

Bridging the gap between lactoferrin and V-ATPase through a multi-stage computational approach

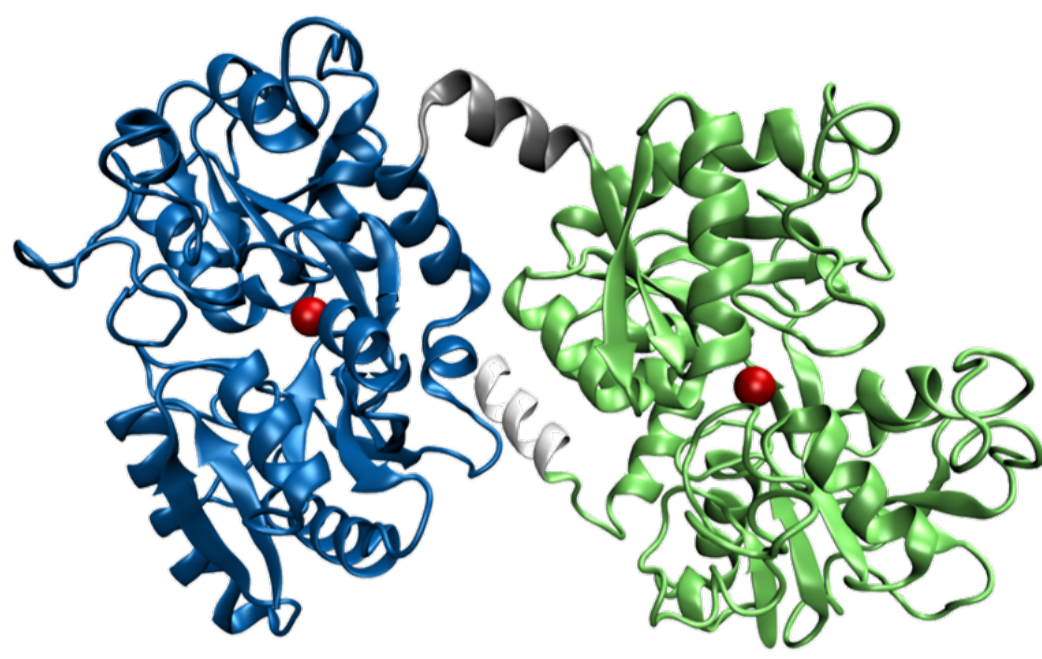
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LACTOFERRIN

