A Protocol for the Analysis of Amino Acid Composition of Peripheral Proteins from a Structural Alignment

By Hélène Kabbech
Supervised by Nathalie Reuter

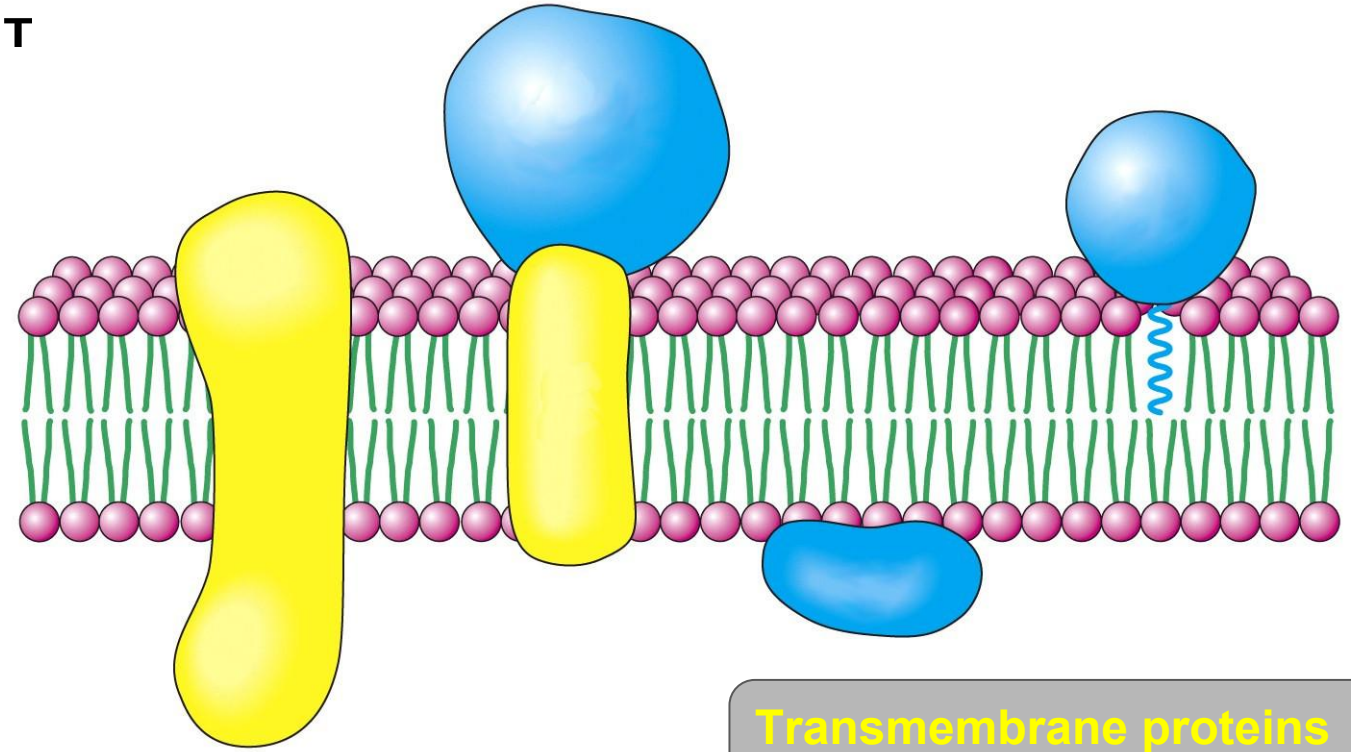


Figure 12.17
***Biochemistry*, Seventh Edition**

Transmembrane proteins
Peripheral proteins

Membrane proteins

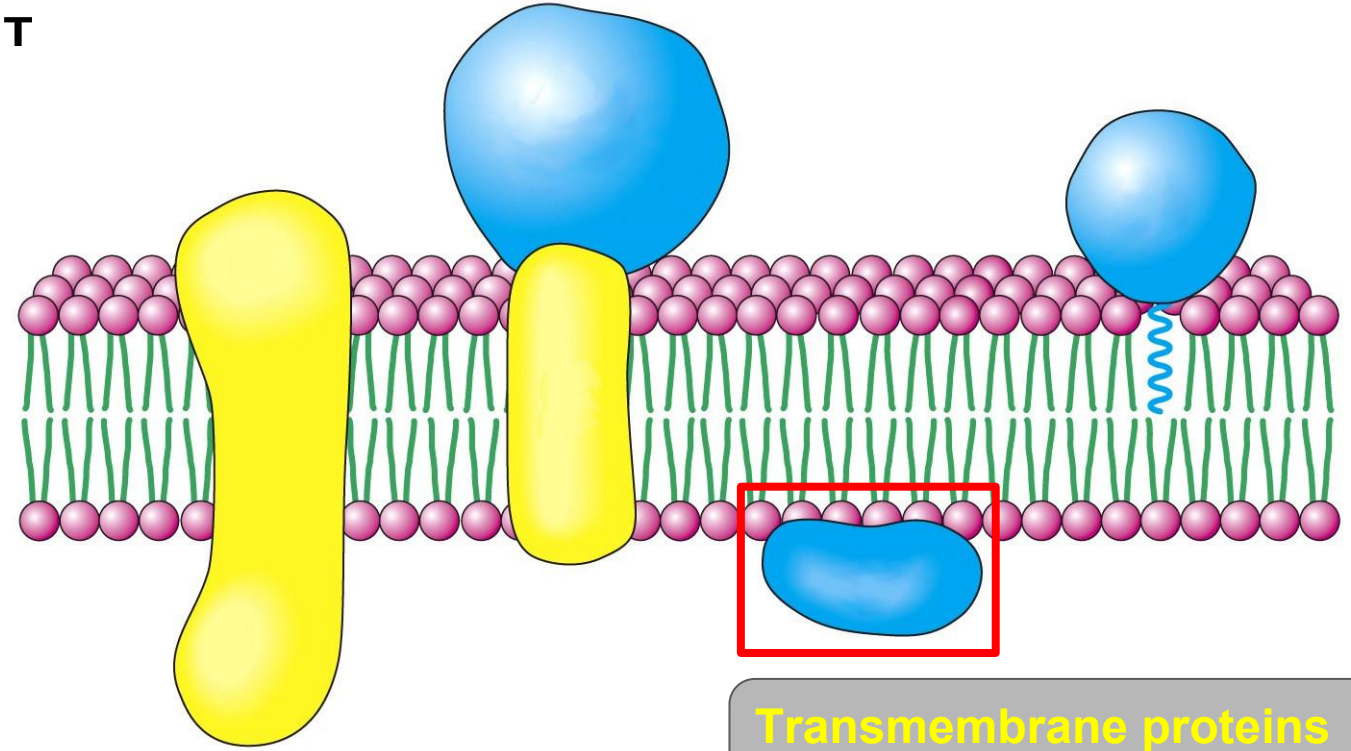


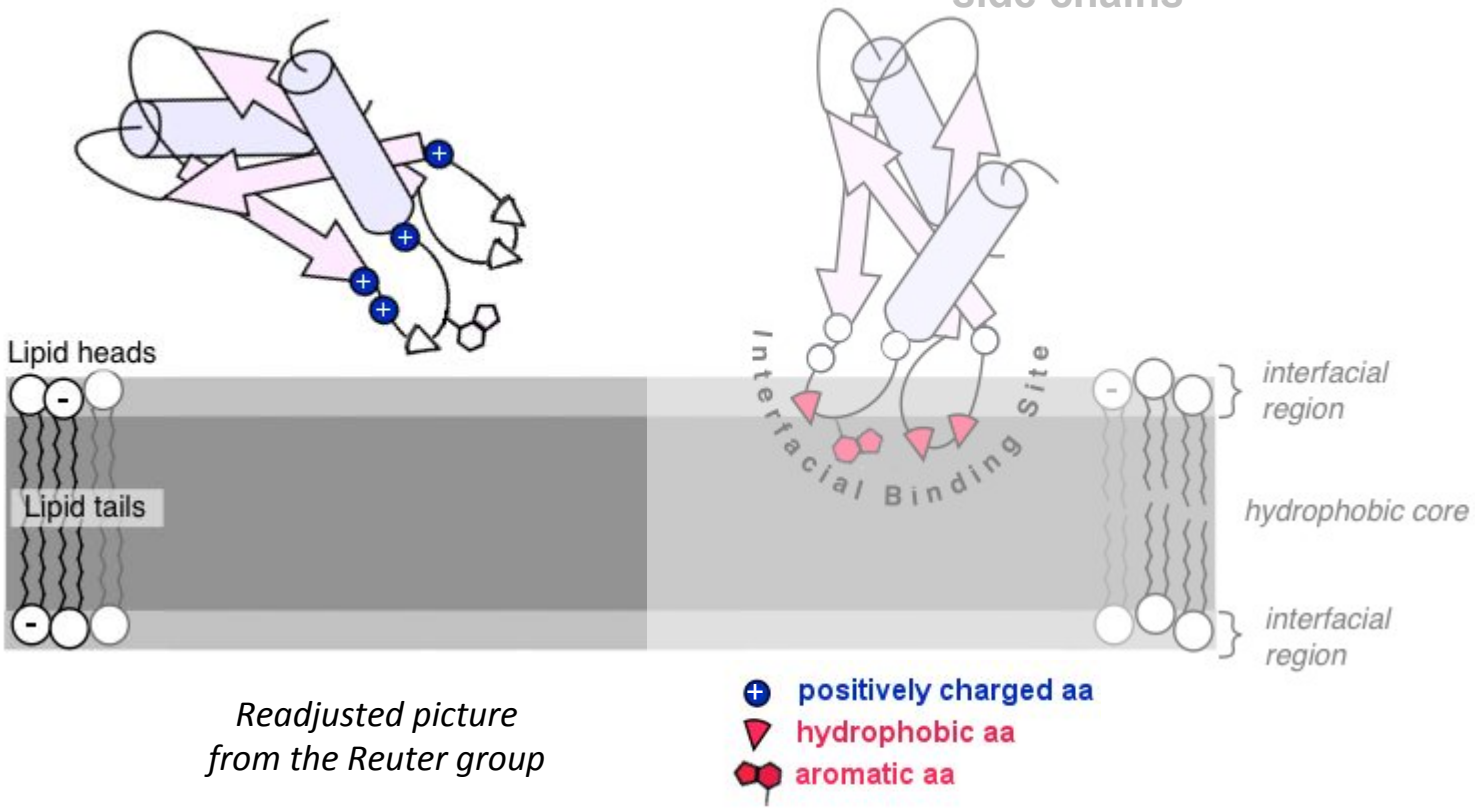
Figure 12.17
***Biochemistry*, Seventh Edition**

