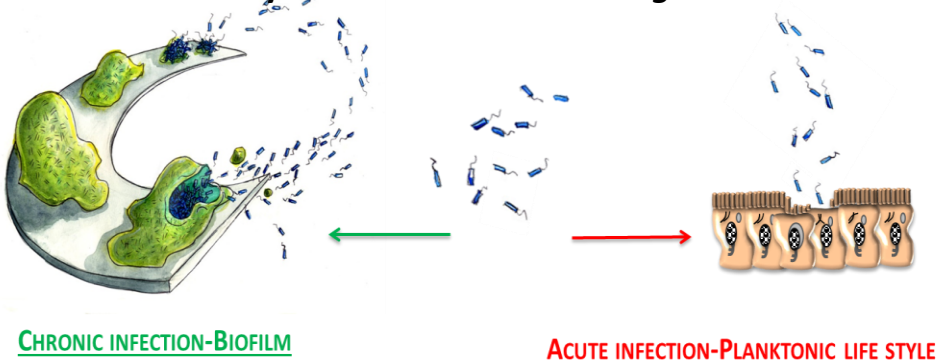


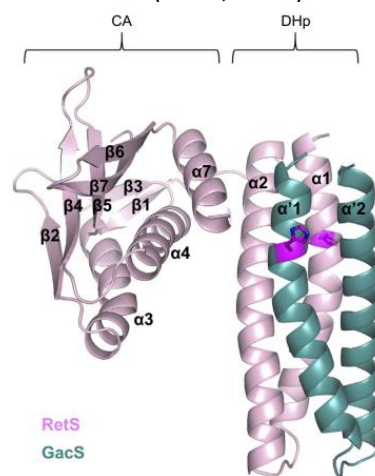
STRUCTURAL AND FUNCTIONAL CHARACTERIZATION OF THE DYNAMIC INTERACTIONS BETWEEN TWO MAJOR MEMBRANE HISTIDINE KINASES CONTROLLING *PSEUDOMONAS AERUGINOSA* INFECTION MODES

Infectious life style of *Pseudomonas aeruginosa*

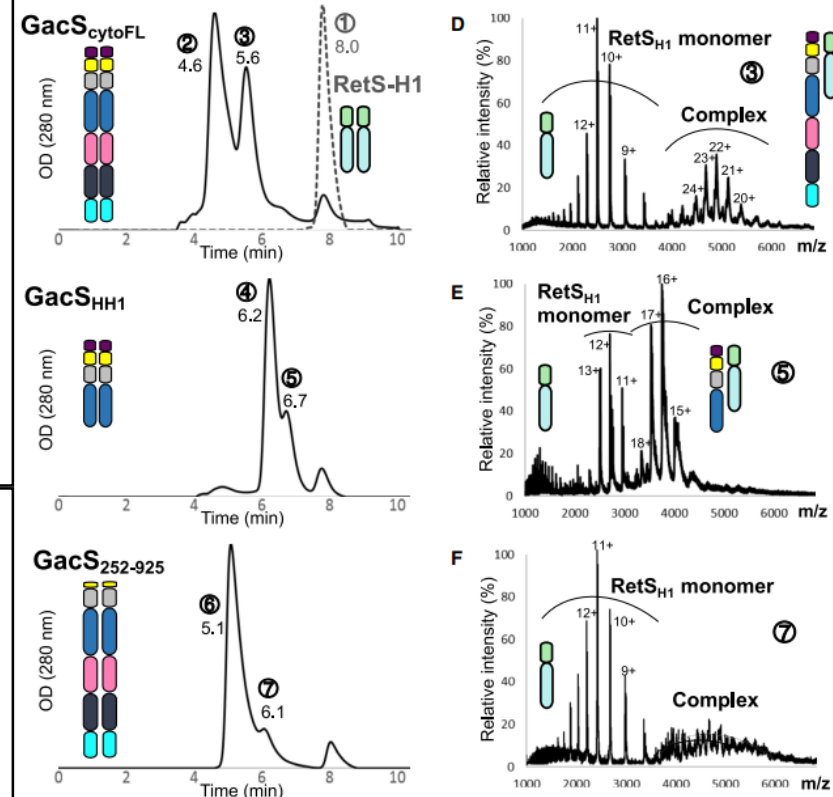


Courtesy of Pflumm 2011, (Anna Lensch artwork)

Crystal structure of a RetS_{DHP}/GacS_{DHP} complex (Kaler, 2021)



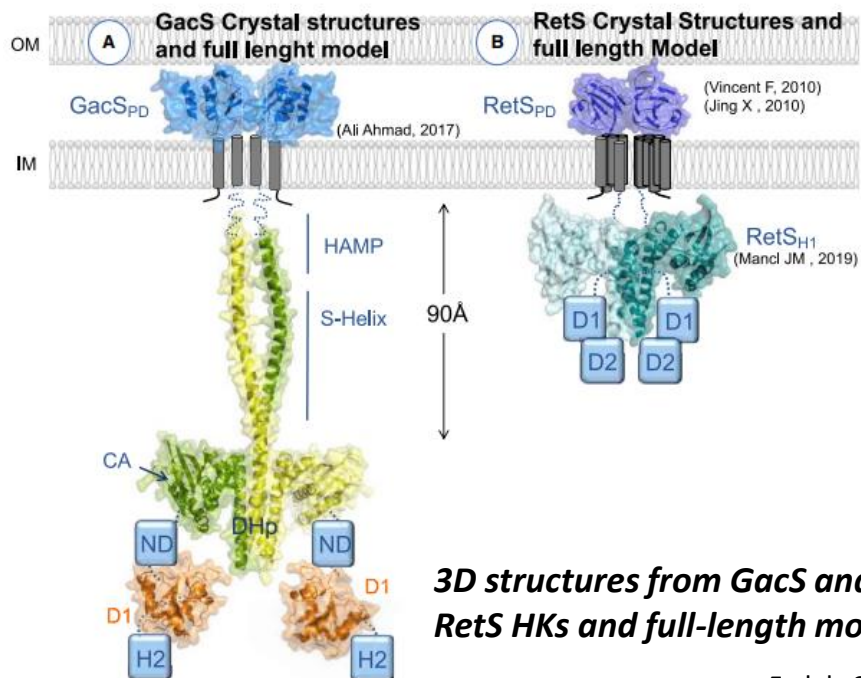
Online SEC-native MS analysis of RetSH1 and different GacS constructs (Fadel, 2022)



How RetS_{DHP} can reach GacS_{DHP}?

OBJECTIVE

- Elucidate the interaction interface of the cytoplasmic domains of GacS and RetS, decipher the amino acid residues accountable for the binding interface.
- Investigate potential nanobodies capable of binding to various GacS cytoplasmic domains to solve the structure of full cytoplasmic region of GacS



3D structures from GacS and RetS HKs and full-length models

Fadel, 2022)