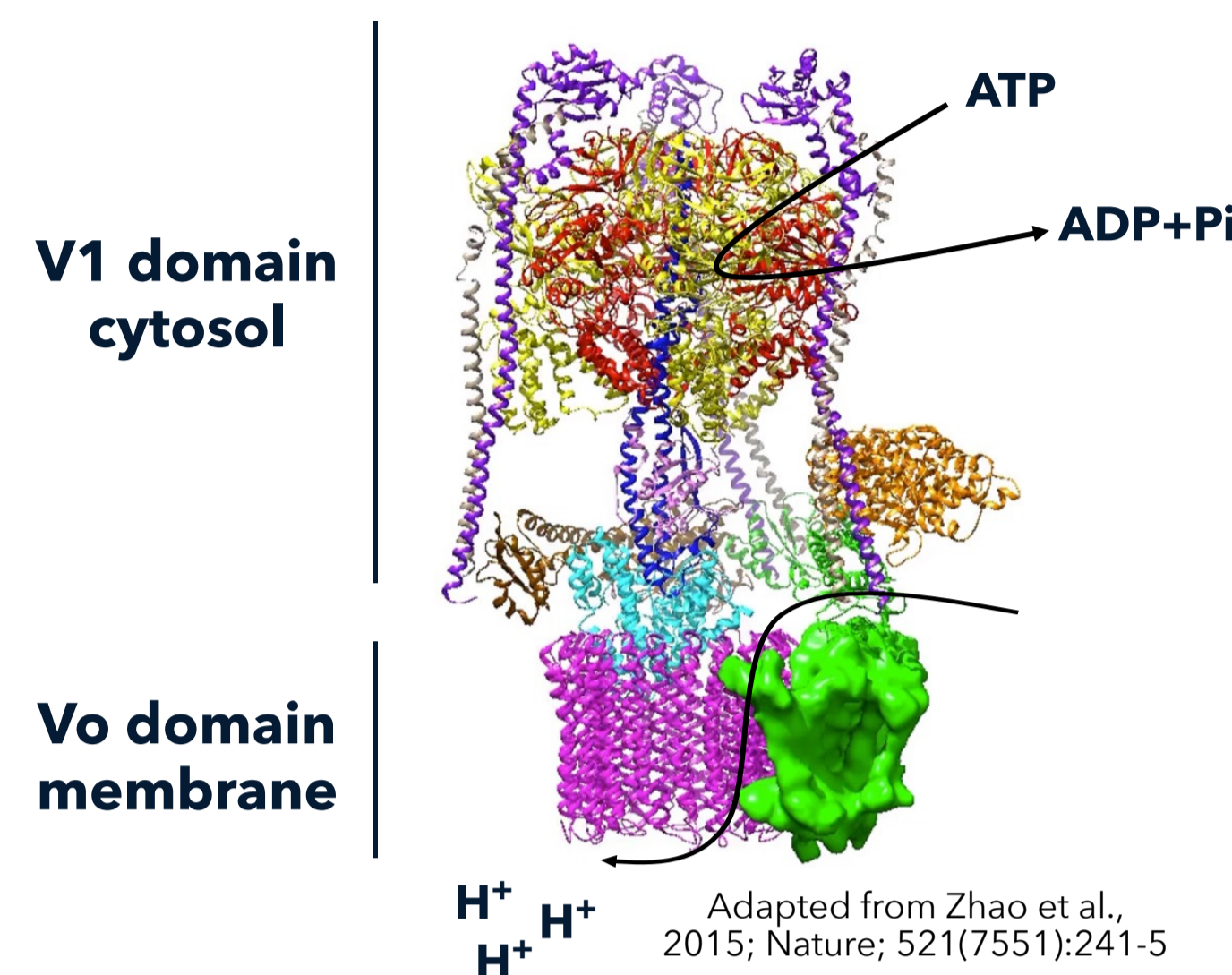
Lactoferrin (Lf) is a versatile milk-derived protein that exhibits strong antifungal and anticancer activities



A common feature among lactoferrin-treated fungal and cancer cells is the **inhibition of V-ATPase**

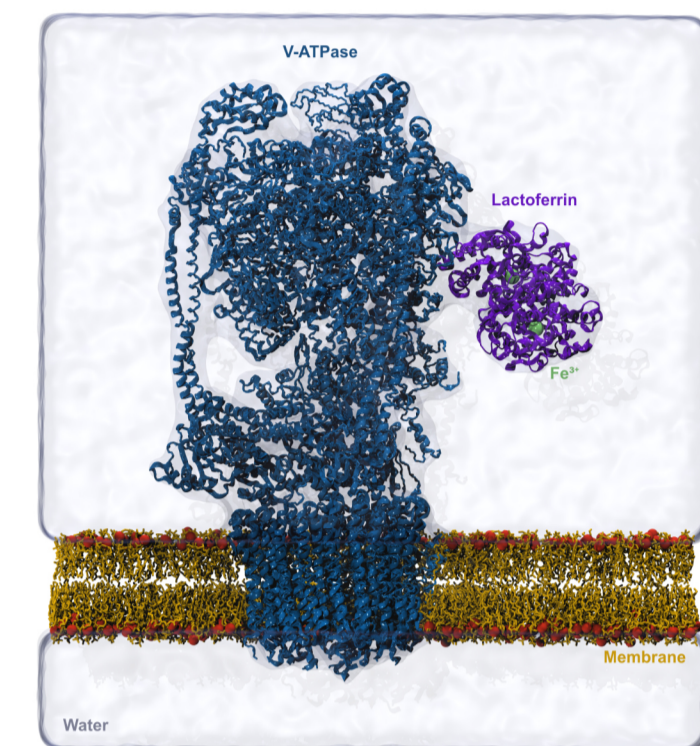
V-ATPASE

Proton pumping ATPase essential for intracellular pH regulation and cellular homeostasis

