Bioinformatical Analysis of *SCR* gene in Brassicaceae species

生物信息**14**小组

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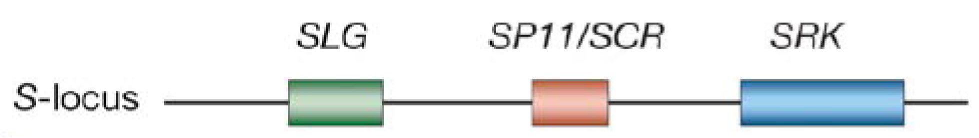
- **Introduction**
- **Methods**
- **Discussion**
- **Acknowledgement**

Inroduction

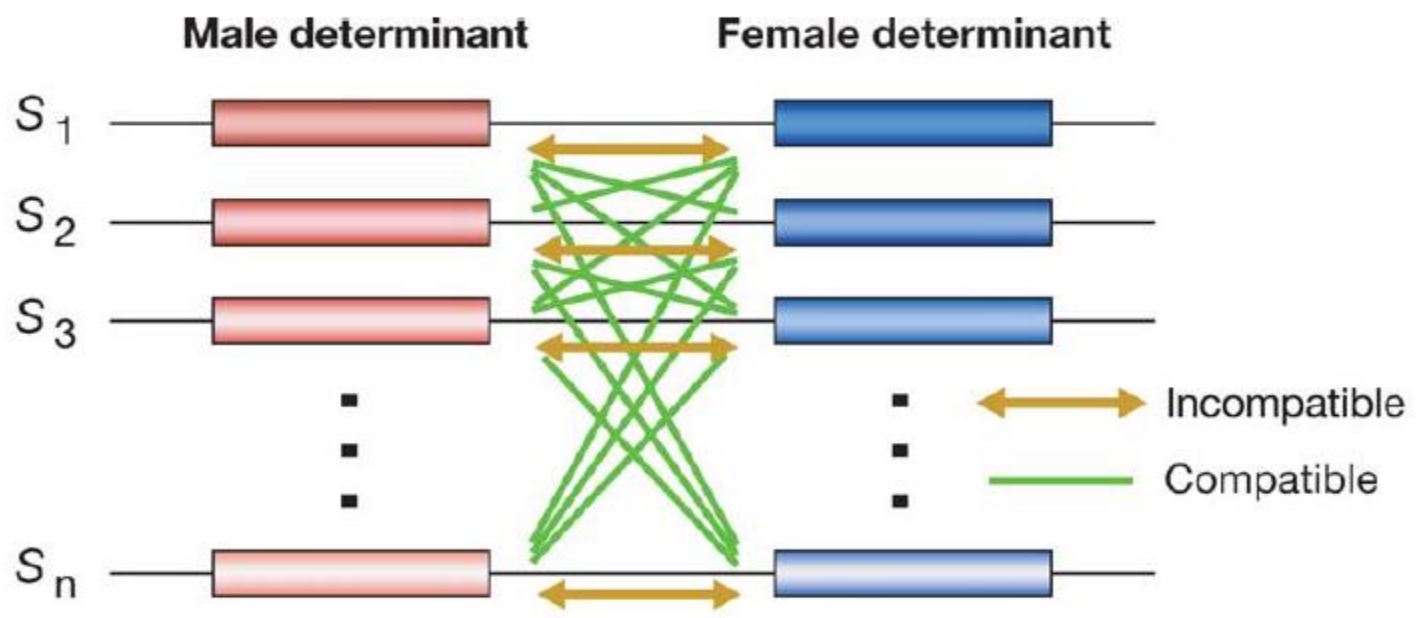
- Self-incompatibility (SI) is an important mechanism used by many angiosperm species for preventing self-fertilization.



- SI is often controlled by a single polymorphic locus, S locus. In Brassicaceae,the S locus contains two specificity-determinant genes.

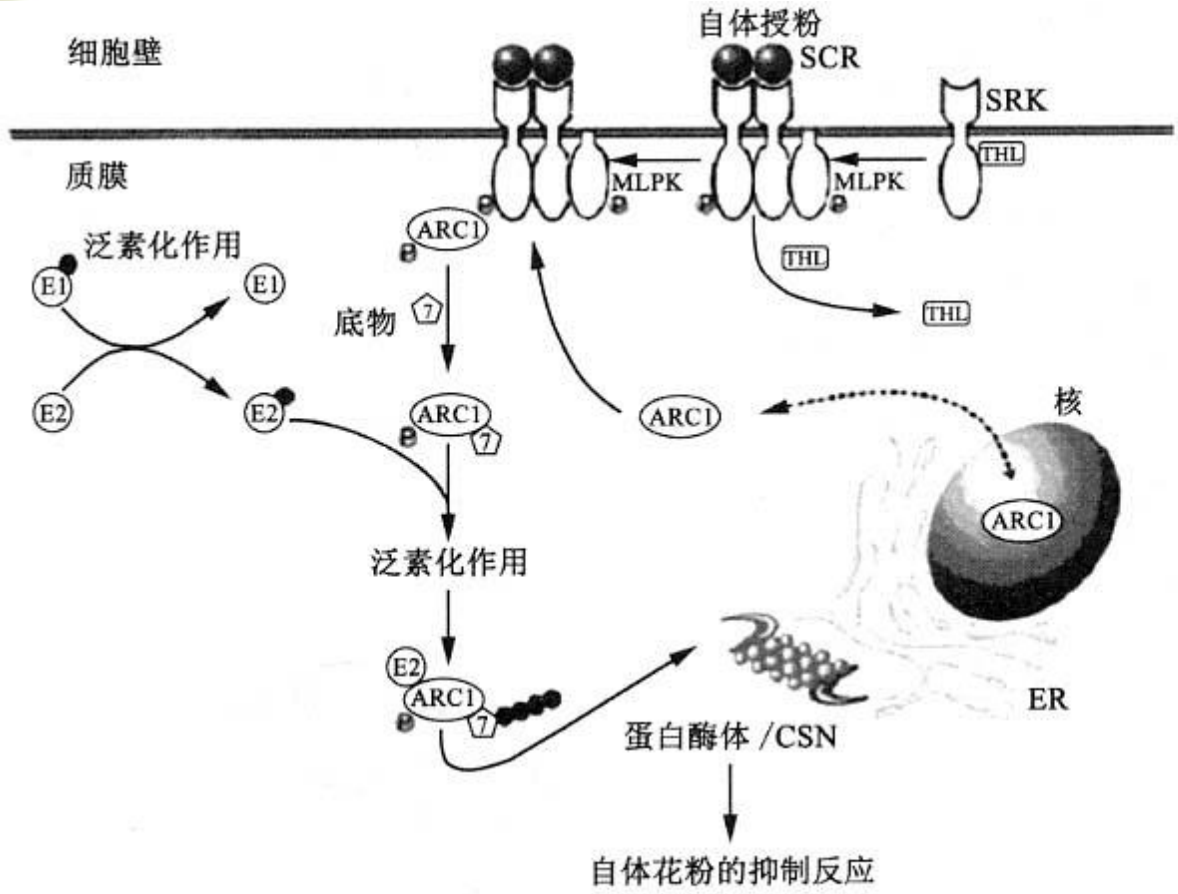
- *SRK* encodes the stigmatic receptor kinase.
- *SCR* encodes a small cys-rich protein localized in the pollen coat, which is the ligand for the *SRK* receptor (Nasrallah, 2002).
- Pollen inhibition occurs when the same S-locus specificity is expressed by both pollen and pistil (Nasrallah, 2002).

