

- Full and Core Window, Add to ends: These are used to calculate the putative and certain transmembrane segments. If a short window is used, one should add some extra residues to ensure that the program sets aside enough residues to span the membrane. A transmembrane segment seems likely to have 21 amino acids in length
- Upper cutoff: The cutoff for predicting certain transmembrane segments.
- Lower cutoff: The cutoff for predicting putative transmembrane segments.
- Charge-pair energy: The weight of a charge-pair. Reasonable values would be 0.0 (maximal weight) to 5.0 (minimal weight) when using GES scale. Only accessible when calculating for eukaryotic proteins
- Critical length: It defines the cutoff to apply or not the Positive-Inside rule. In the case of eukaryotic proteins, if this rule is not applied, the Compositional Distance method is used.

Default values are provided for all parameters.