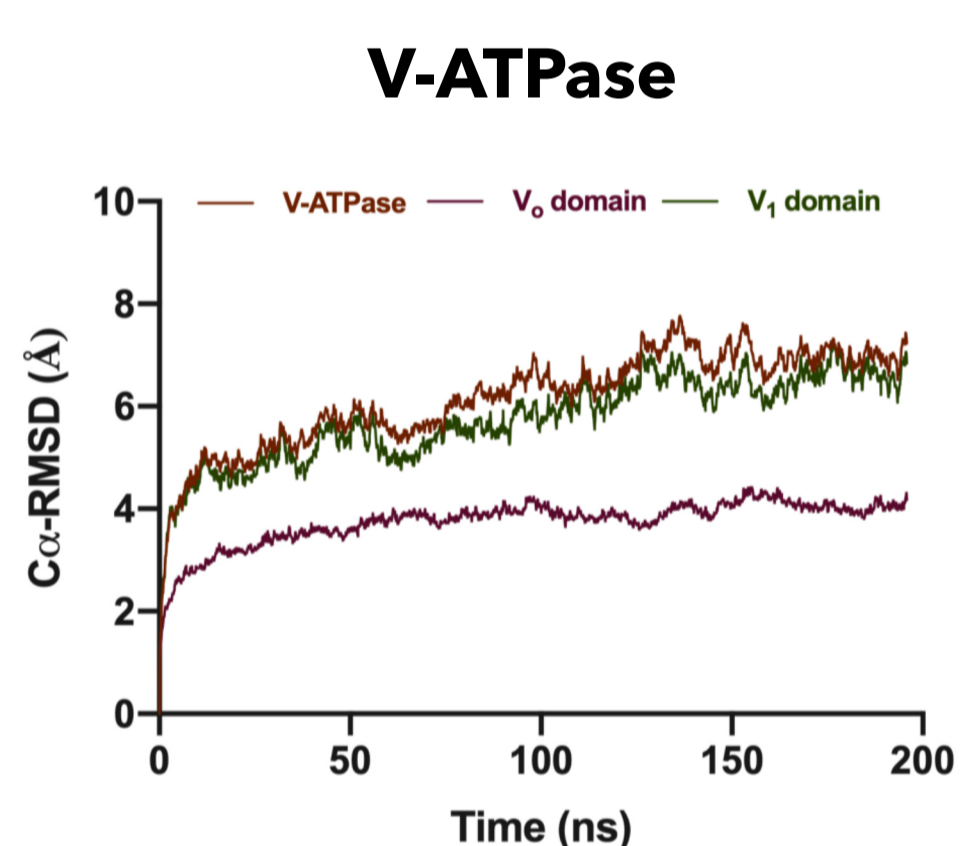
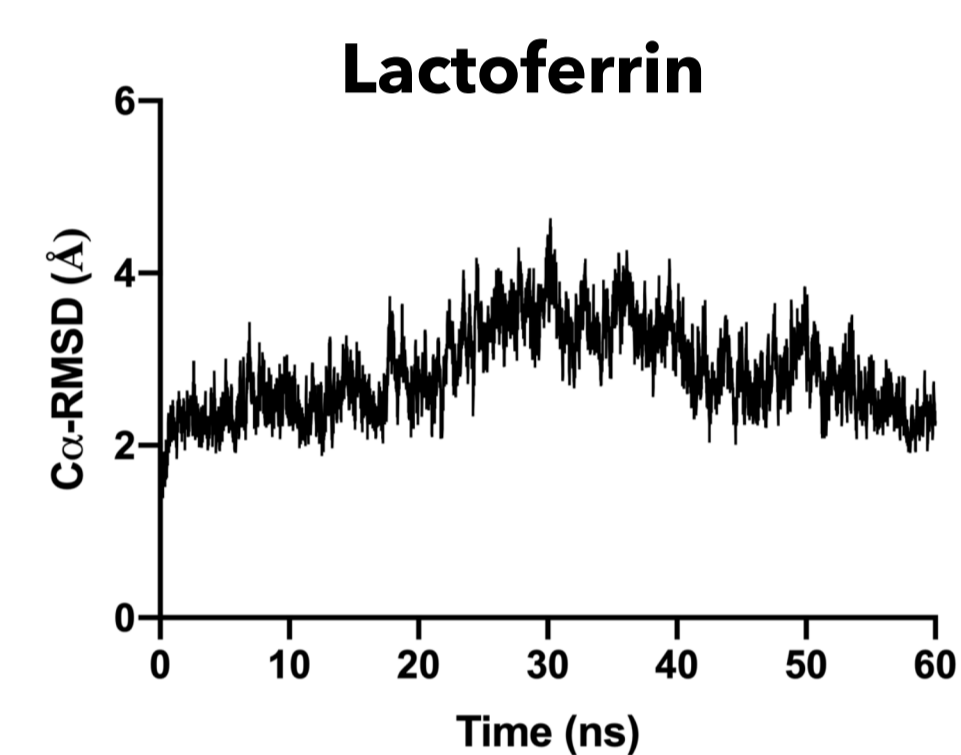