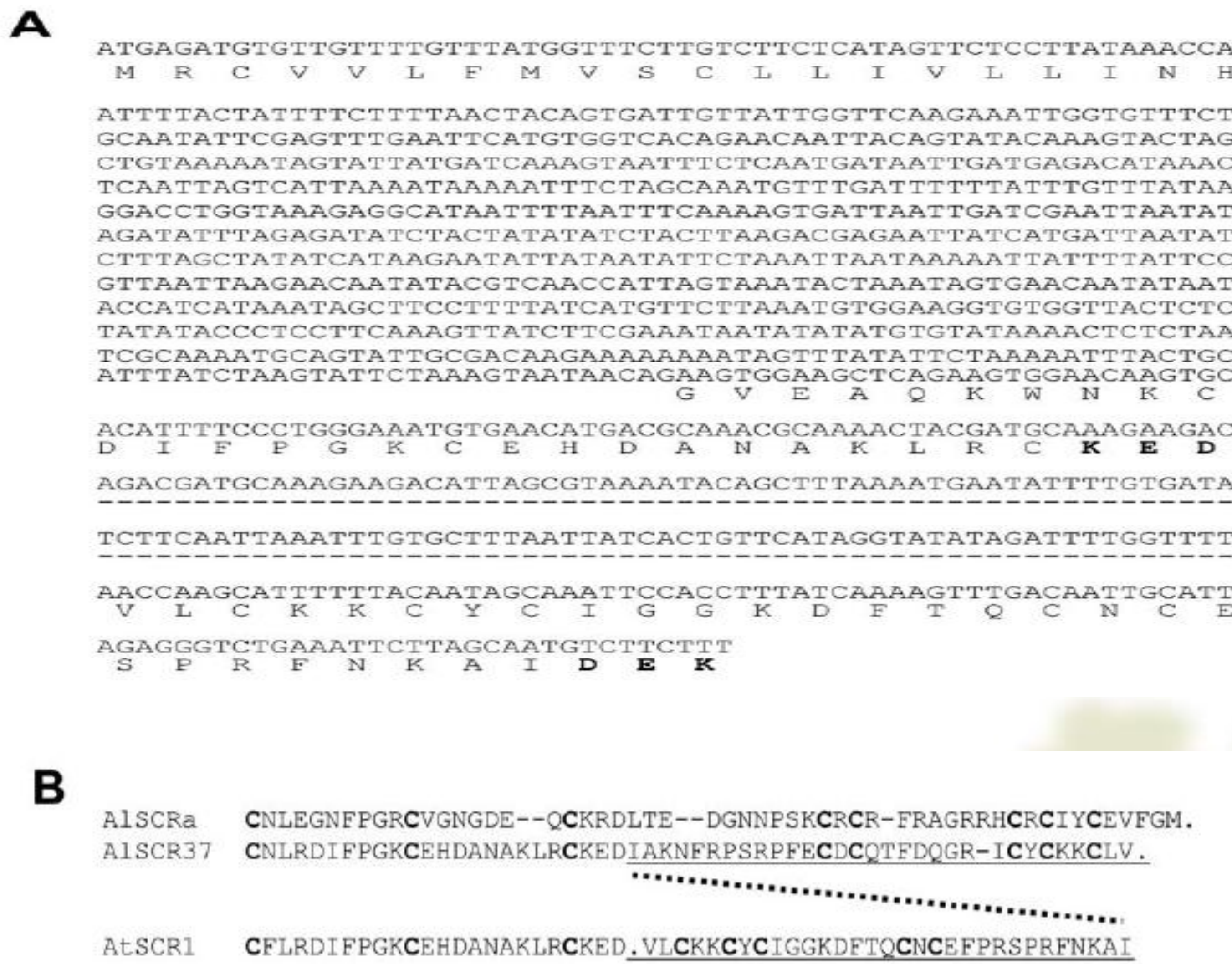
- **Classic genetic studies unraveled two distinct forms of SI, the gametophytic (GSI) and the sporophytic (SSI).**