Transmembrane proteins
Peripheral proteins

Membrane proteins

1 **Long-range nonspecific electrostatic forces**

2 **Intercalation of hydrophobic side chains**

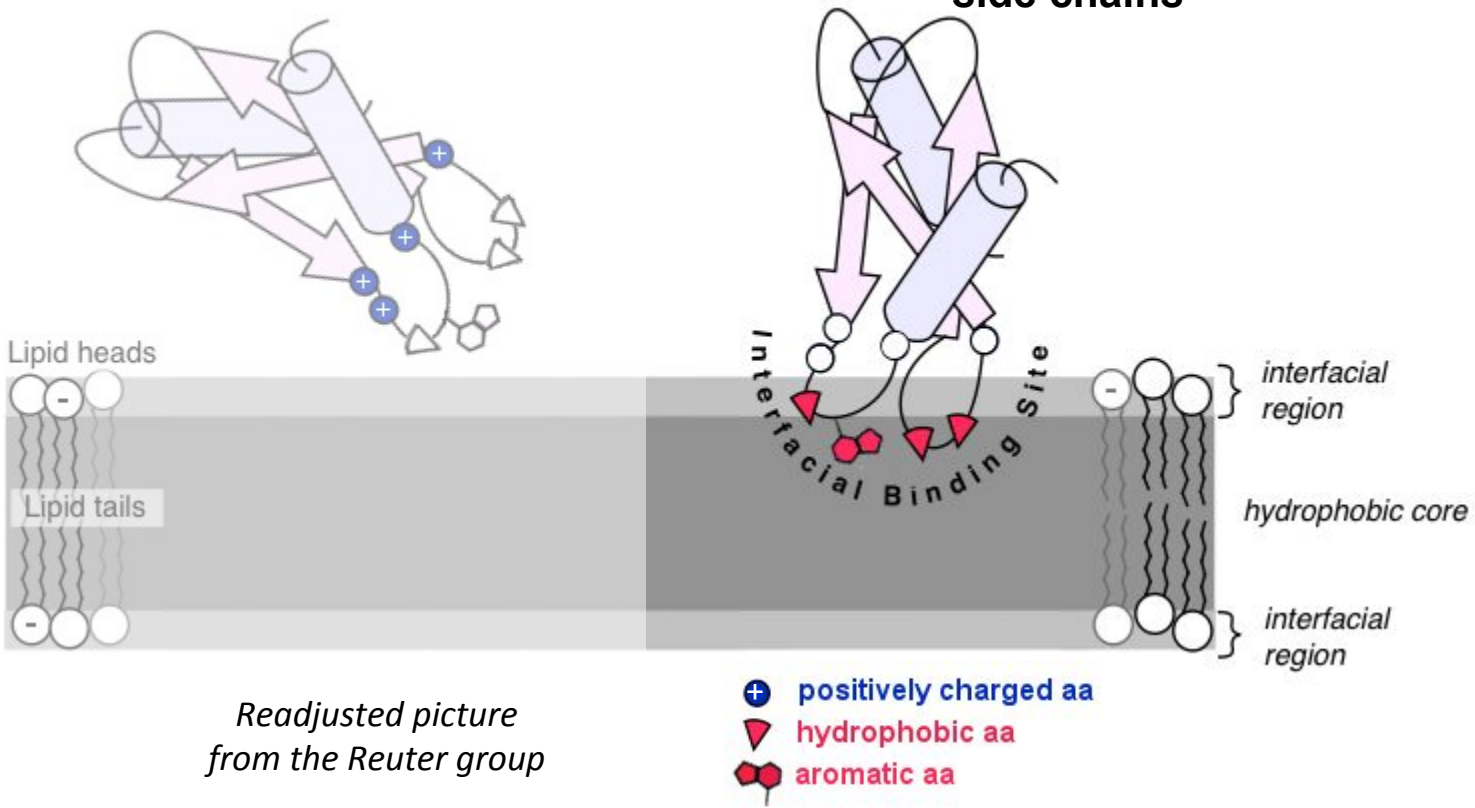


Readjusted picture from the Reuter group

Textbook model of peripheral proteins

1 Long-range nonspecific electrostatic forces

2 Intercalation of hydrophobic side chains

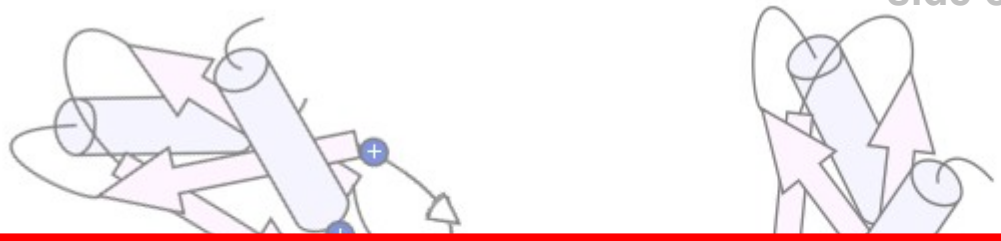


Readjusted picture from the Reuter group

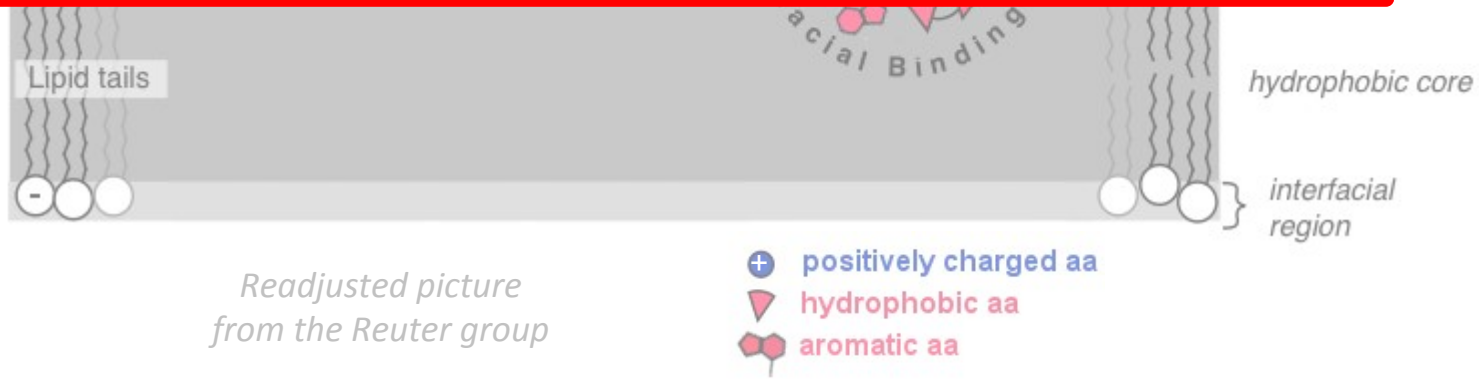
Textbook model of peripheral proteins

1 Long-range nonspecific electrostatic forces

2 Intercalation of hydrophobic side chains



Some well-studied peripheral proteins do not fit this model.
Need to **update this textbook model**.

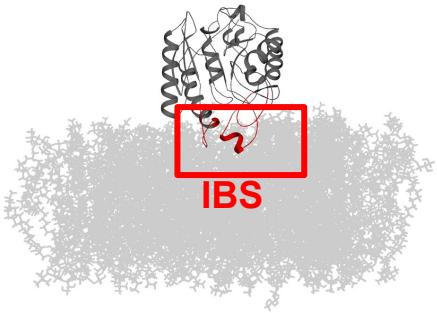


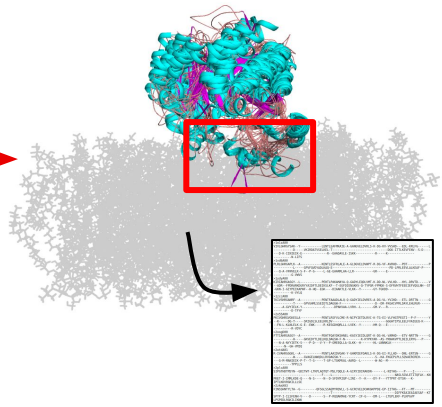
Readjusted picture from the Reuter group

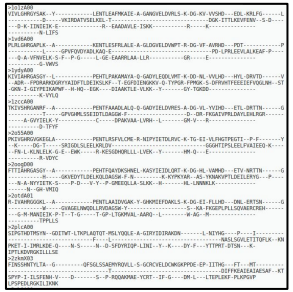
Textbook model of peripheral proteins

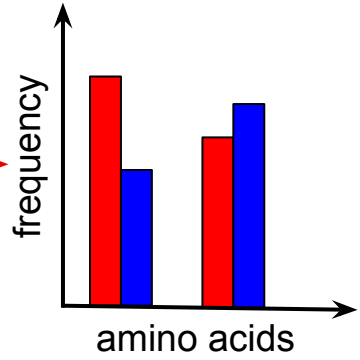
Develop and test a protocol to analyse amino acid composition at the membrane binding site of peripheral proteins.

