

Differential effects of Oleuropein and Hydroxytyrosol on Aggregation and Stability of CFTR NBD1-ΔF508 Domain

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Supplementary Materials

Table S1. Ligand-mNBD1-ΔF508 docking scores of BIA and Oleuropein full fitness and ΔG values for most stable docked molecules shown in Figure 3.

Name	Full Fitness kcal/mol	ΔG kcal/mol
BIA	-1630.1	-6.37
Oleuropein	-1585.0	-8.36
Hydroxytyrosol	-1626.3	-6.25

Table S2. ANOVA analysis of DSF experiments.

ANOVA Analysis			
<i>mNBD1-ΔF508 vs Name</i>	<i>F</i>	<i>P-value</i>	<i>F crit</i>
mNBD1-ΔF508 + 1mM ATP	43.40	0.00275	7.709
mNBD1-ΔF508 + 5mM ATP	302.88	0.00006	7.709
mNBD1-ΔF508 + 1mM BIA	10.86	0.03006	7.709
mNBD1-ΔF508 + 1.5mM ATP + 1mM BIA	194.59	0.00015	7.709
mNBD1-ΔF508 + 100μM Oleuropein	0.29	0.61671	7.709
mNBD1-ΔF508 + 100μM Hydroxy-Tyrosol	0.07	0.79986	7.709
mNBD1-ΔF508 + 500μM Hydroxy-Tyrosol	0.34	0.59343	7.709
mNBD1-ΔF508 + 1mM Hydroxy-Tyrosol	0.85	0.40977	7.709
mNBD1-ΔF508 + 1mM Hydroxy-Tyrosol + 1mM BIA	13.72	0.02076	7.709

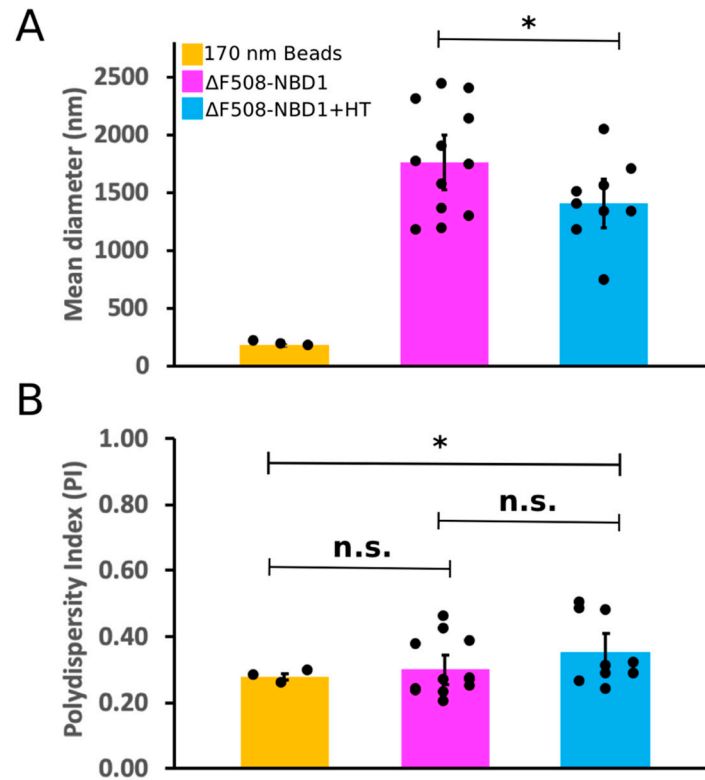


Figure S1. NBD1-ΔF508 aggregates incubated with Hydroxytyrosol are smaller in diameter and mostly monodispersed. **A)** Mean diameter of NBD1-ΔF508 aggregates measured by dynamic light scattering in the absence (n=4, 12 replicates) or presence of 100 μM Hydroxytyrosol (n=3, 9 replicates), **p*-value = 0.032. Aggregate diameter in absence and presence of Hydroxytyrosol was significantly larger compared to 170 nm beads (3 replicates), *p*-value = 7.17E-08 and *p*-value = 3.21E-06, respectively. **B)** mean polydispersity measurement for control (n=4, 12 replicates) and Hydroxytyrosol incubated (n=3, 9 replicates) NBD1-ΔF508 aggregates compared to 170 nm beads, **p*-value = 0.0387 and n.s. = not significant (*p*-value > 0.05). Data plotted as mean ± SEM. Significant differences were analyzed by unpaired Student's *t*-test.