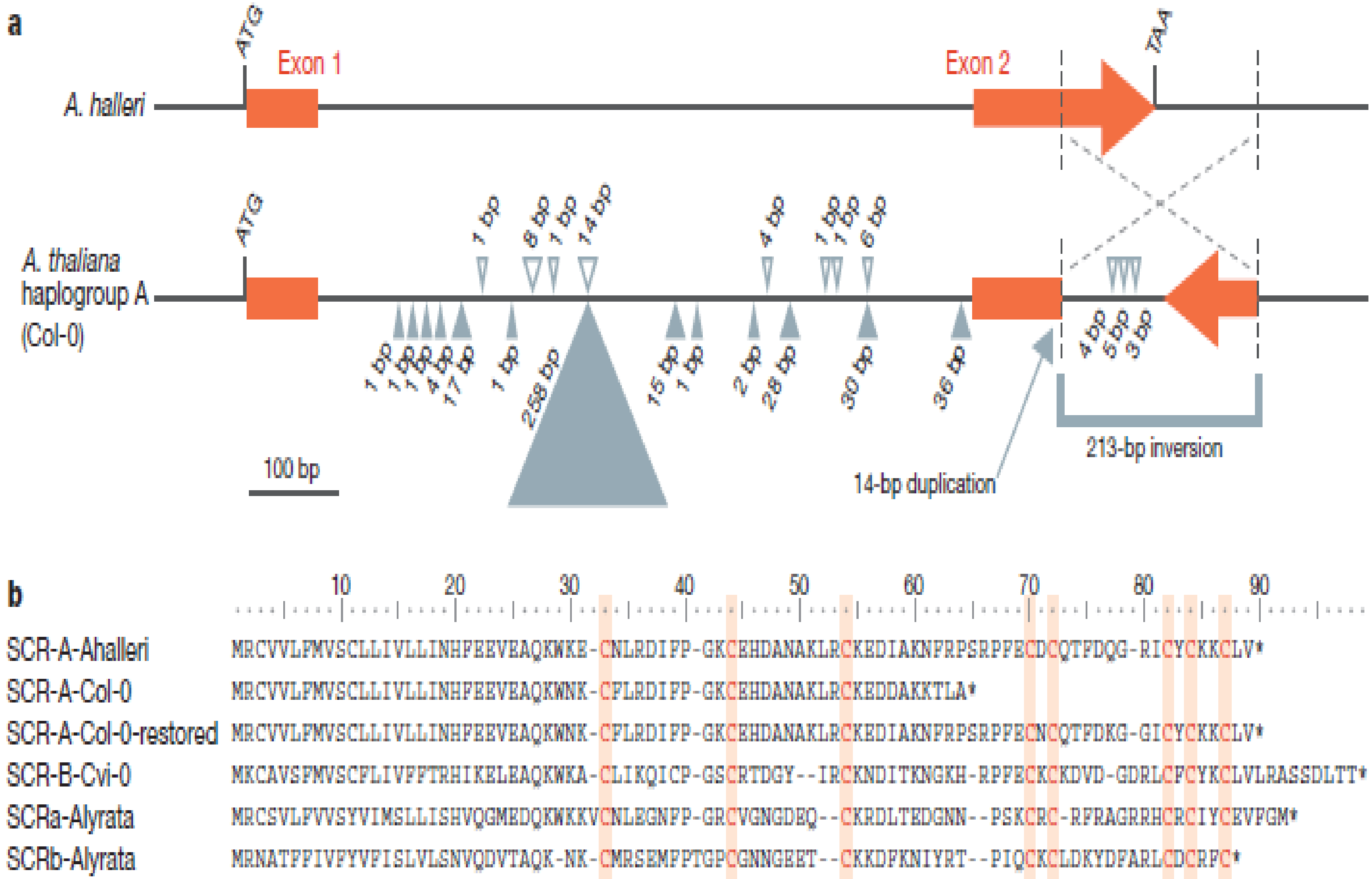
Seiji Takayama et al ,2005

Signal transduction of Self-incompatibility reaction





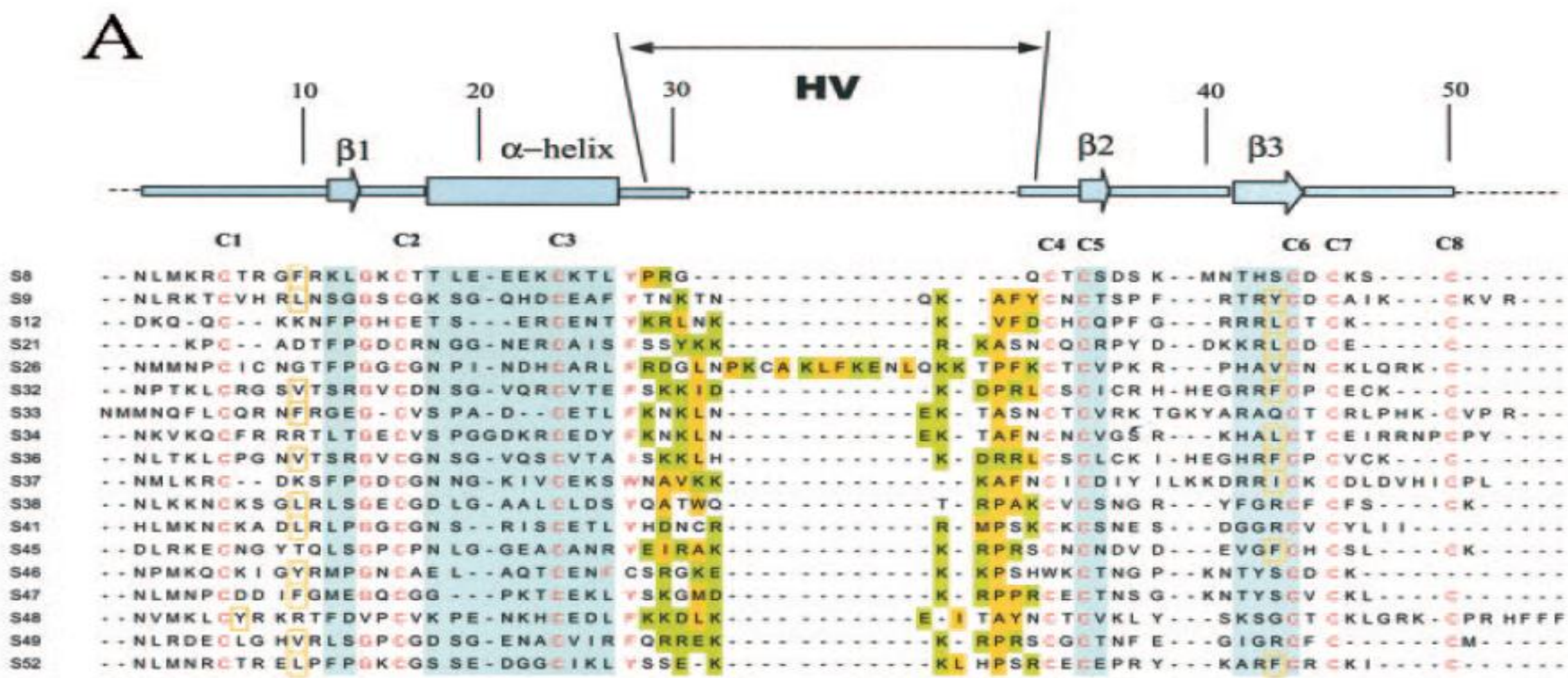
Boggs et al,2009



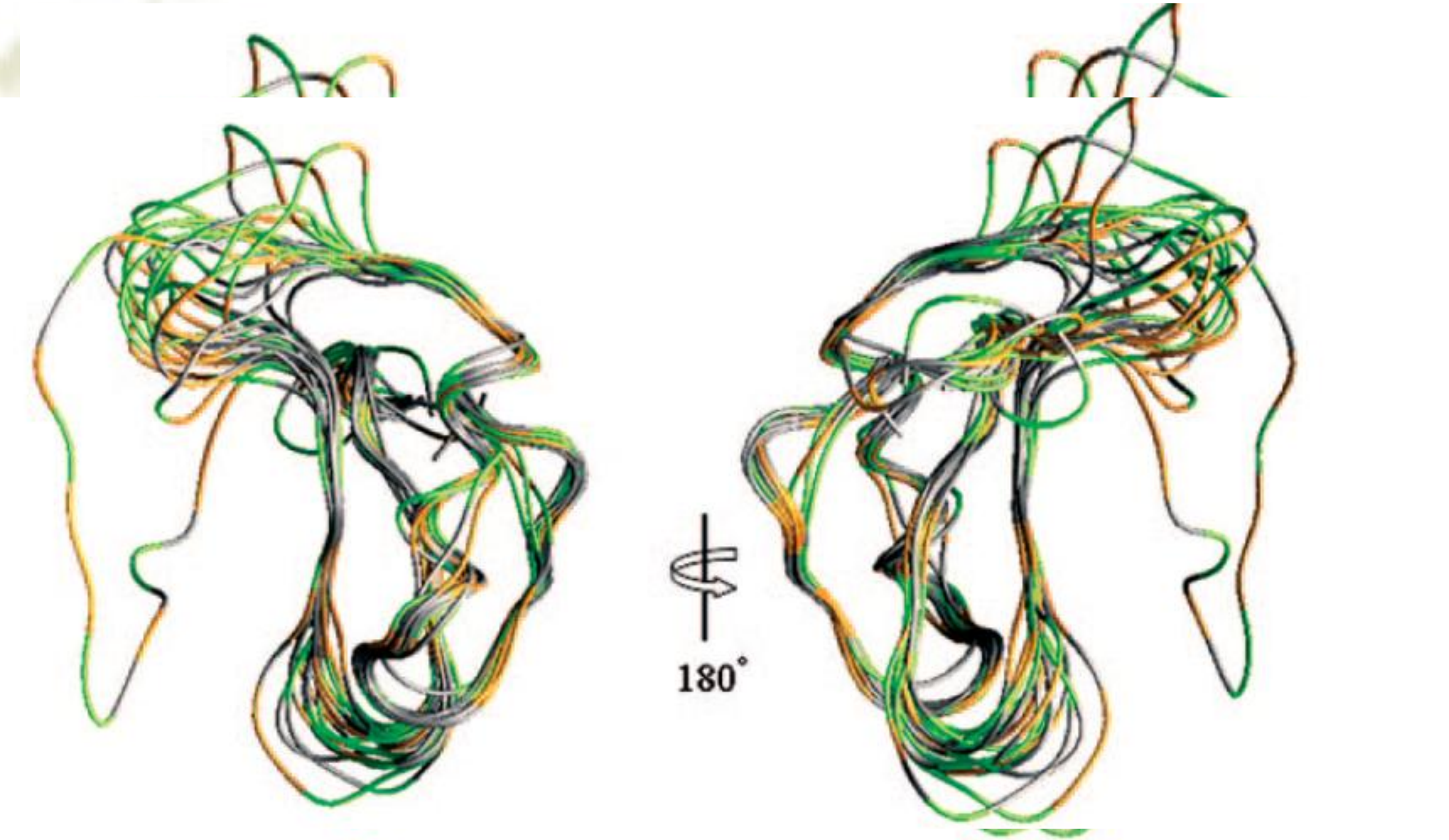
Takashi et al,2010

Methods