Aim of the project









Domains with known IBS

Structural superposition of related domains

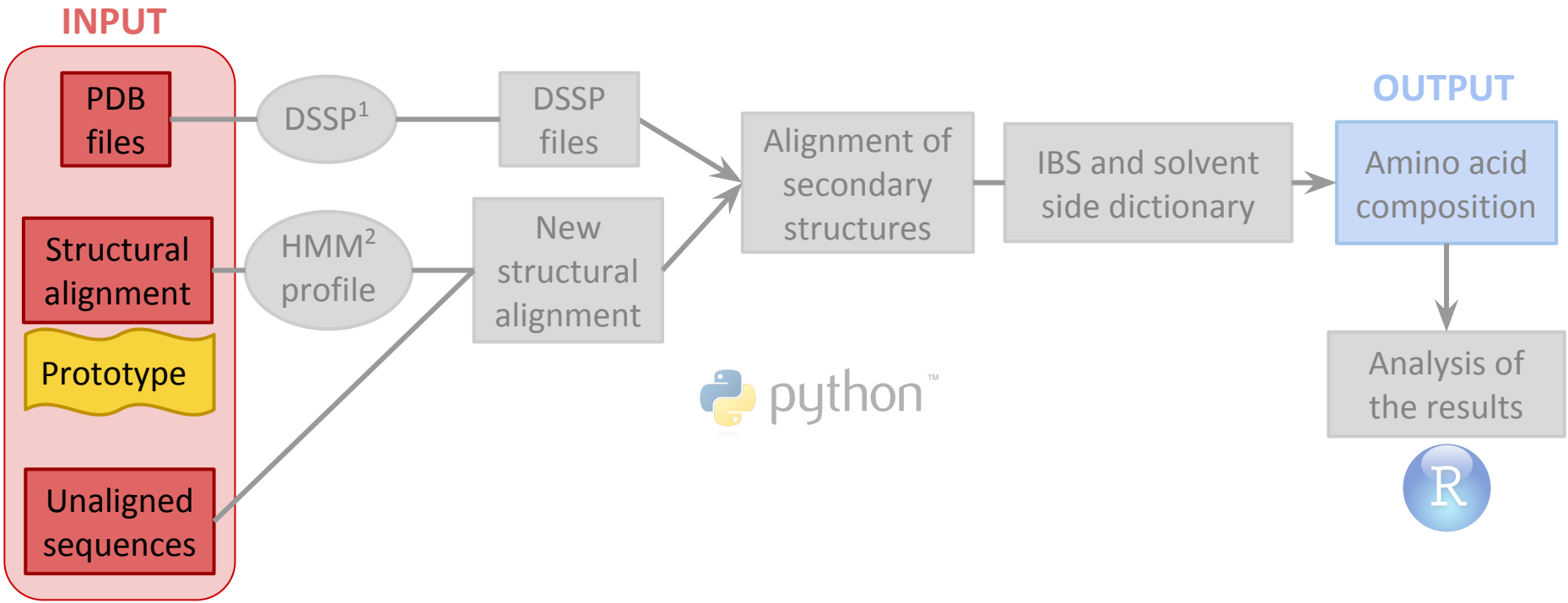
CATH

+ Sequence data

Pfam

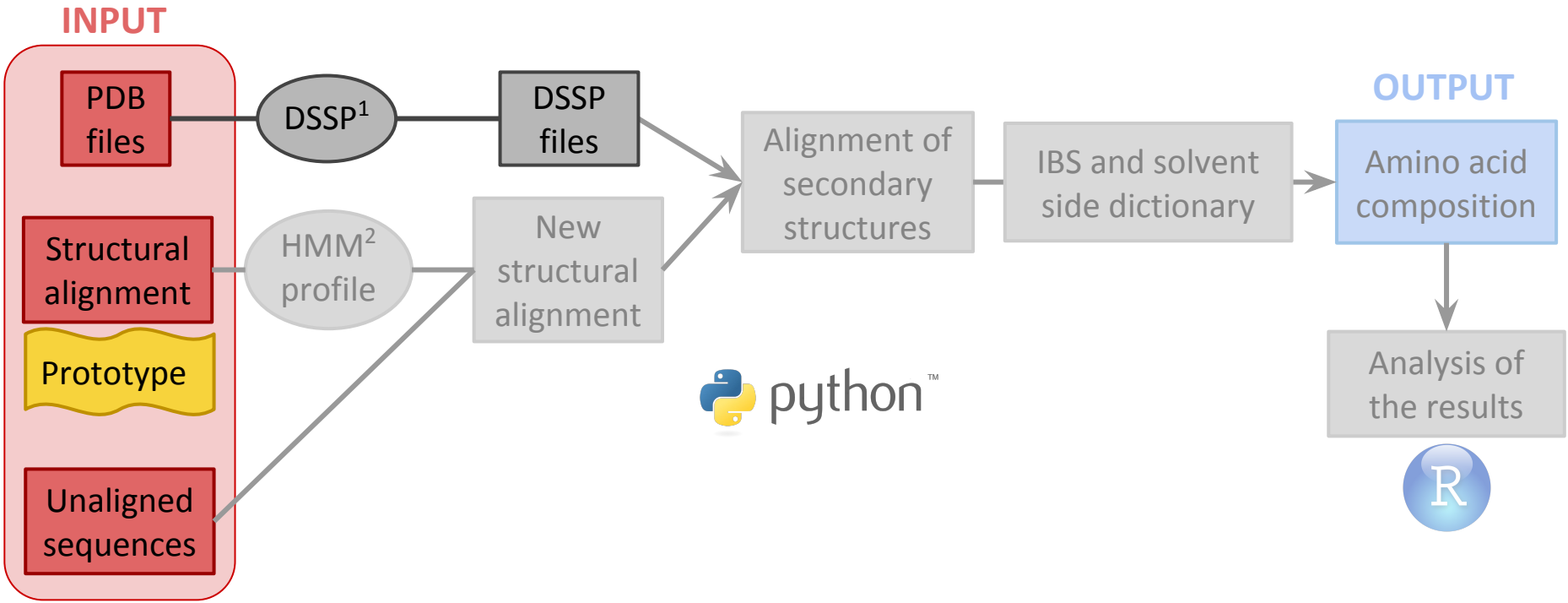
Statistics on aa composition