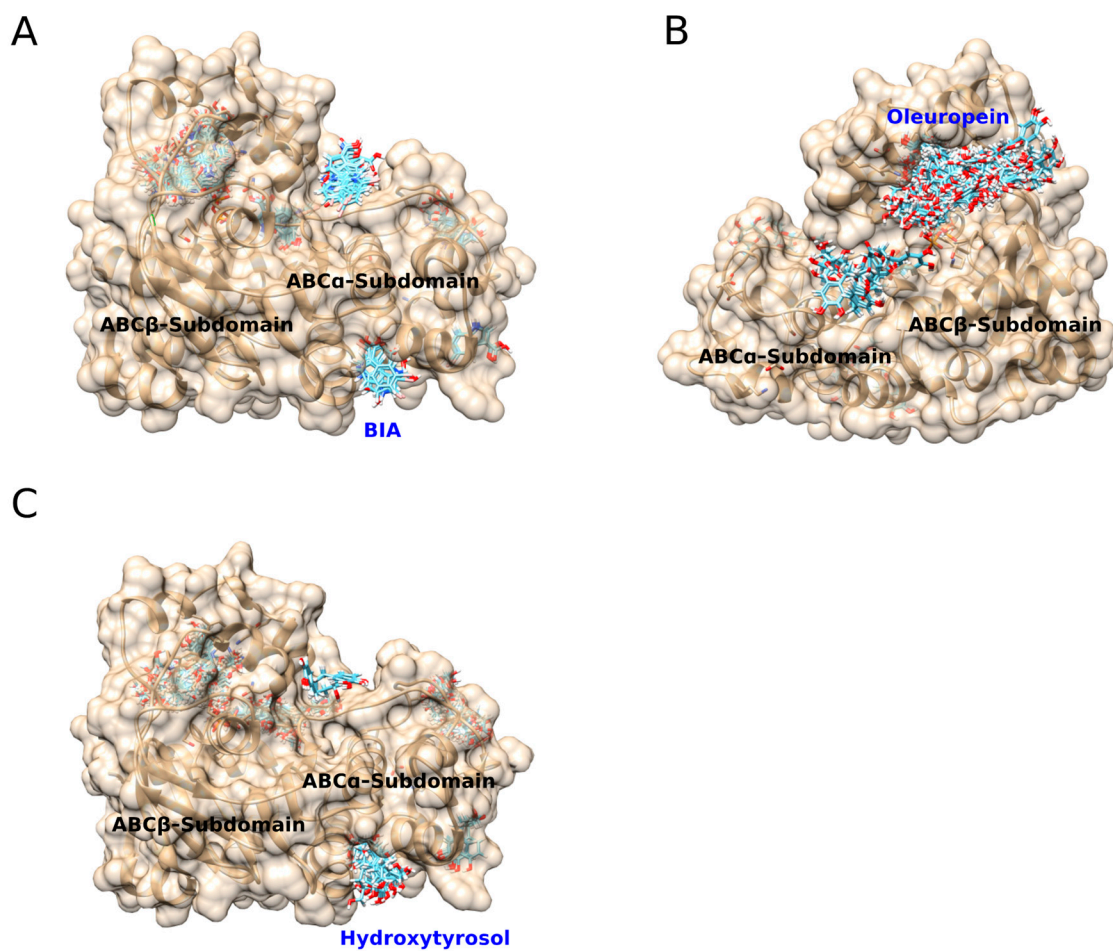


Figure S2. Full SwissDock predicted binding modes for BIA, Oleuropein, and Hydroxytyrosol to mNBD1- Δ F508. Note the majority of predicted binding modes for BIA and Hydroxytyrosol overlap. The majority of Oleuropein binding modes are in the ATP binding cleft.