Solution Structure of S_8-SP11

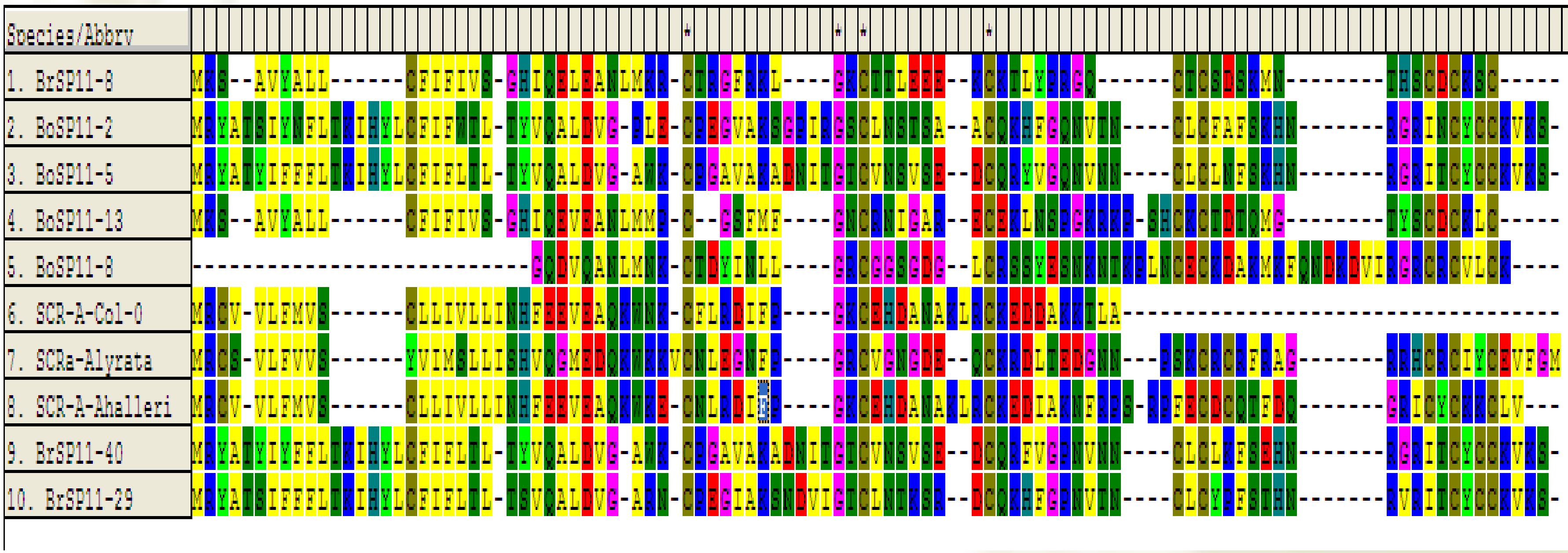


Mishima,et al,2003



Mishima et al,2003

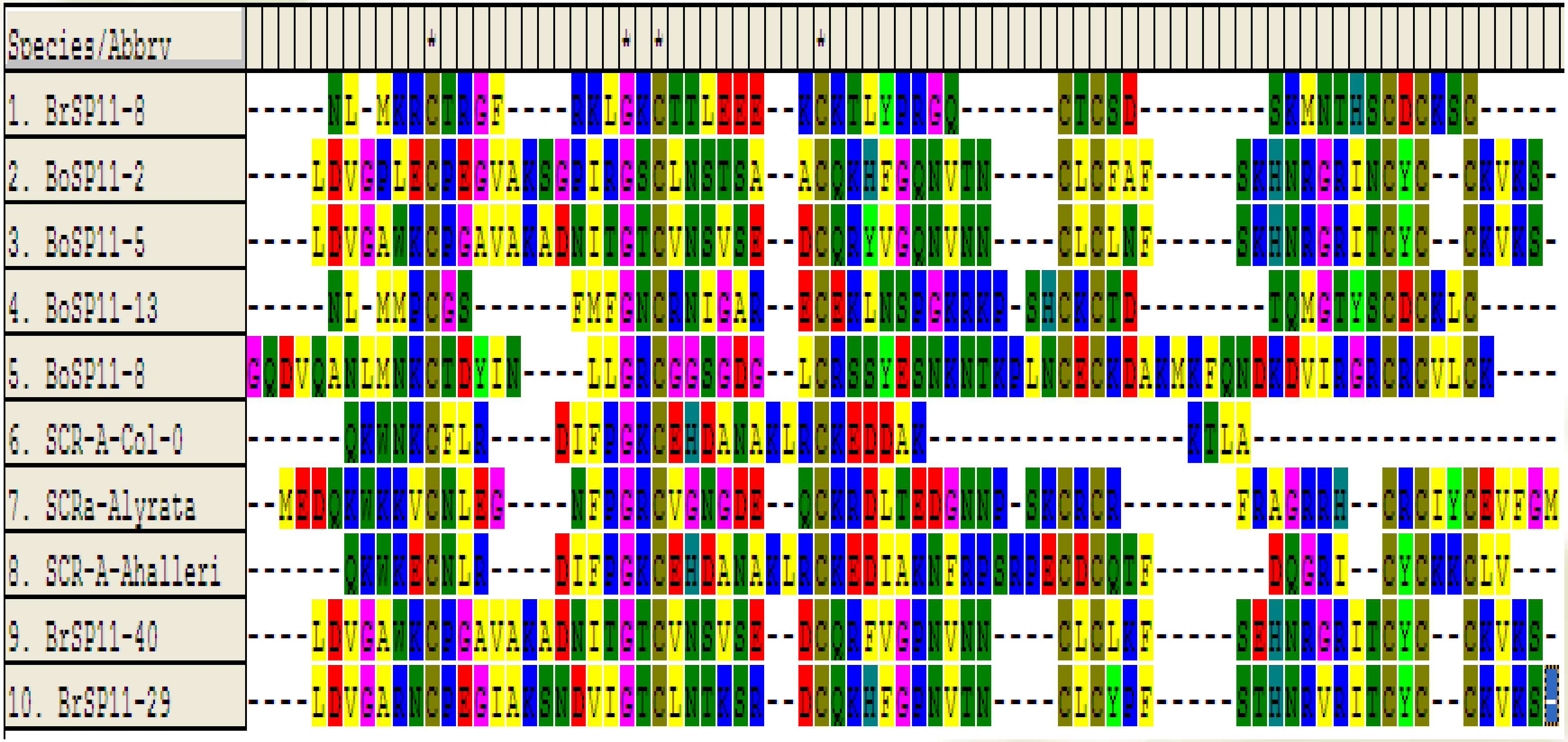
Sequence Alignment of allelic SP11s

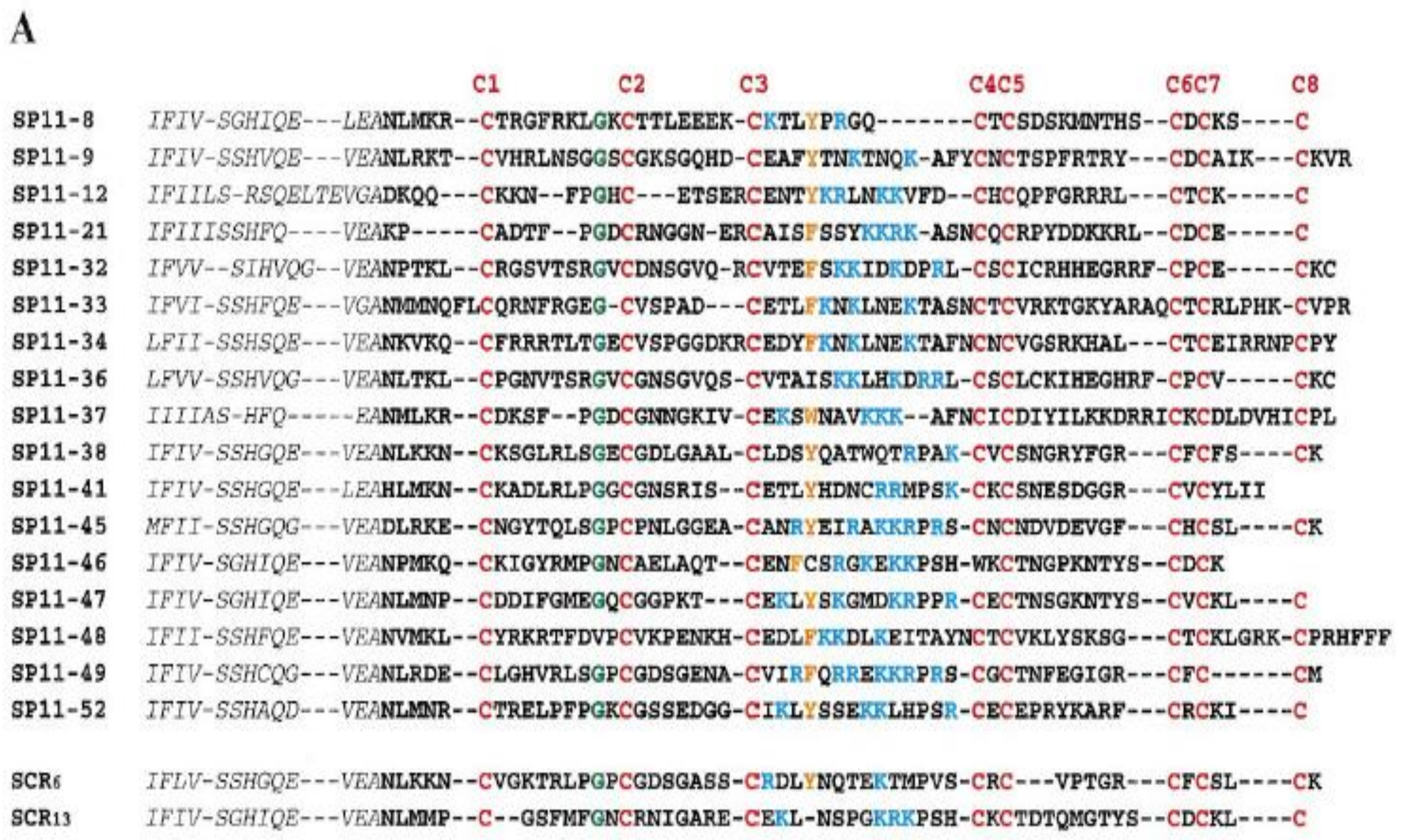


Signal Peptide Predition

gene name	Cut Site		Cut Seq
BrSP11-8	24	25	LEA-NL
BrSP11-40	29	30	VQA-LD
BrSP11-29	29	30	VQA-LD
BoSP11-2	29	30	VQA-LD
BoSP11-5	29	30	VQA-LD
BoSP11-13	24	25	VEA-NL
BoSP11-8			
SCR-A-Col_0	26	27	VEA-QK
SCRa-Alyrata	23	24	VQG-ME
SCRa-Ahalleri	26	27	VEA-QK