Protocol summary



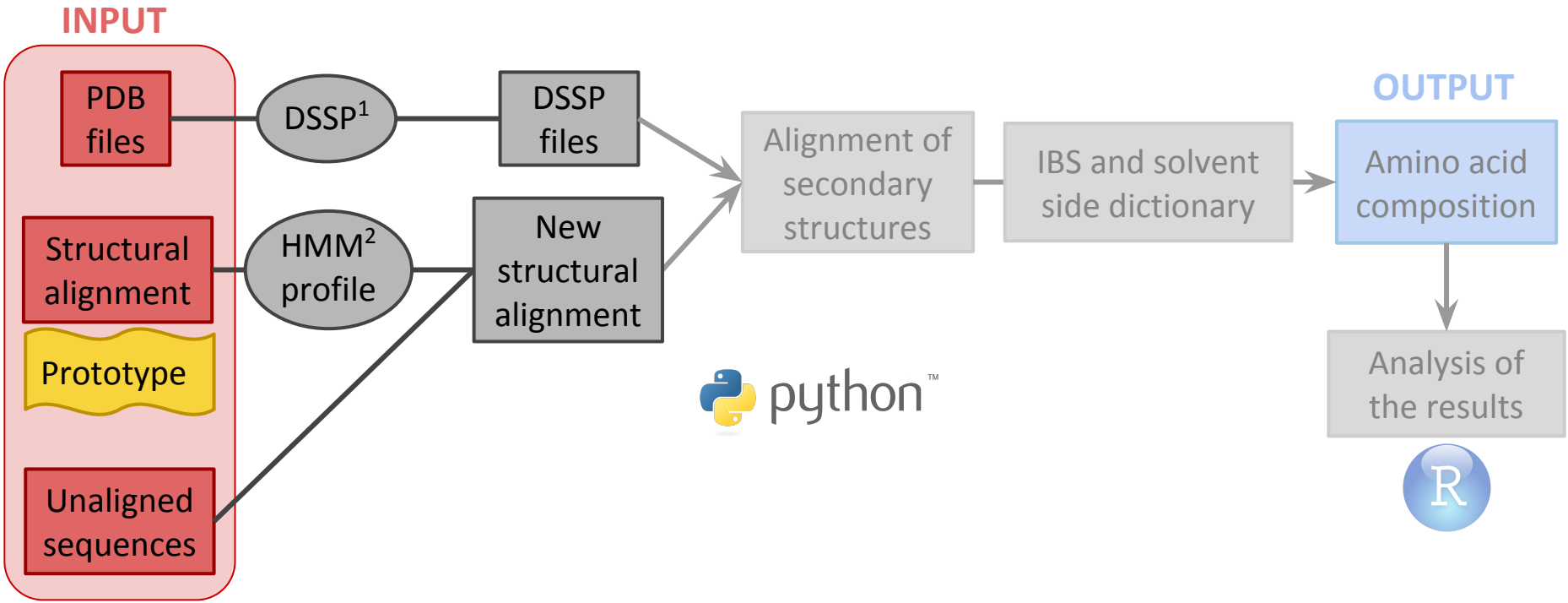
[1] Kabsch W & Sander C. (1983)
[2] Eddy S R. (1998)

Automated pipeline



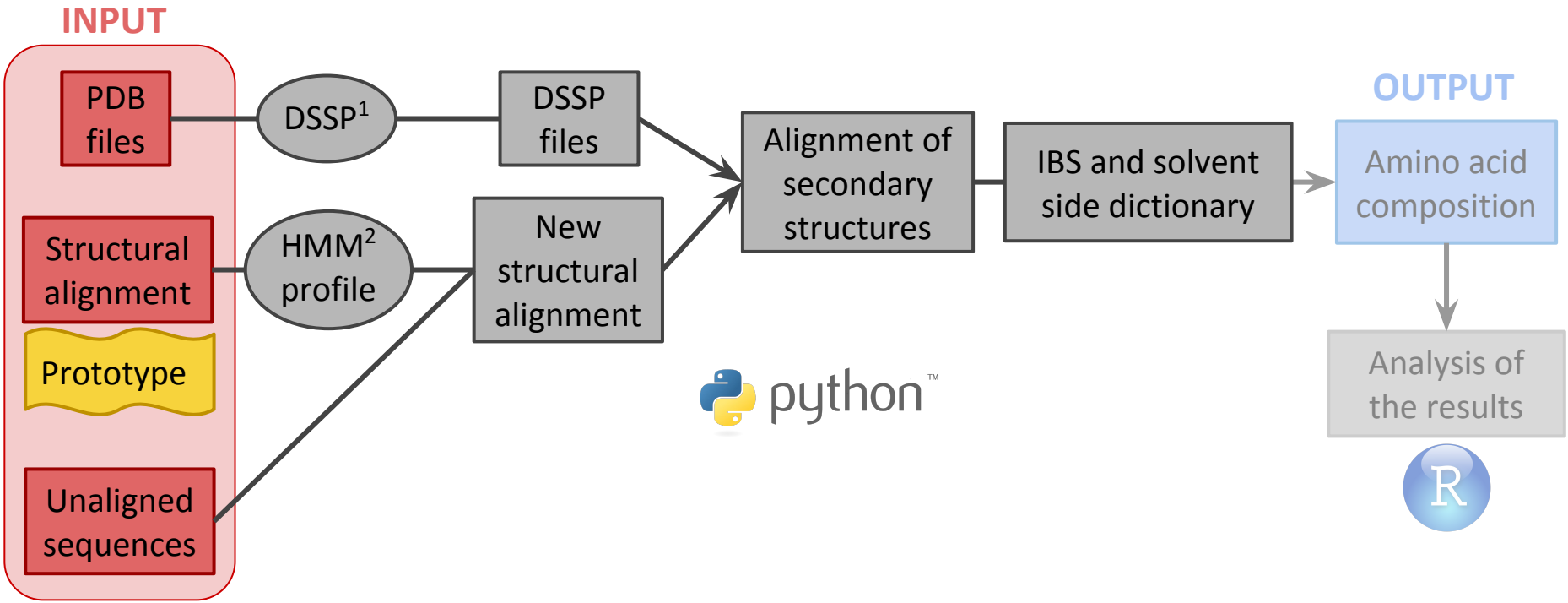
[1] Kabsch W & Sander C. (1983)
[2] Eddy S R. (1998)