OUR AIMS

- Find how Lactoferrin and V-ATPase interact
- Identify key binding residues

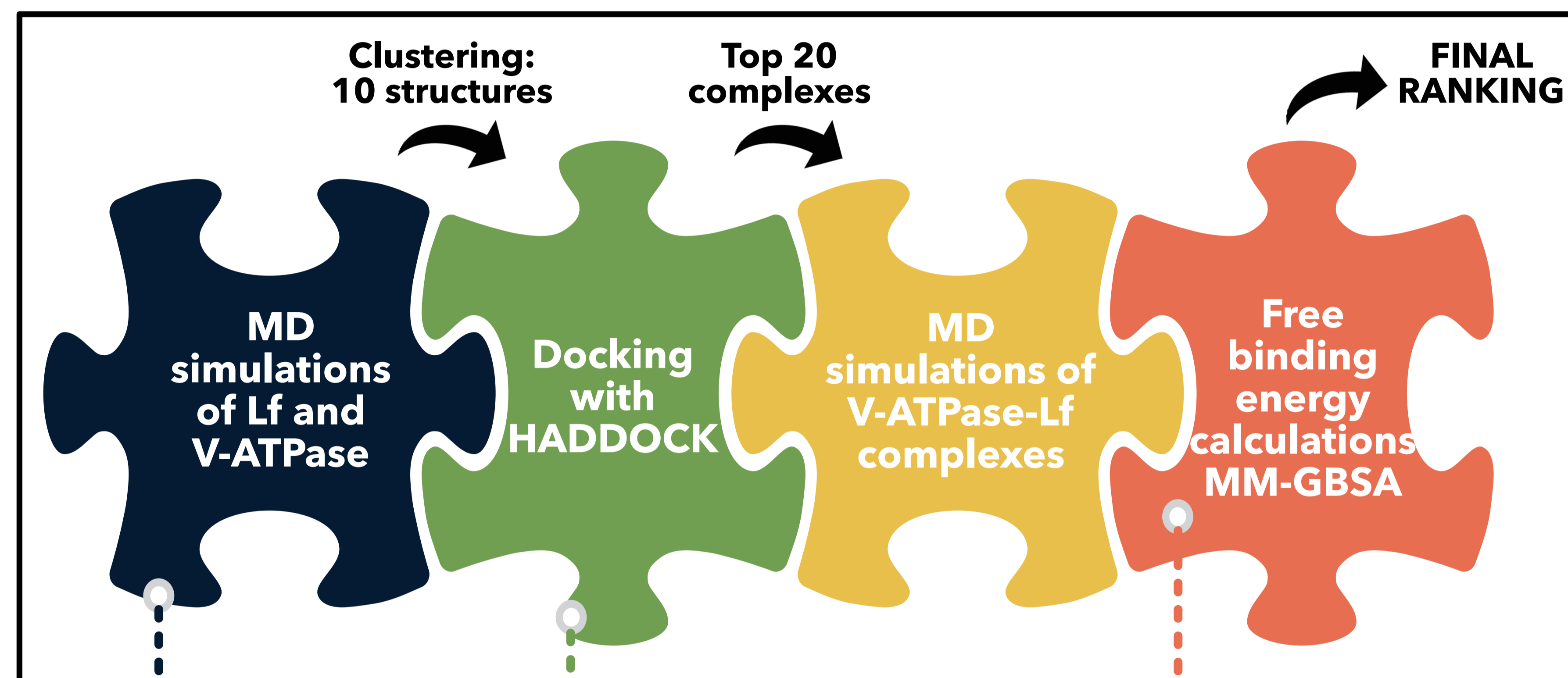


MD simulations of individual proteins



RMSD of molecular dynamics simulations of Lf (60 ns) and V-ATPase (200 ns).