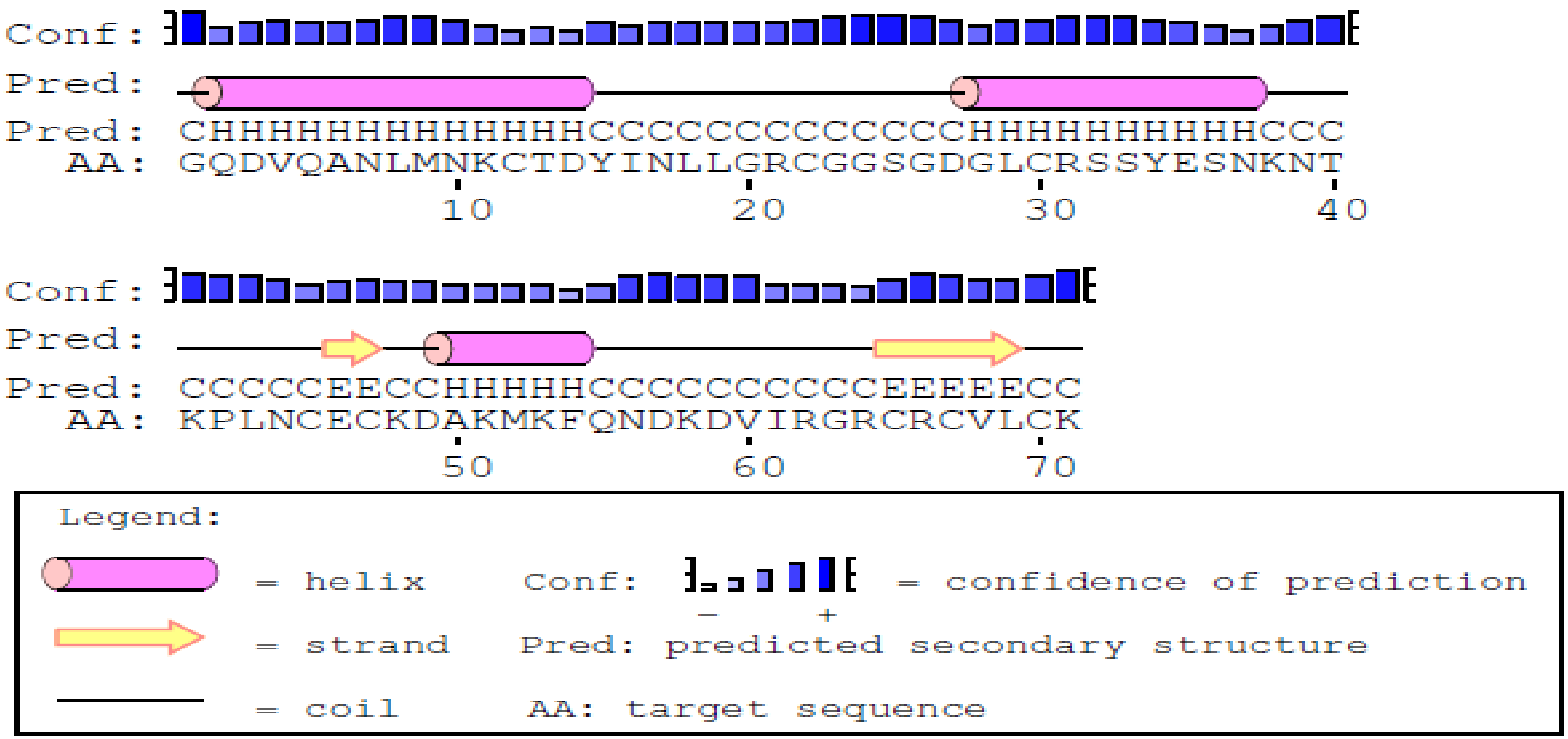
Alignment after remove signal peptide



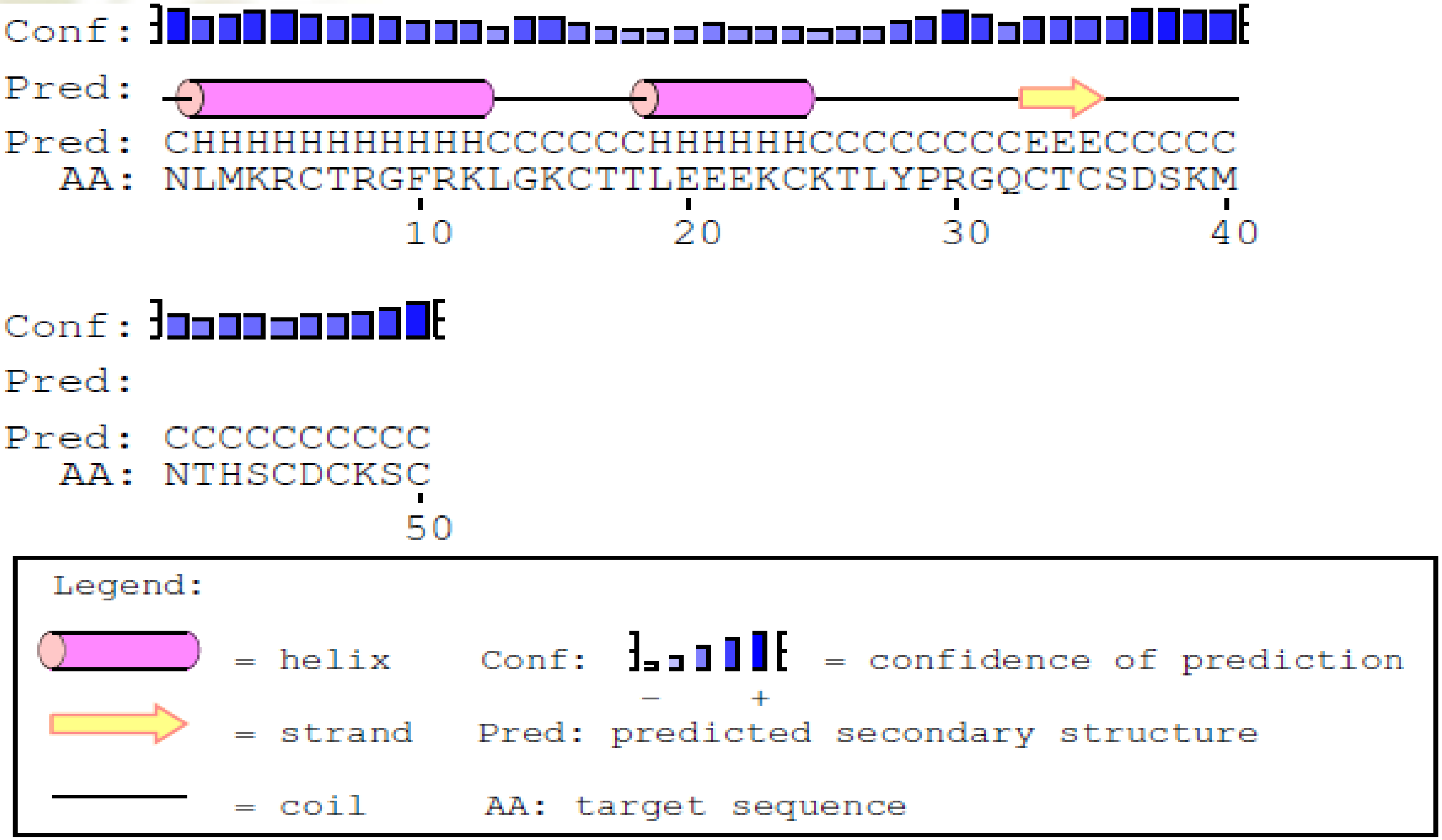


Watanabe et al,2000

Secondary Structure prediction

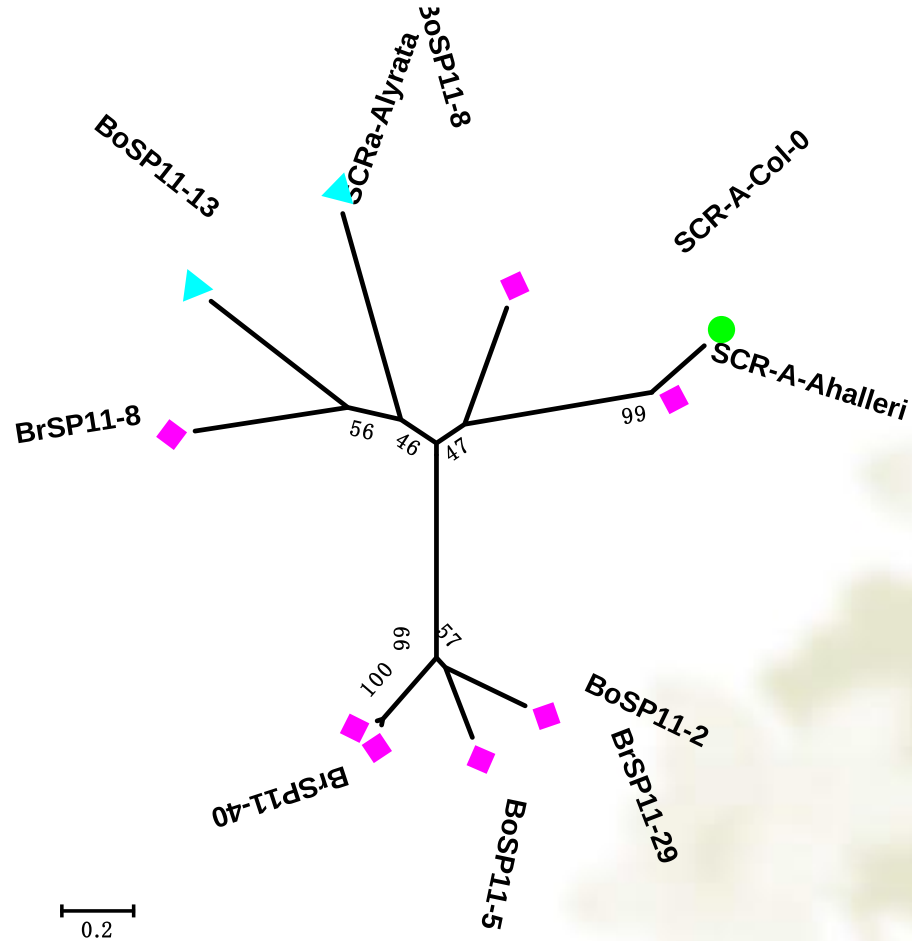


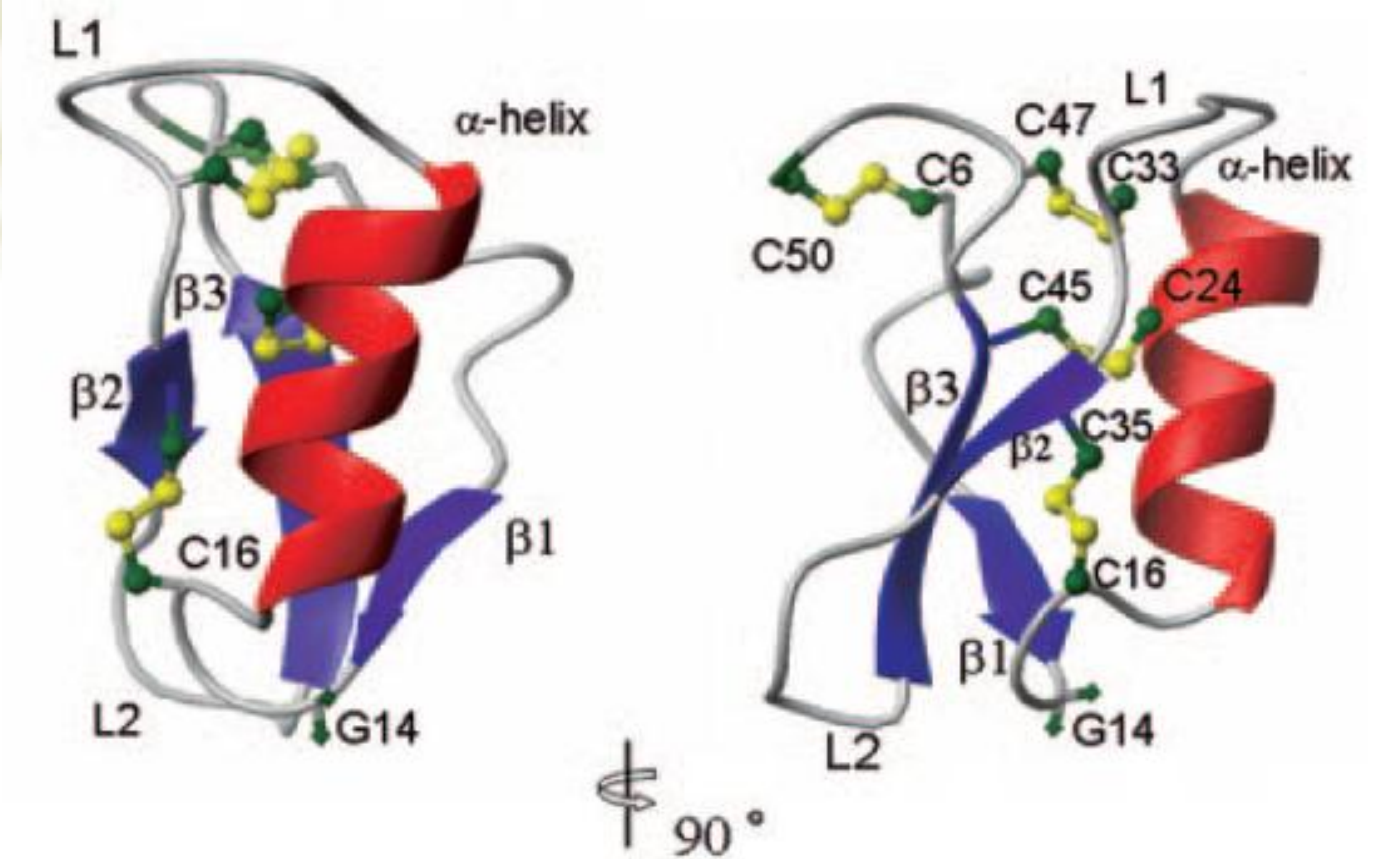
BoSP11-8 secondary struction



BoSP11-8 secondary structure

Phylogenetic tree of SP11s





Mishima et al,2003

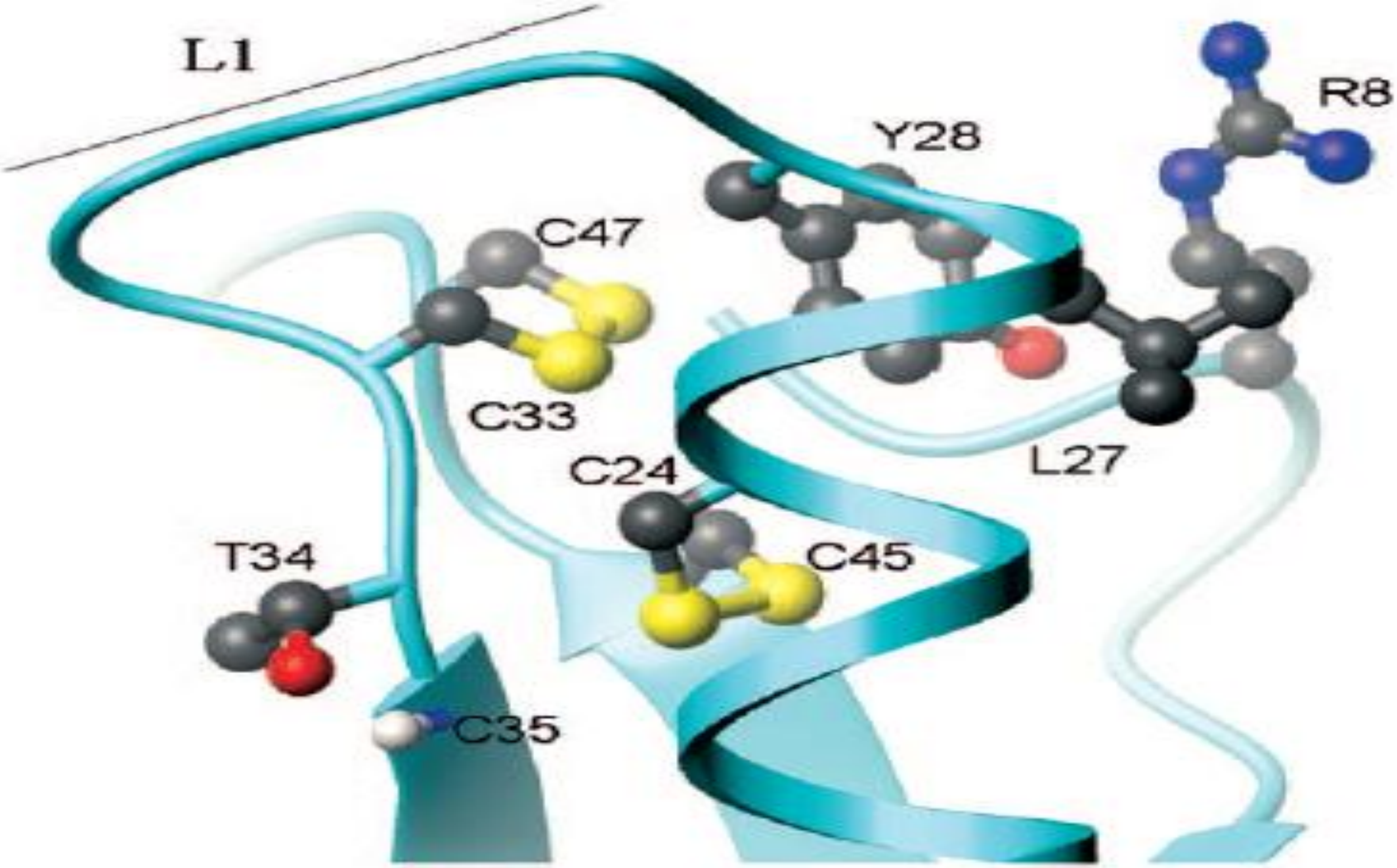


FIG. 3. **Protein-core forming residues and loop L1.** The *ribbon representation* and the *ball-and-stick models* of the side chain around the protein core. The *ball-and-stick model* of the backbone amide group of Cys-35 is also depicted. The L1 loop, referred to as HV, is guided by the *solid line*.

Discusstion

- Here,we align different SP11 genes in *Brassica rapa*,*Brassica oleracea*,*Arabidopsis thaliana* and *Arabidopsis lyrata,*with a finding that 8 conserved cysteine residues exists in every SP11.But no hyper-variable region(HV) is found.
- As a result of too low identity between SP11-8 and other SP11s,we can’t do homology modeling.But based on 8 conserved cysteine,we presume that other SP11s share the similar structure.

Acknowledgement

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