Automated pipeline



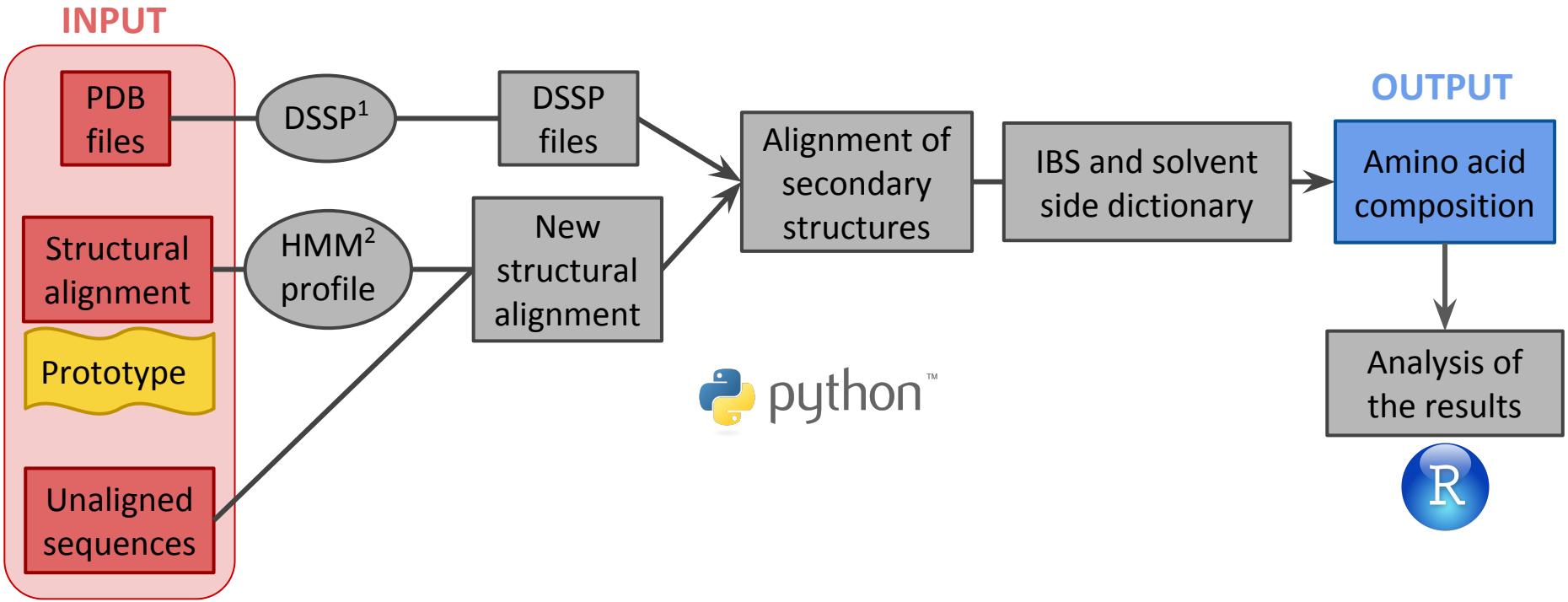
[1] Kabsch W & Sander C. (1983)
[2] Eddy S R. (1998)

Automated pipeline



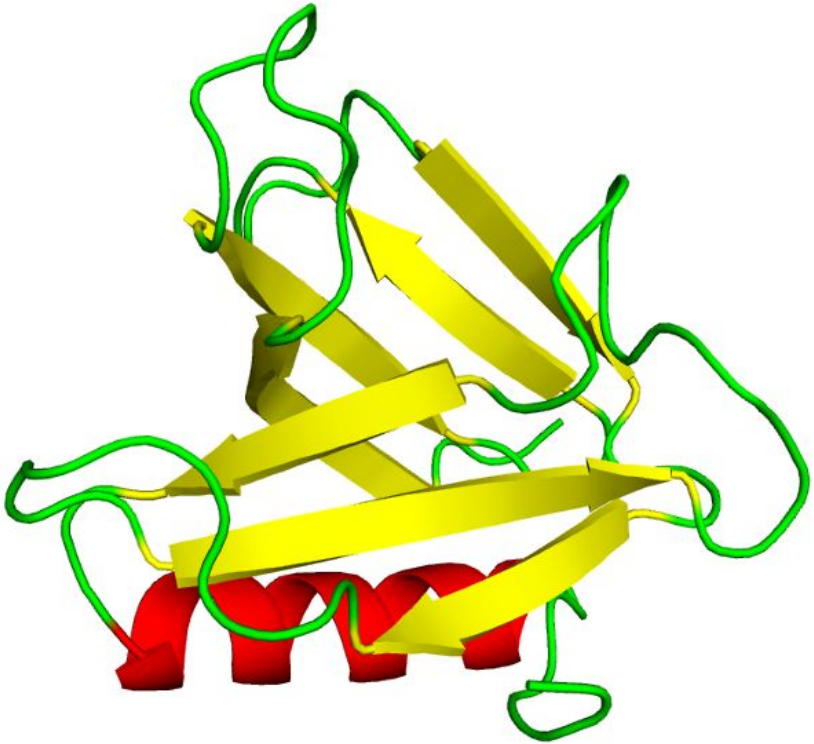
[1] Kabsch W & Sander C. (1983)
[2] Eddy S R. (1998)

Automated pipeline



[1] Kabsch W & Sander C. (1983)
[2] Eddy S R. (1998)

Automated pipeline

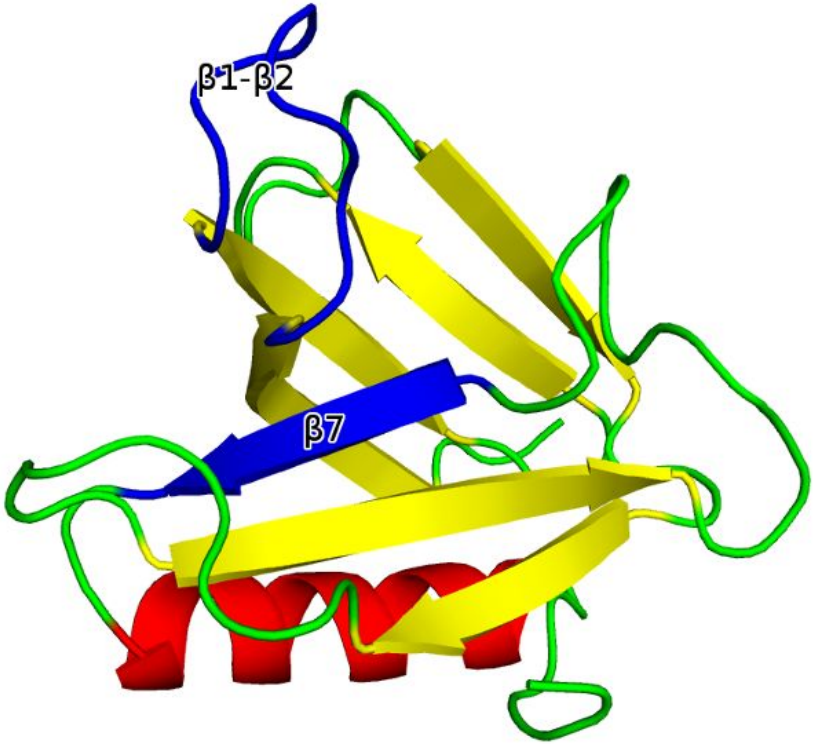


PH domain (1dyn)