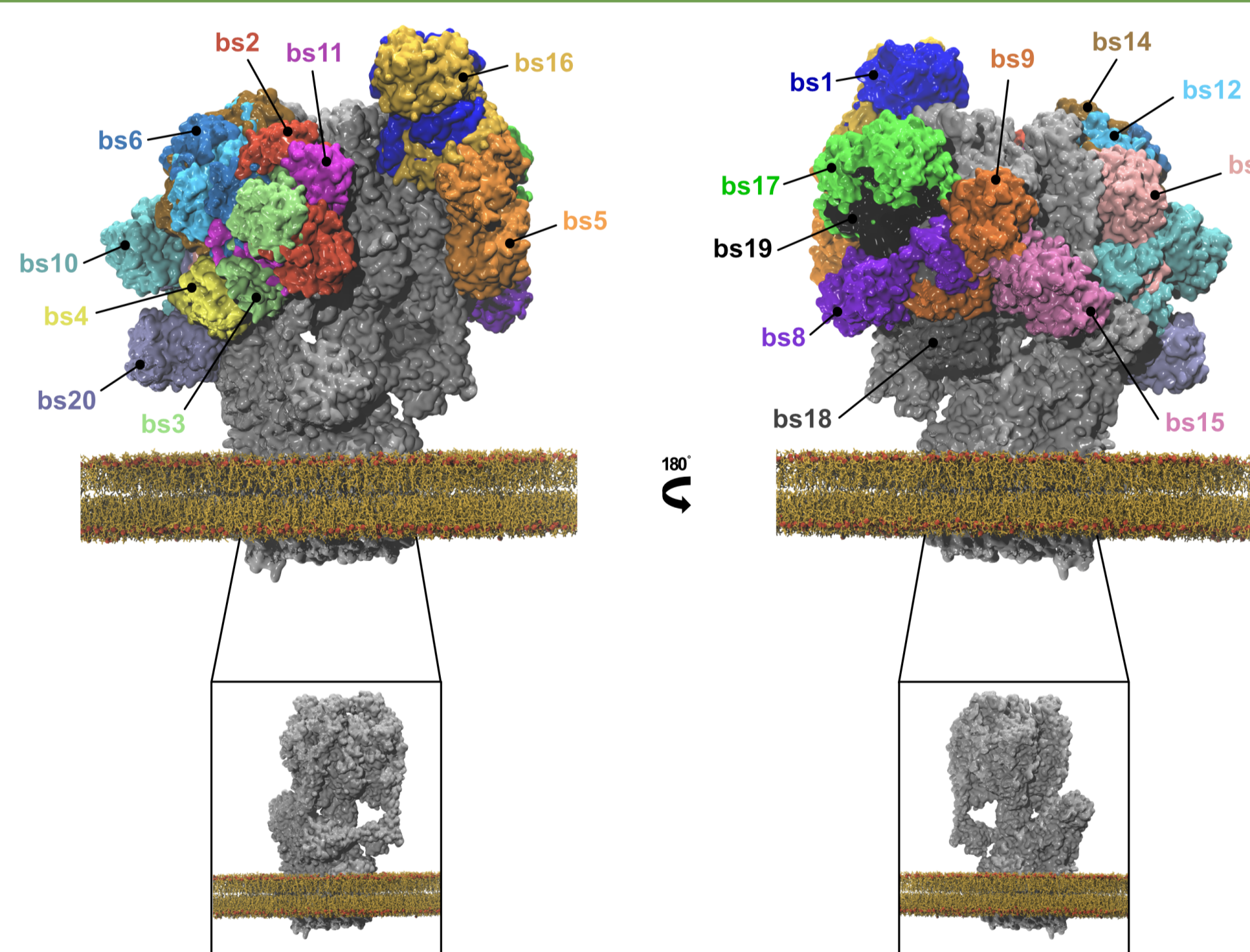
WORKFLOW AND RESULTS



INTERACTIVE VIEW OF TOP 4 COMPLEXES

