Identification of Benzoxazin-3-one Derivatives as Novel, Potent, and Selective Non-steroidal Mineralocorticoid Receptor Antagonists

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Supporting Information

Table S1. Data collection and refinement statistics.

Crystal	MR C808S/S801L-spironolactone	MR C808S/S810L/A976V-compound **1d**
Data collection		
Space group	$C222_1$	$P3_2$
Unit cell dimensions		
a, b, c (Å)	91.5, 171.5, 42.4	62.6, 62.6, 75.5
α, β, γ (°)	90, 90, 90	90, 90, 120
Resolution range (Å)	40–2.12	40–1.35
Observed reflections	116007	264961
Unique reflections	19366	71863
Redundancy	6.0 (3.9)	3.7 (2.5)
Completeness (%)	98.6 (90.3)	98.6 (88.4)
I/σ	26.2 (2.4)	22.2 (2.2)
R_{sym} [a]	0.059 (0.515)	0.045 (0.410)
Molecules in ASU	1	1
Refinement		
Resolution (Å)	40–2.11 (2.16-2.11)	40–1.35 (1.38-1.35)
Reflections	18299	68224
R_{cryst} [b]	0.196 (0.295)	0.162 (0.311)
R_{free} [b]	0.240 (0.358)	0.184 (0.319)
Number of atoms		
Protein	2034	2134
Ligand/Ion	29	61
Water	45	355
Average B value ($Å^2$)	34.7	15.2
Rms deviation from ideal geometry		
bond lengths (Å)	0.010	0.008
bond angles (°)	1.22	1.30
Ramachandran plot		
Preferred regions	98.4	98.0
Allowed regions	1.6	2.0

[a] $R_{sym} = \Sigma h \Sigma j \, |<I(h)> - I(h)j| \, / \, \Sigma h \Sigma j \, <I(h)>$, where $<I(h)>$ is the mean intensity of symmetry-related reflections. [b] $R_{cryst} = \Sigma \, ||F_{obs}| - |F_{calc}|| \, / \, \Sigma \, |F_{obs}|$. R_{free} was calculated for randomly chosen 5% of reflections excluded from refinement. Values in parentheses are for the highest resolution shell.

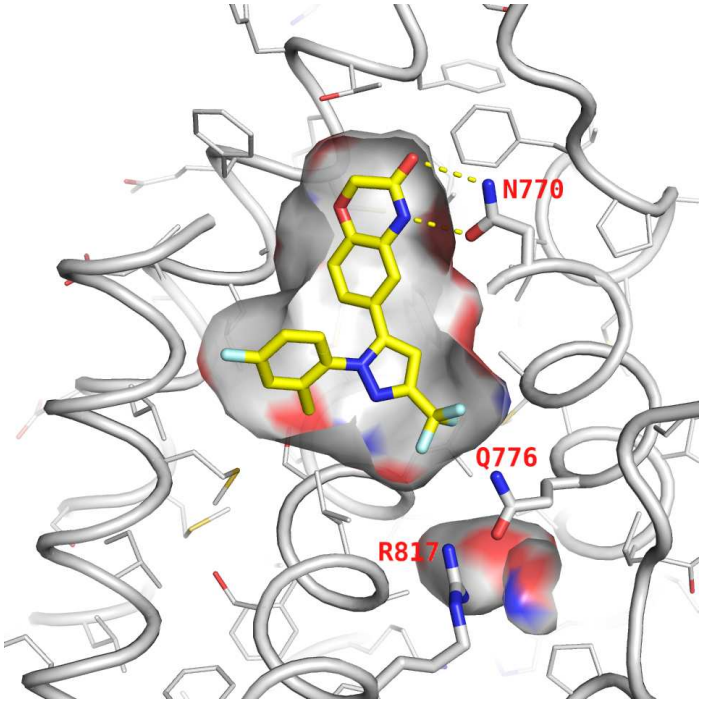

Figure S1. Docking model of compound **14n**. The compound **14n** was docked to the X-ray crystal structure of MR/compound **1d** complex. The hydrogen bonds are shown as yellow dotted lines.