*Bc*PI-PLC (1gym)

Peripheral proteins studied

Vonkova I *et al.* (2015)

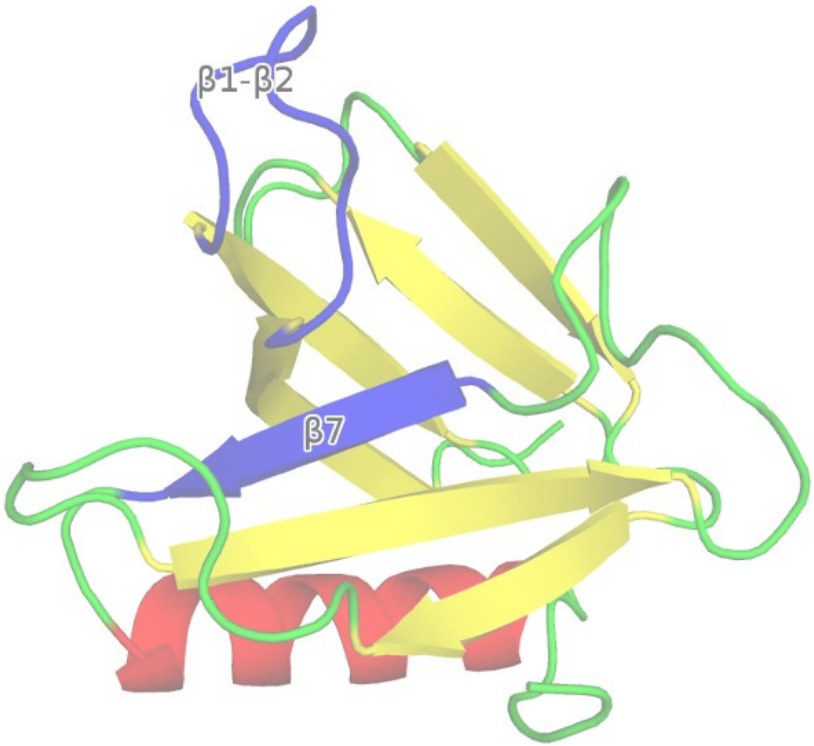


PH domain (1dyn)

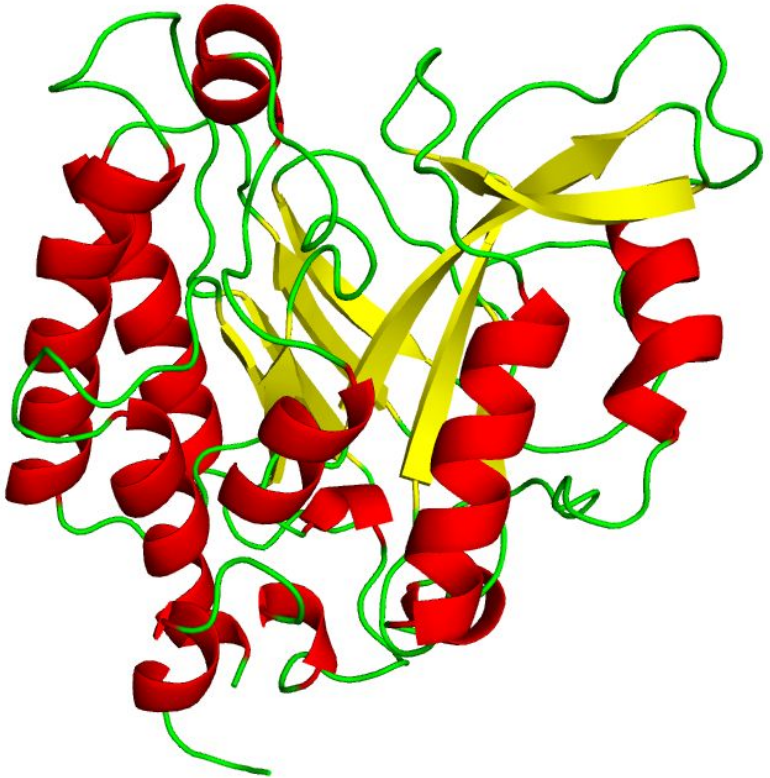
***Bc*PI-PLC (1gym)**

Peripheral proteins studied

Vonkova I *et al.* (2015)



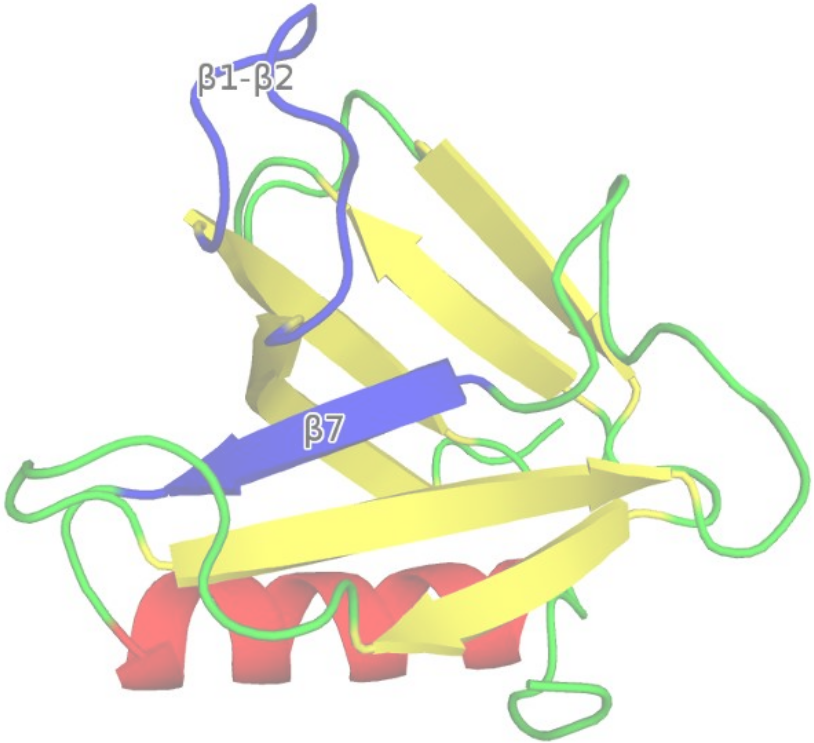
PH domain (1dyn)



***Bc*PI-PLC (1gym)**

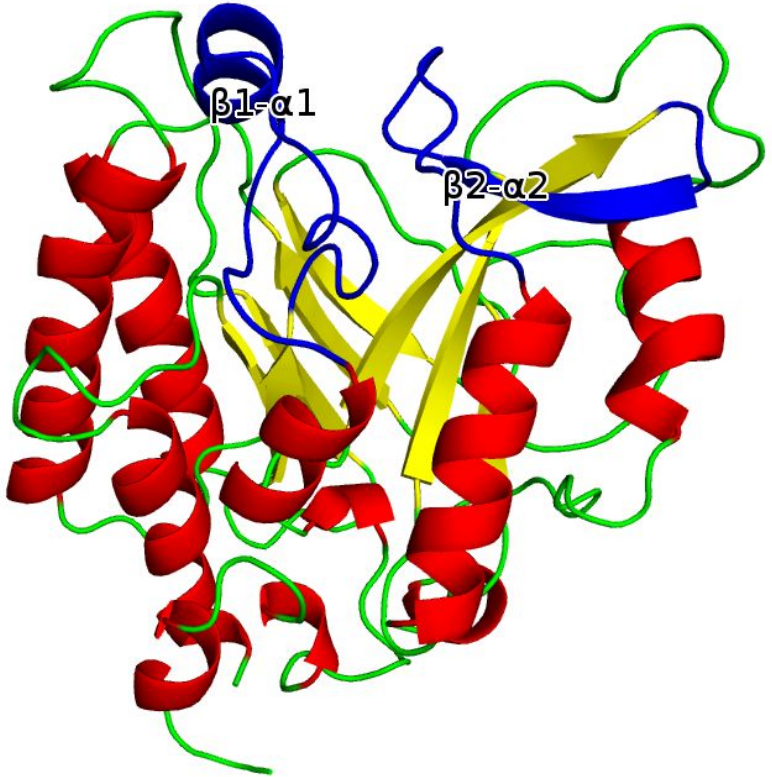
Peripheral proteins studied

Vonkova I *et al.* (2015)