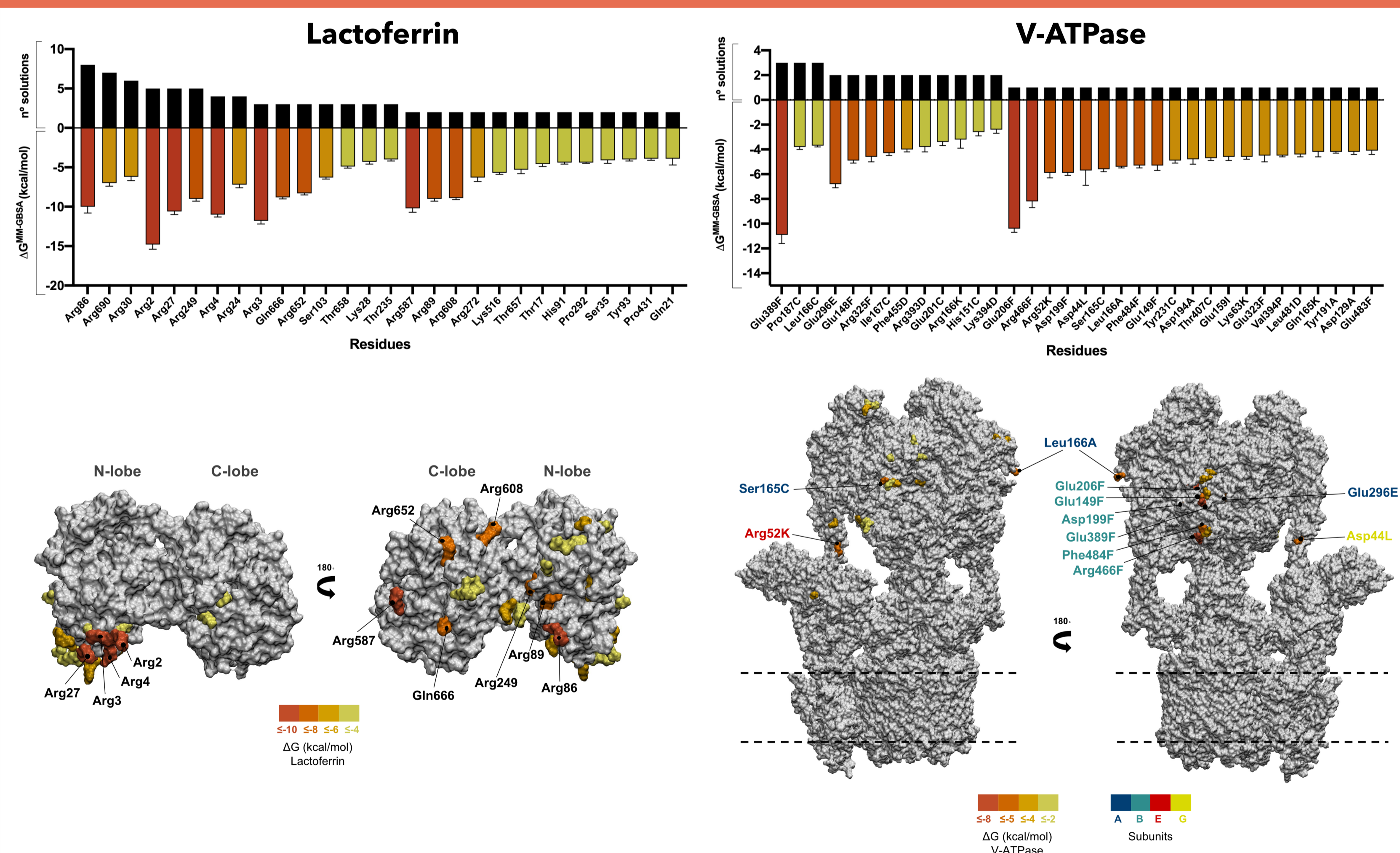


HADDOCK results



Representation of the top 20 complexes based on HADDOCK score.

