Supplementary Materials

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

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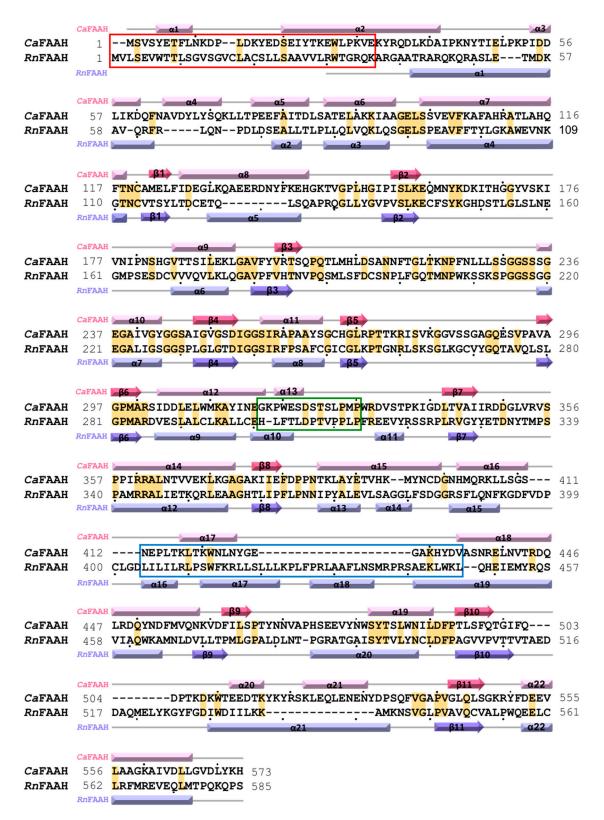
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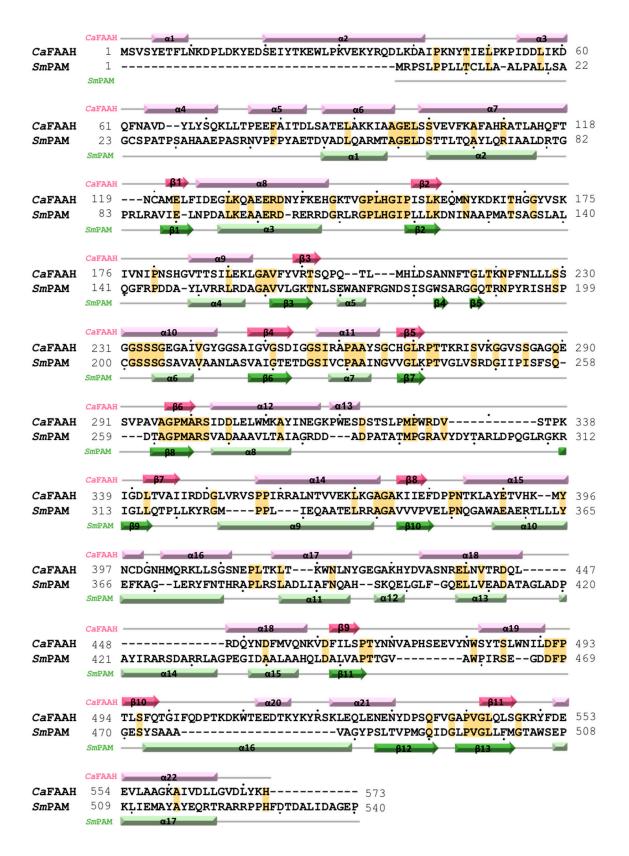
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Supplemental Figure S1. Structure-based sequence alignment of CaFAAH with RnFAAH. Identical residues between CaFAAH and RnFAAH are highlighted in yellow. The red box indicates the monotopic transmembrane domain of RnFAAH. The green box shows the oligomerization 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.

СаҒААН ВјМАЕ2	CaFAAH al al az	60
СаҒААН ВјМАЕ2	CaFAAH α4 α5 α6 α7 61 QFNAVDYLYSQKLLTPEEFAITDLSATELAKKIAAGELSSVEVFKAFAHRATLAHQFTNC 1 MISLADLQRRIETGELSPNAAIAQS-HA BjMAE2 α1 α2	120 27
СаҒААН ВјМАЕ2	CaFAAH β1 α8 β2 121 AMELFIDEGİKQAEERDNYFKEHGKTVGPİHGI PISLKEQMNYKDKITHGGYVSK 28 AIEAREKEVHAFVRHDKSARAQASGPLRGIAVGIKDIIDTANMPTEMGSEIY BjMAE2 β1	175 79
СаҒААН ВјМАЕ2		
СаҒААН ВјМАЕ2		295 191
СаҒААН ВјМАЕ2	CaFAAH β6 α12 α13 β7 296 AGPMARSIDDLELWMKAYINEGKPWESDSTSLPMPWRDVSTPKIGDLTVAIIRDDGLVRV 192 LFGARAEDLARGLLAMTGRSEFSGIVPAKAPRIGVVRQEFAGAV BjMAE2 β6 α6	
СаҒААН ВјМАЕ2	CaFAAH α14 β8 α15 α16 356 SPPIRRALNTVVEKLKGAGAKIIEFDPPNTKLAYETVHKMYN-CDGNHMQRKLLSGSNEP 236 EPAAEQGLQAAIKAAERAGASVQAIDLPEAVHEAWRIHPIIQDFEAHRALAWEFSEHHDE BjMAE2 α7 β8 α8 α9	
СаҒААН ВјМАЕ2	CaFAAH α17 α18 β9 415 LTKLTKWNLNYGEGAKHYDVASNRELNVTRDQLRDQYNDFMVQNKVDFILSPTYNNVA 296 IAPMLRASLDATVGLTPKEYDEARRIG-RRGRRELGEVFEGVDVLLTYSAPGTA BjMAE2 α10	
СаҒААН ВјМАЕ2	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	
СаҒААН ВјМАЕ2	CaFAAH β11 α22 531 YDPSQFVGAPVGLQLSGKRYFDEEVLAAGKAIVDLLGVDLYKH 573 379 KVGGLPIGVQVIARFGNDAHALATAWFLEDALAKSG 414 BjMAE2 β10 β11 α13	

Supplemental Figure S2. Structure-based sequence alignment of *Ca*FAAH with *Bj*MAE2. Identical residues between *Ca*FAAH and *Bj*MAE2 are highlighted in yellow. The secondary structure elements in *Ca*FAAH and *Bj*MAE2 are shown in the vicinity of the sequences. Black dots, either above or below the sequence, indicate every tenth residue in *Ca*FAAH and *Bj*MAE2.



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