PH domain (1dyn)

Gauffel C et *al*. (2013)



***Bc*PI-PLC (1gym)**

Peripheral proteins studied

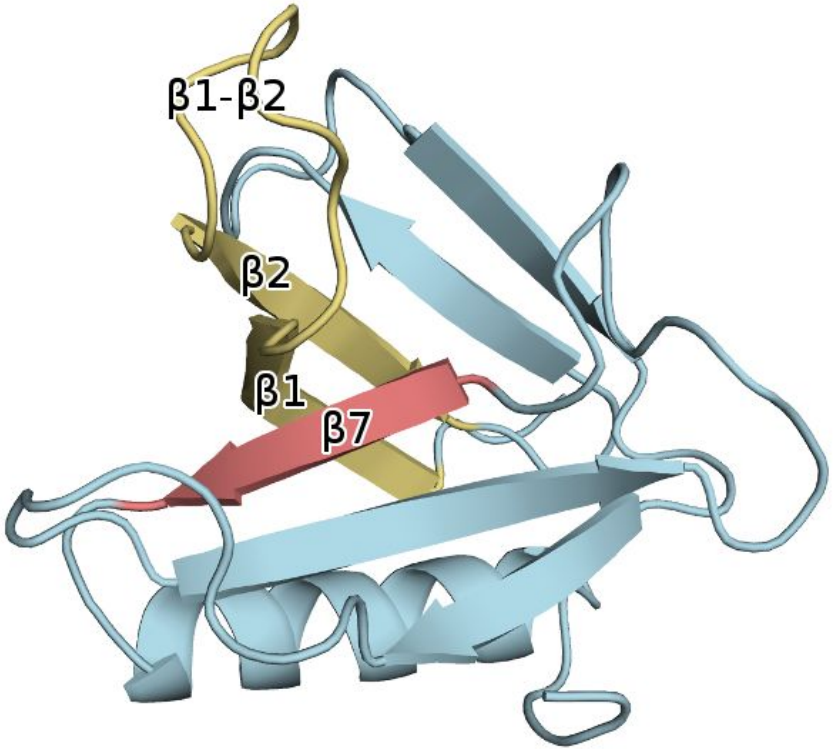
Dataset : 27 PH domains

Prototype : 1dyn

Protein function : targeting proteins

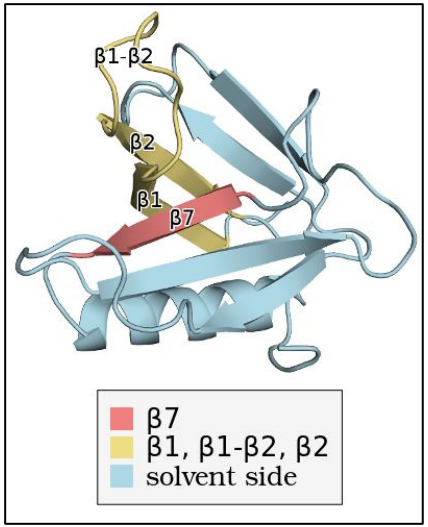
Experimental : All domains bind the membrane

Vonkova I *et al.* (2015)



