

Supplementary Material

The *Staphylococcus aureus* Two-Component System AgrAC Displays Four Distinct Genomic Arrangements That Delineate Genomic Virulence Factor Signatures

Kumari Sonal Choudhary¹, Nathan Mih^{1,2}, Jonathan Monk¹, Erol Kavvas¹, James T. Yurkovich^{1,2}, George Sakoulas³, Bernhard O. Palsson^{1,2,3*}

¹Systems Biology Research Group, Department of Bioengineering, University of California, San Diego, CA

²Bioinformatics and Systems Biology Program, University of California, San Diego

³Department of Pediatrics, University of California, San Diego

***Correspondence:**

Bernhard O. Palsson

palsson@eng.ucsd.edu

SUPPLEMENTARY FIGURE

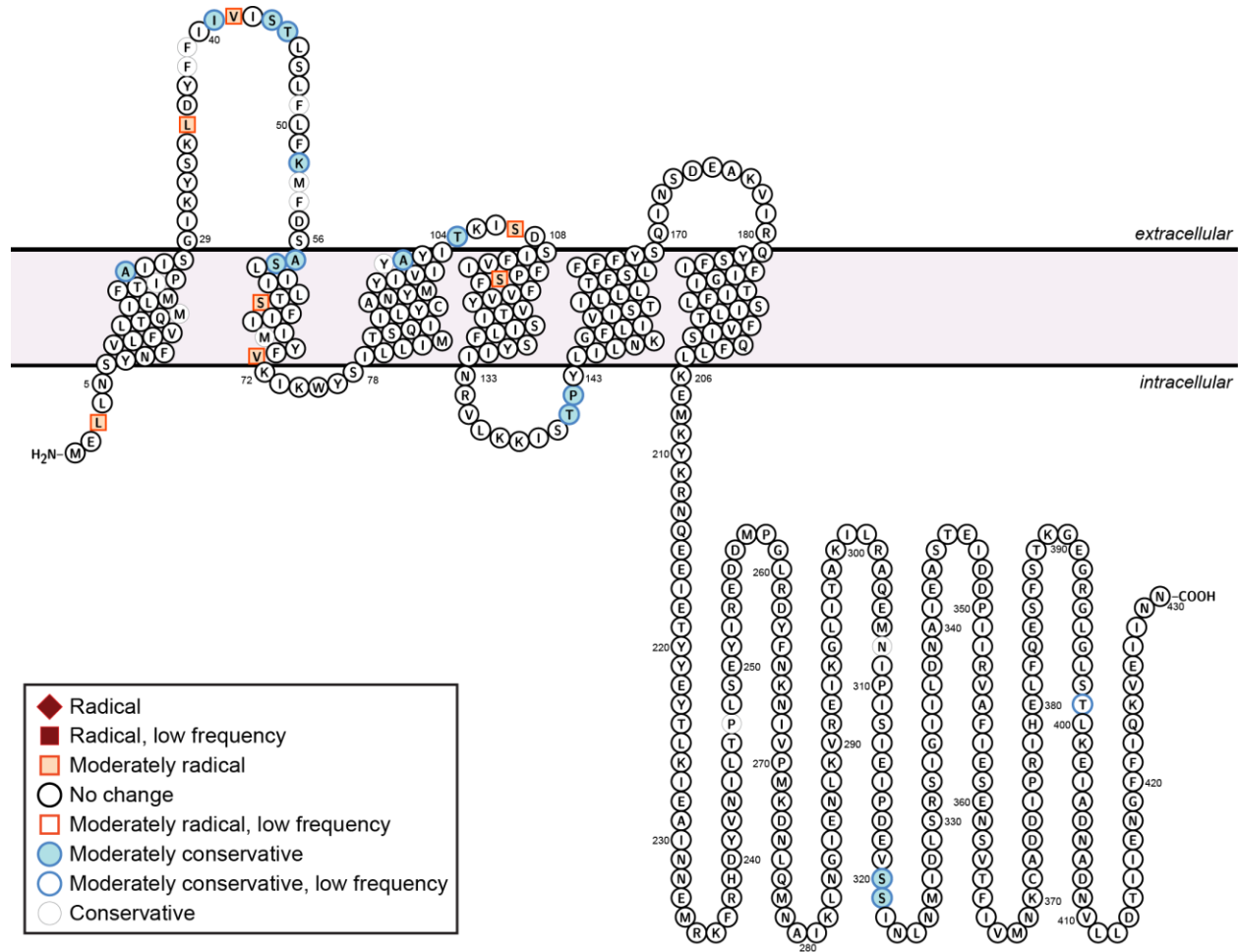


Figure 7: Comparison of AgrC in type IV strains with AgrC-I reference sequence. The predicted topology of AgrC-I reference sequence from CCTOP with highlighted amino acid residues that tend to diverge in type IV strains. The color coding is per biochemical and biophysical property of the amino acid residue mutated. Radical, moderate and conservative are the nomenclature given in the order of amino acid divergence with radical being vast difference between amino acid properties and could change the properties of the protein. Conservative change depicts the amino acid substitution which can be tolerated by the protein. Low frequency: amino acid variations that occurred only in very few strains.