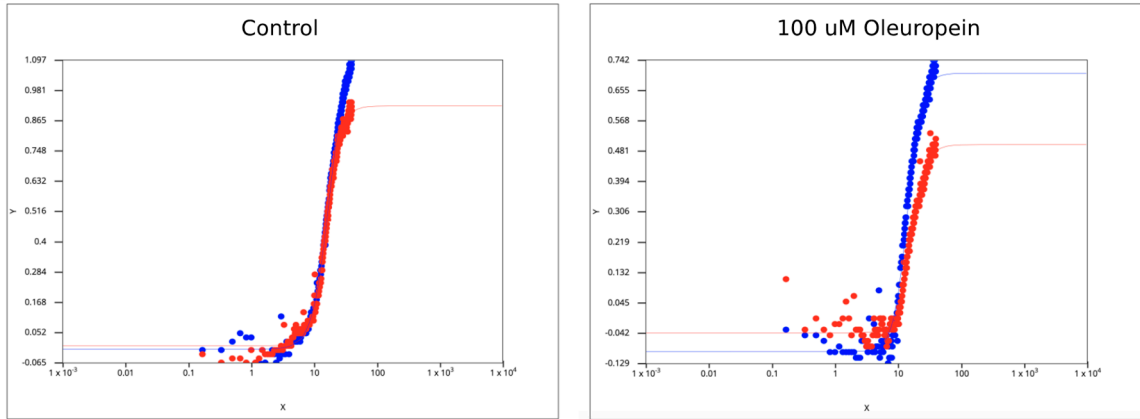
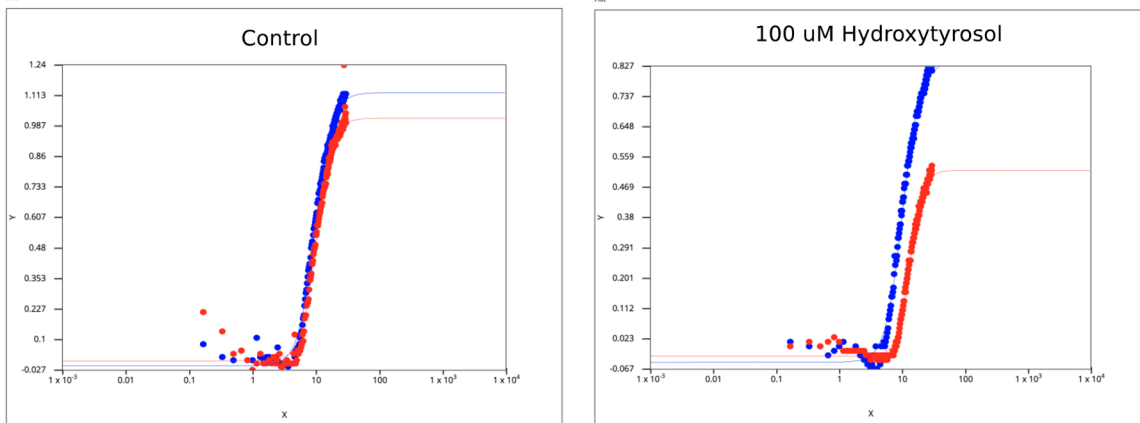
A**B**

Figure S3. Curve fitting of mNBD1-ΔF508 aggregation data from Figure 1C & D. **A)** Representative results for control (left panel) and 100 μ M Oleuropein (right panel) data fitted with logistics equation. **B)** Representative results for control (left panel) and 100 μ M Hydroxytyrosol (right panel) data fitted with four parameter logistics equation.