

Supplementary Materials

Comparison of *Candida albicans* Fatty Acid Amide Hydrolase Structure with Homologous Amidase Signature Family Enzymes

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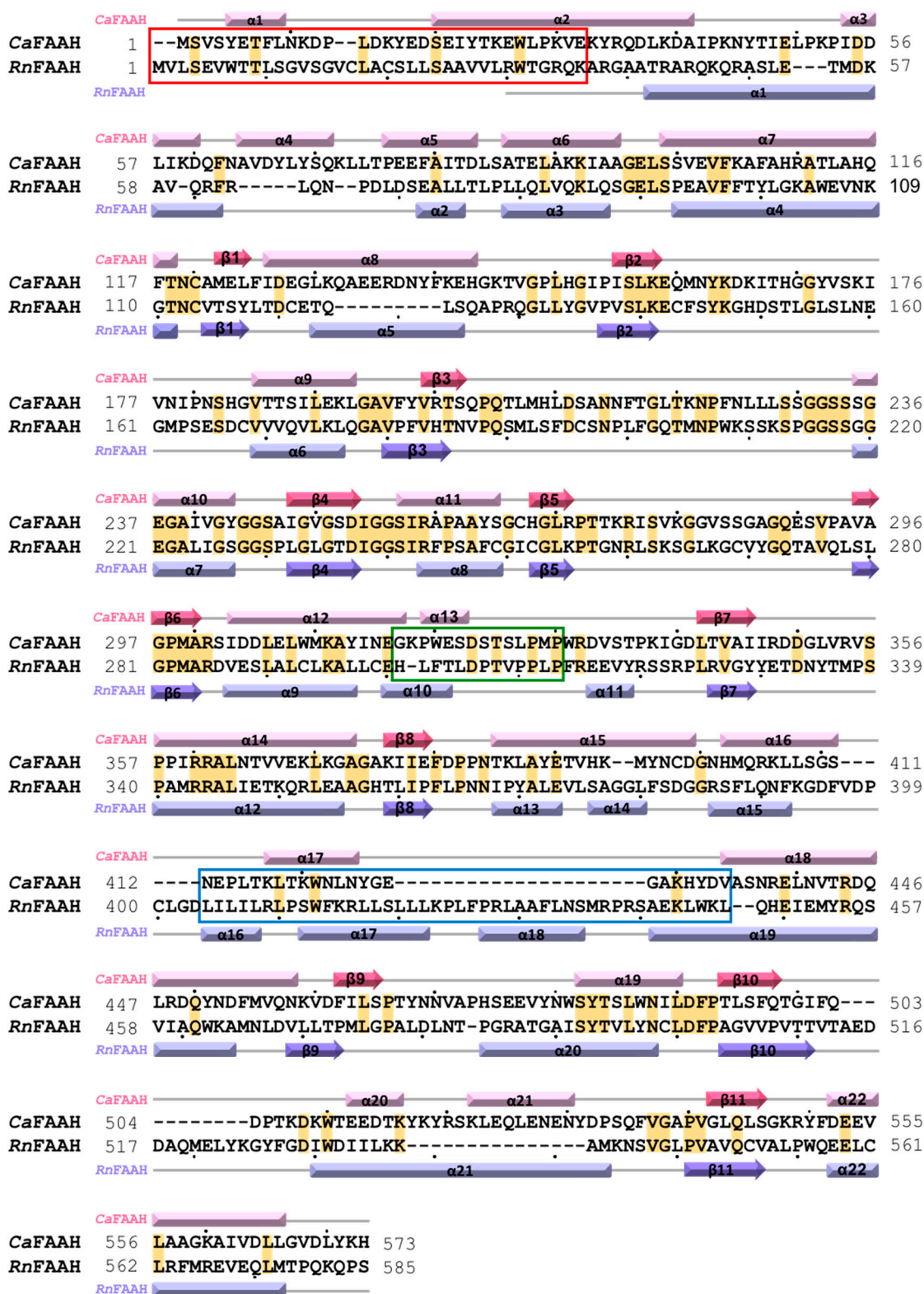
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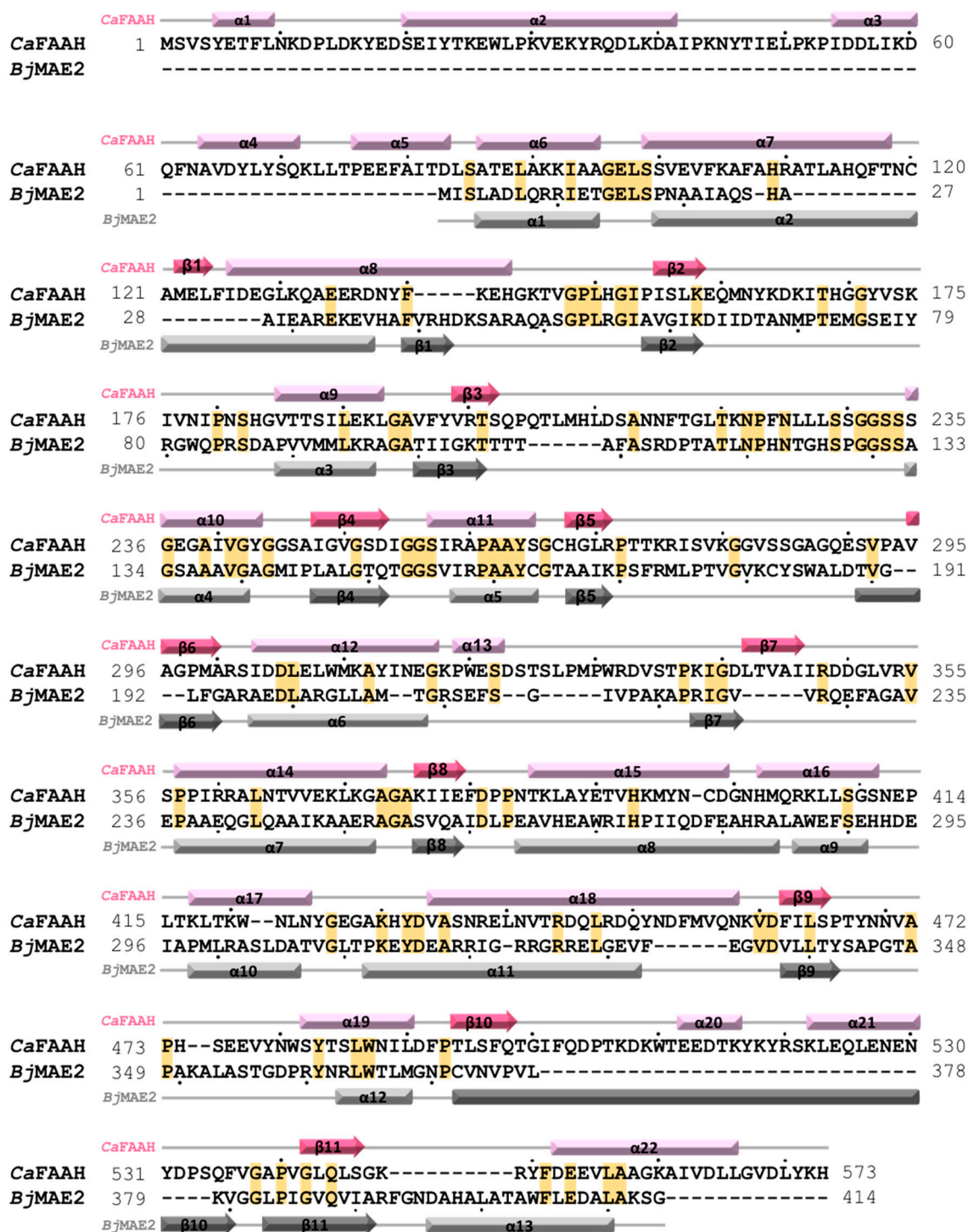
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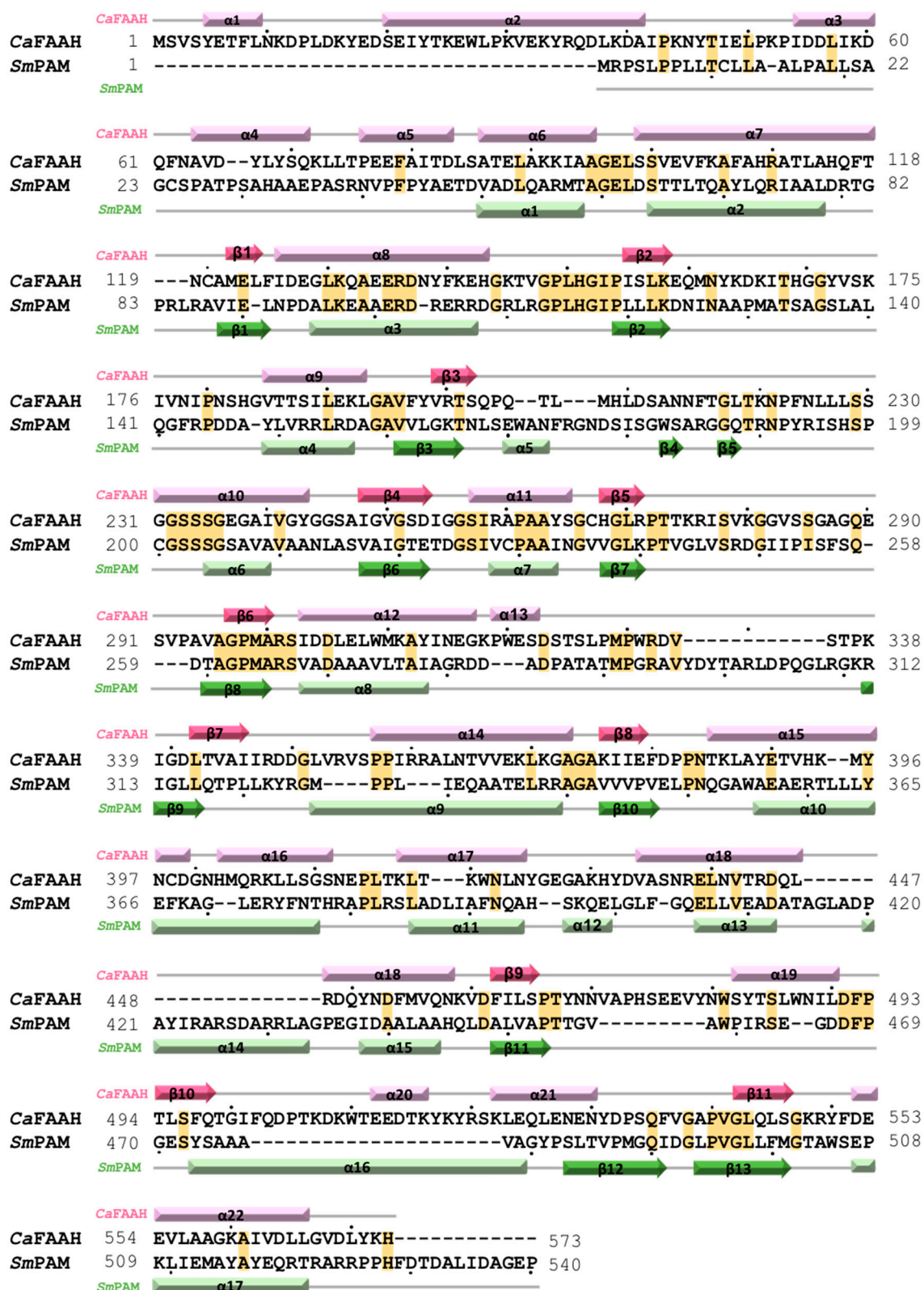
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Supplemental Figure S1. Structure-based sequence alignment of CaFAAH with RnFAAH. Identical residues between CaFAAH and RnFAAH are highlighted in yellow. The red box indicates the monotopic transmembrane domain of RnFAAH. The green box shows the oligomerization domain and the blue box represents the hydrophobic cap in RnFAAH. The secondary structure elements in both FAAHs are shown in the vicinity of their sequences. Black dots, either above or below the CaFAAH and RnFAAH sequences, indicate every tenth residue.



Supplemental Figure S2. Structure-based sequence alignment of *CaFAAH* with *BjMAE2*. Identical residues between *CaFAAH* and *BjMAE2* are highlighted in yellow. The secondary structure elements in *CaFAAH* and *BjMAE2* are shown in the vicinity of the sequences. Black dots, either above or below the sequence, indicate every tenth residue in *CaFAAH* and *BjMAE2*.



Supplemental Figure S3. Structure-based sequence alignment of *CaFAAH* with *SmPAM*. Identical residues within *CaFAAH* and *SmPAM* are highlighted in yellow. The secondary structure elements in *CaFAAH* and *SmPAM* are shown in the vicinity of the sequences. Black dots, either above or below the sequences, indicate every tenth residue in *CaFAAH* and *SmPAM*.