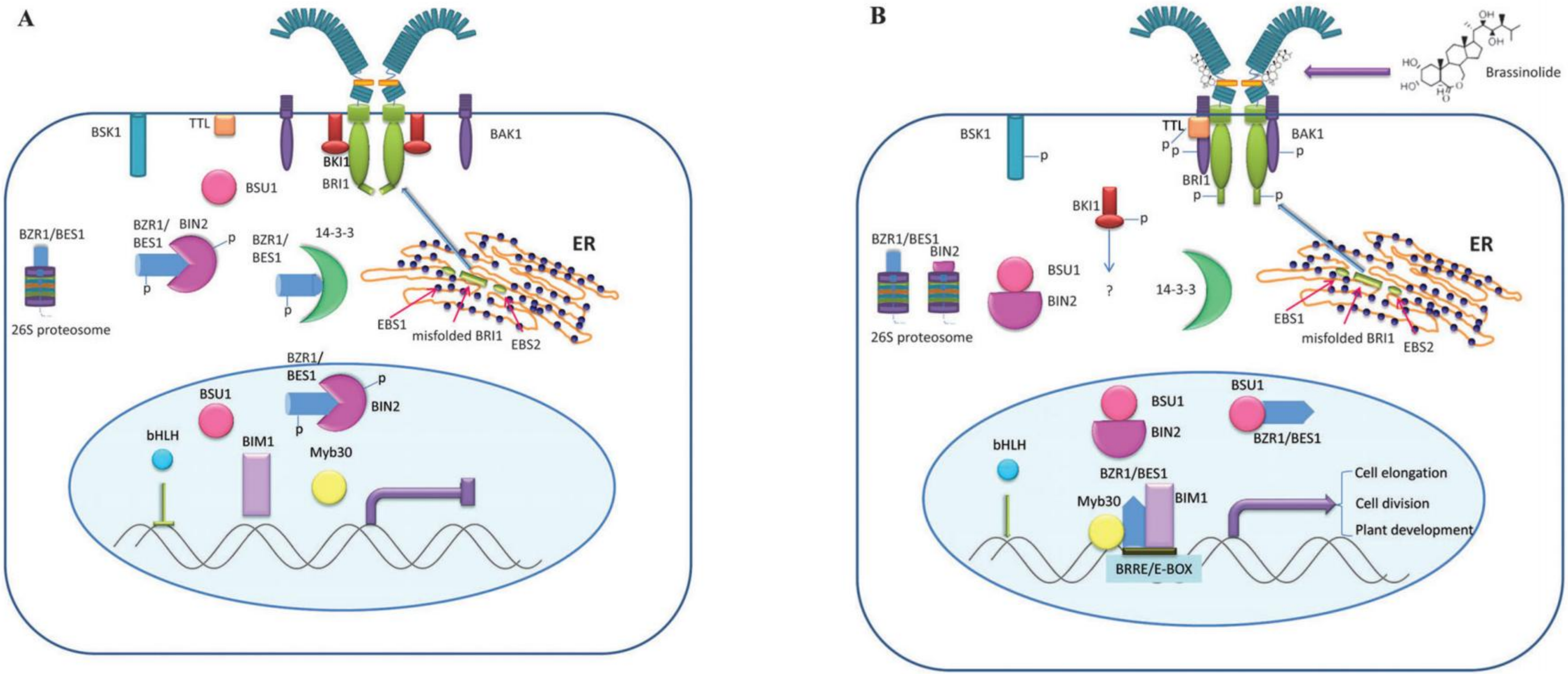




- 在芽休眠与解除过程中，环境信号经由RLK感知后，通过磷酸化级联（包括MAPK和CDPK途径）调控ABA、茉莉酸等信号和转录因子网络，从而实现对休眠状态的精细调控。

Jiang et al. (2024) Horticulture Research

Li et al. (2019) BMC Genomics



- **BR** 参与调节下胚轴伸长、细胞分裂、地上部分发育、叶片发育、根发育、生殖发育、开花时间和衰老以及胁迫响应等过程。
- 文中 **BRI1** 属于 **LRR - RLK**，在 **BR** 信号转导起始阶段发挥关键作用。在茶树中可能也存在类似的 **LRR - RLK** 参与激素信号感知。

Yang et al. (2011) Molecular Plant

# 感谢聆听，恳请指正！