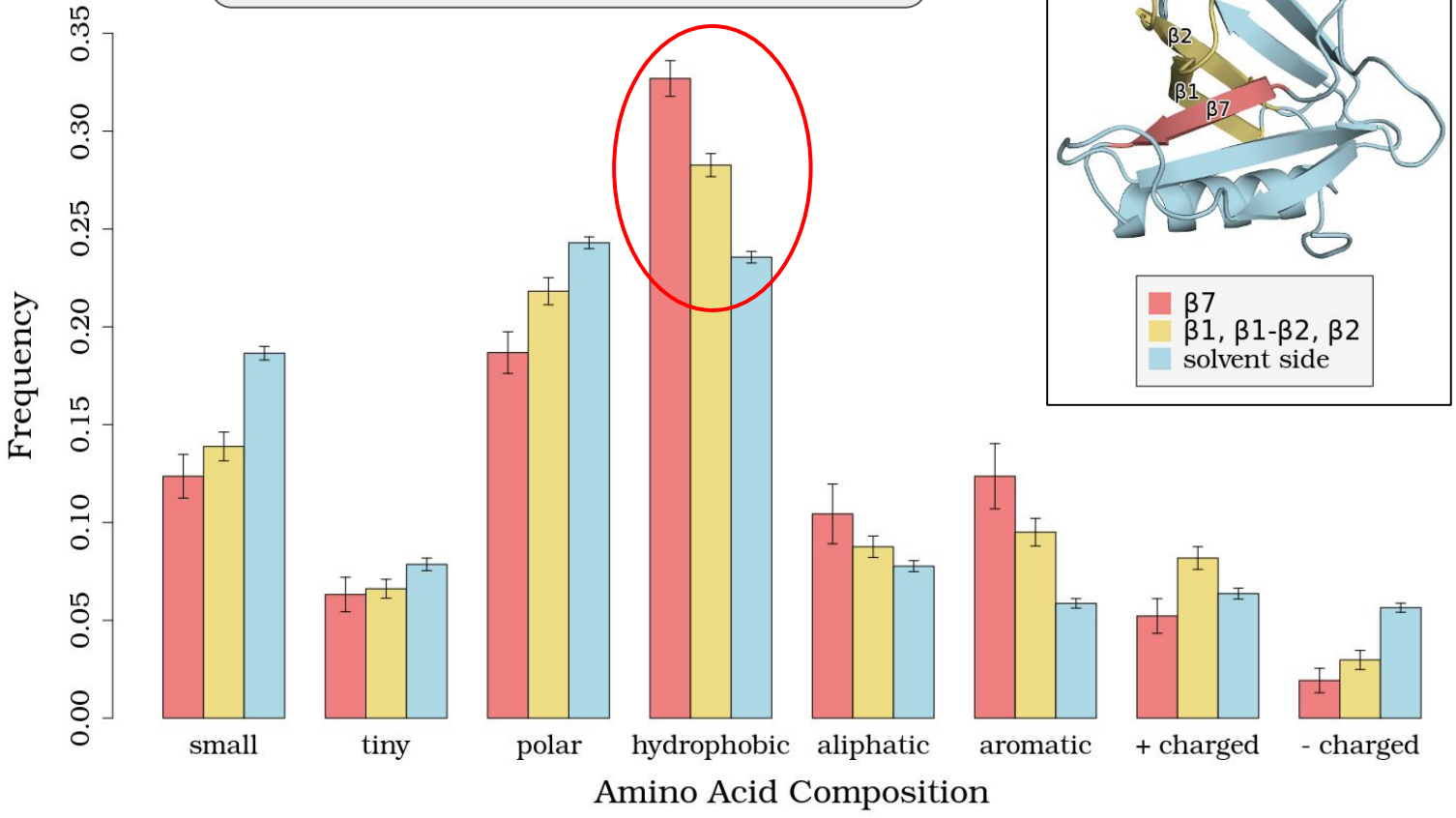
PH domains : Analysis strategy

1 Long-range nonspecific electrostatic forces



PH domains : Results

2 Intercalation of hydrophobic side chains



PH domains : Results

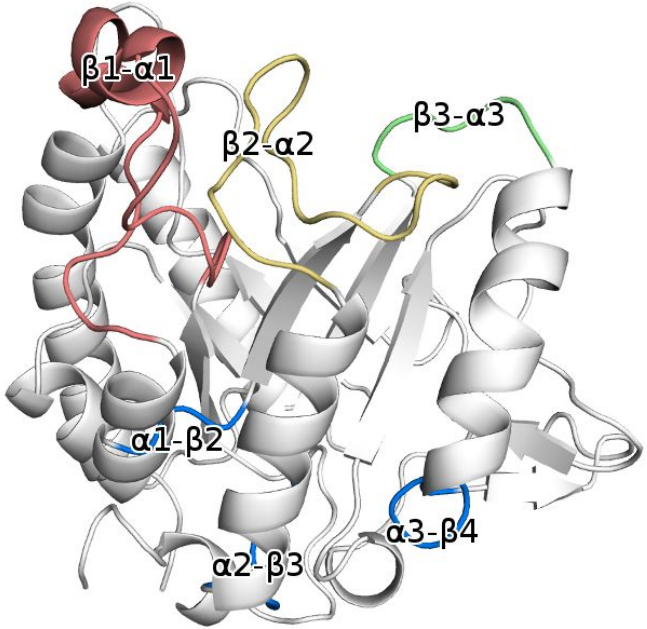
Dataset : 58 PI-PLC-X

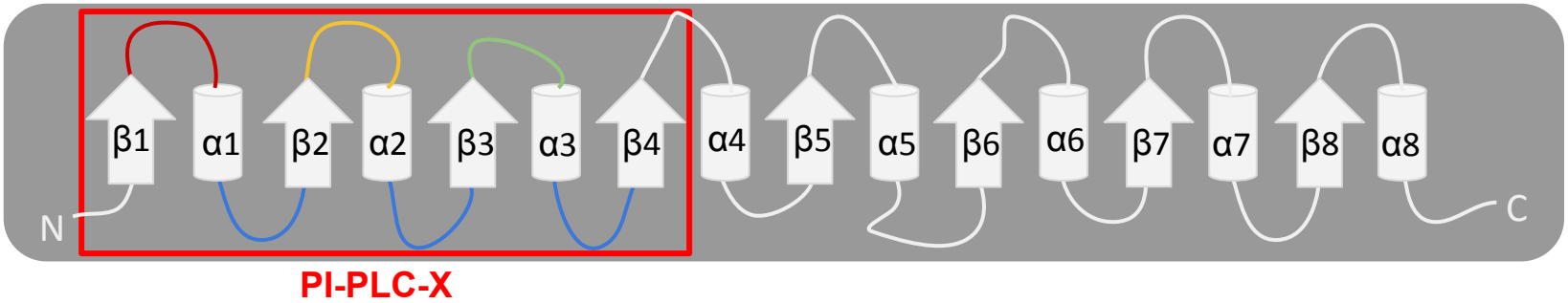
Prototype : 2plc

Protein function : Catalyzing the hydrolysis of PIP2

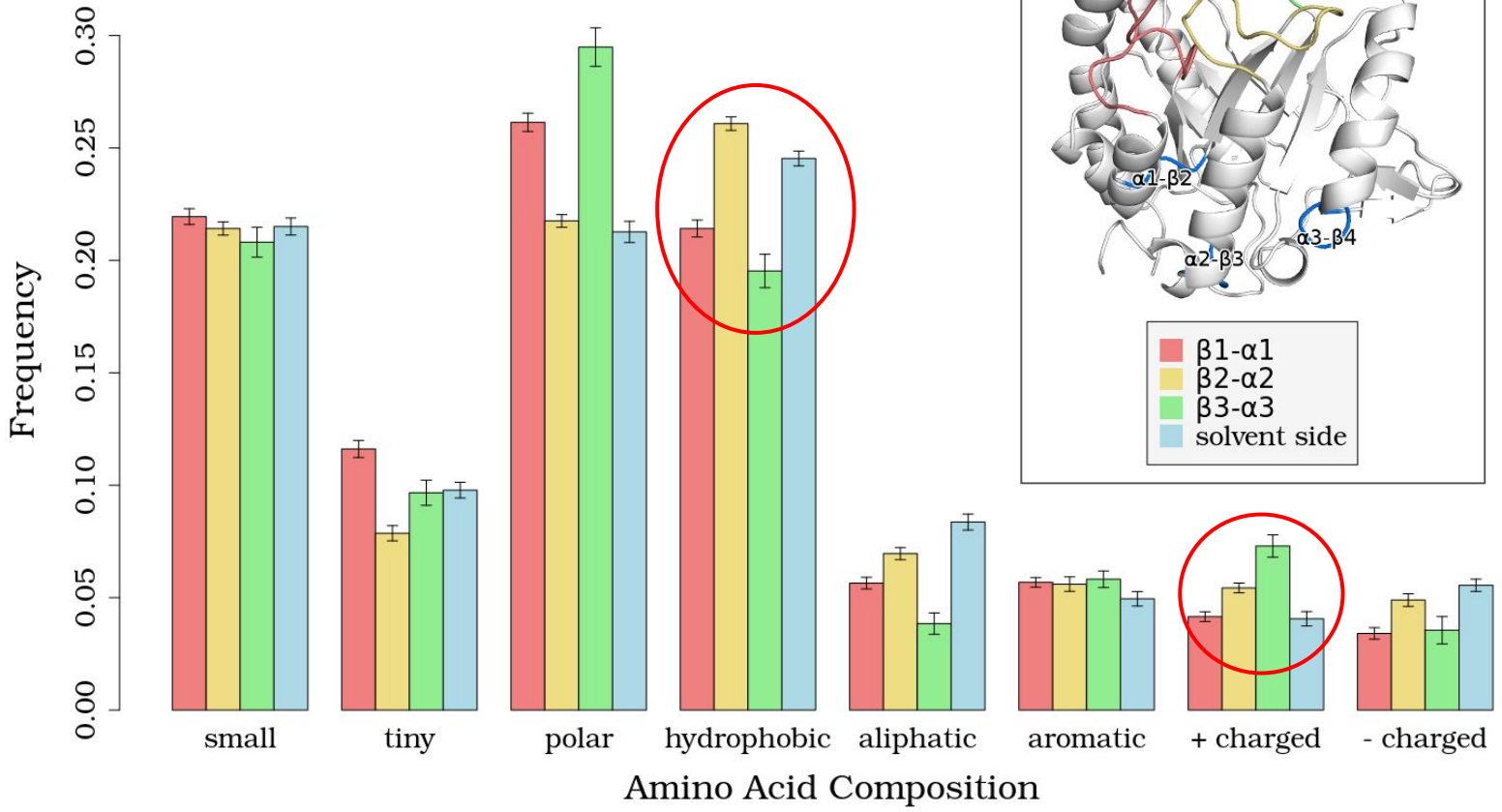
Experimental : *Bc*PI-PLC, *Sa*PI-PLC and *Lm*PI-PLC bind the membrane

Gauffel C et *al*. (2013)



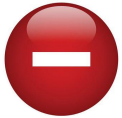


PI-PLC-X : Analysis strategy



PI-PLC-X : Results

- Automated pipeline
- Applicable to other domain families (ex : C2 domains, Fyve domains)
- Added sequences whose structure is unknown
- Comparison within the protein domains



- Verification of the new alignment generated
- Unknown structures = Delineation of the IBS depends on the prototype
- Add comparison between peripheral proteins and non-membrane proteins

Conclusion : *Pro et contra* of the pipeline

Thank you for your attention !