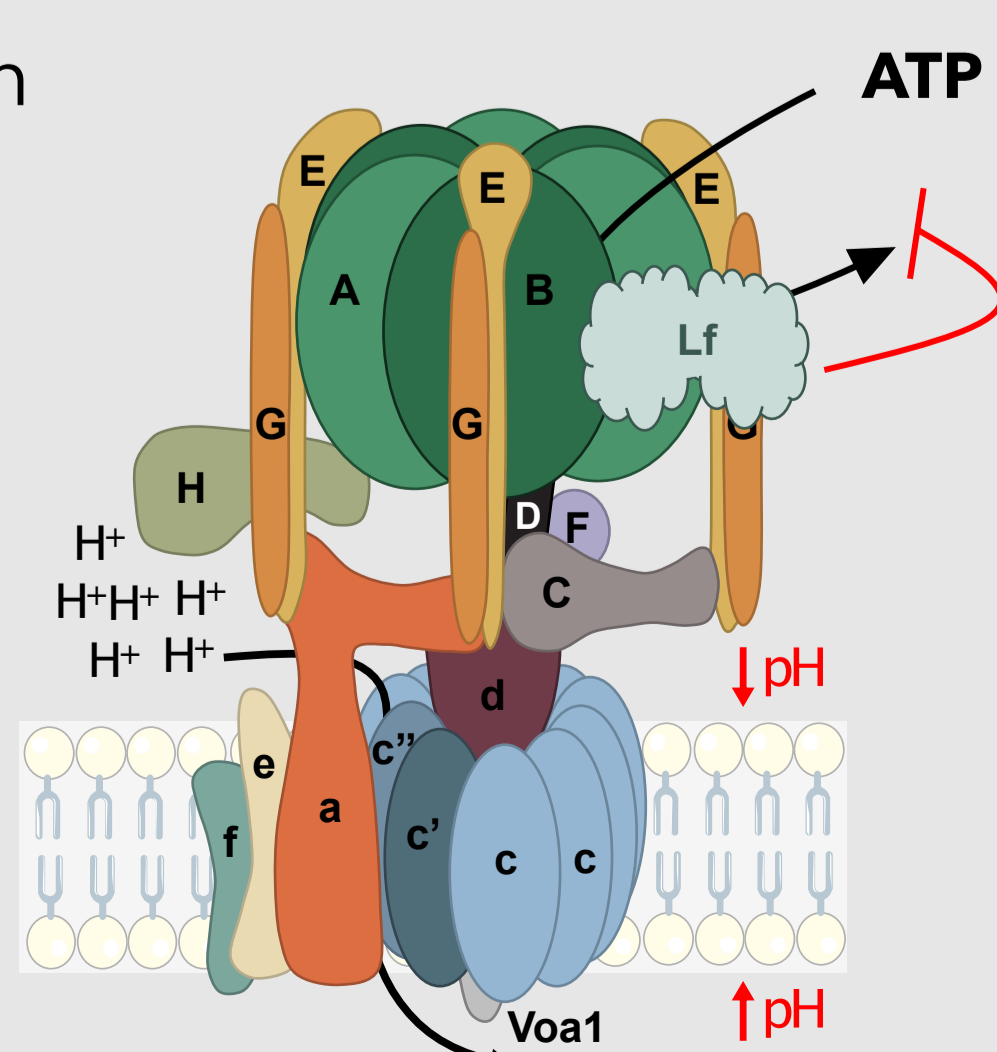
MM-GBSA results



Analysis of the critical lactoferrin and V-ATPase binding residues based on the decomposition of the binding free energy calculated using the MM-GBSA method.

CONCLUSIONS

- Lf binds in the interface between subunits A and B of V-ATPase inhibiting ATP hydrolysis
- A few residues of Lf and V-ATPase were identified as critical for the interaction, which will aid the rational design of experimental studies



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