Supplementary Material

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

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SUPPLEMENTARY FIGURE

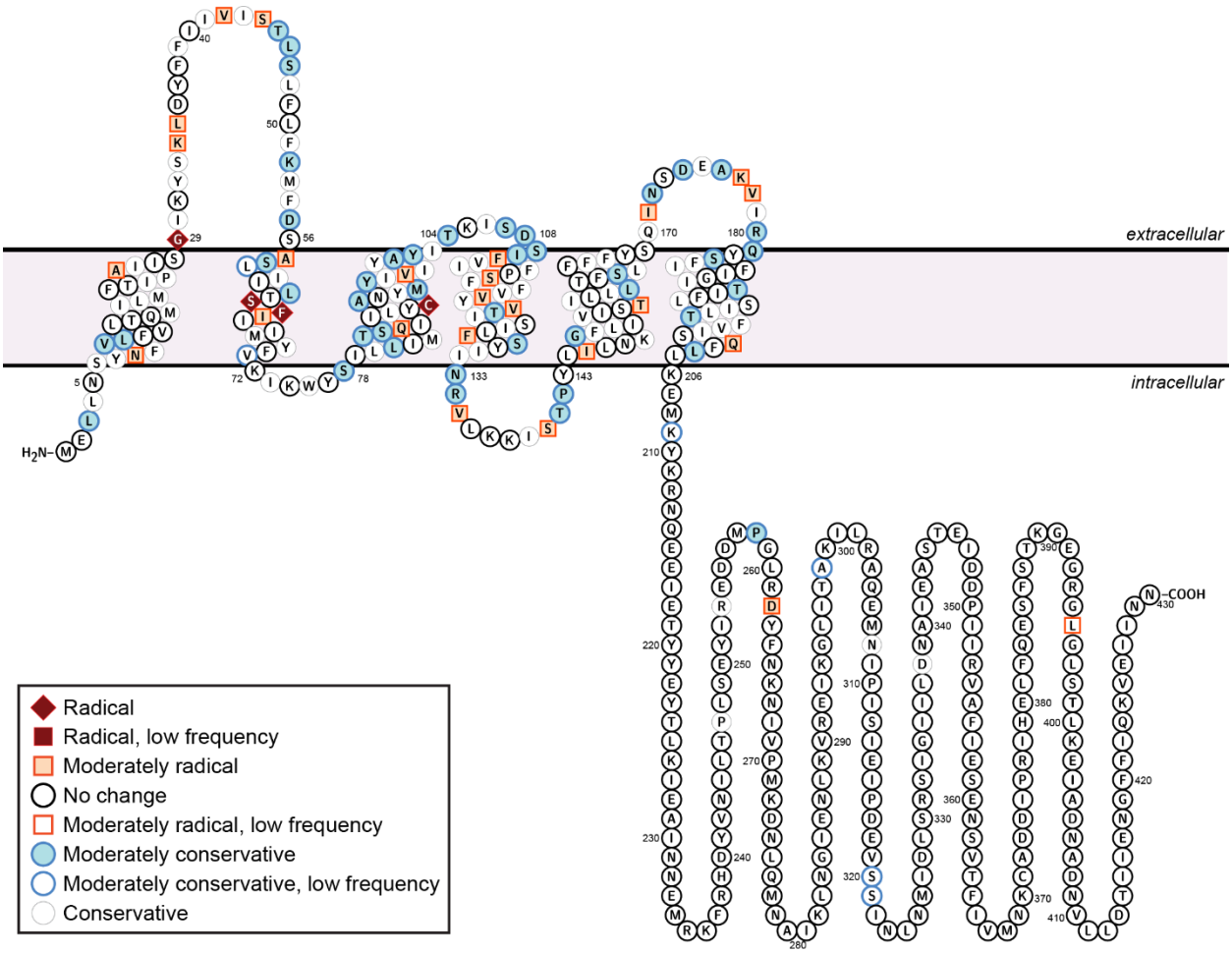


Figure 6: Comparison of AgrC in type III strains with AgrC-I reference sequence. The predicted topology of AgrC-I reference sequence from CCTOP with highlighted amino acid residues that tend to diverge in type III strains. The color coding is per biochemical and biophysical property of the amino acid 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.