

SUPPORTING INFORMATION

Synthesis and Biological Evaluation of a New Series of 1,2,4-triazolo[1,5-*a*]-1,3,5-triazine as Human A_{2A} Adenosine Receptor Antagonists with Improved Water Solubility

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Table 1. Elemental analyses of all synthesized compounds.

compd	formula	MW	Calcd			Found		
			% C	%H	%N	%C	%H	%N
8	C ₁₂ H ₁₃ N ₇ O	271.28	53.13	4.83	36.14	52.78	4.77	35.99
7	C ₁₇ H ₂₂ N ₈ O ₃	386.41	52.84	5.74	29.00	52.91	5.72	29.04
11	C ₂₁ H ₂₈ N ₈ O ₃	440.50	57.26	6.41	25.44	57.45	6.46	25.71
10	C ₁₅ H ₂₀ N ₈ O ₃	360.37	49.99	5.59	31.09	50.09	5.66	30.89
12	C ₁₆ H ₂₂ N ₈ O ₃	374.40	51.33	5.92	29.93	51.15	5.78	29.78
13	C ₁₈ H ₂₆ N ₈ O ₃	402.45	52.72	6.51	27.84	52.88	6.53	28.00
14	C ₁₉ H ₂₈ N ₈ O ₅	448.48	50.88	6.29	24.99	50.66	6.09	24.76
37	C ₂₂ H ₃₃ N ₉ O ₅	503.55	52.47	6.61	25.03	52.65	6.65	25.13
38	C ₁₆ H ₁₉ N ₉ O ₅ F ₆	531.31	36.17	3.60	23.72	36.25	3.54	23.81
9	C ₁₄ H ₁₅ N ₈ O ₃ F ₃	432.31	38.90	3.50	25.92	39.02	3.53	25.90
31	C ₁₈ H ₂₃ N ₈ O ₃ F ₃	456.42	47.37	5.08	24.55	47.51	5.12	24.62
30	C ₁₂ H ₁₃ N ₈ O ₃ F ₃	374.28	38.51	3.50	29.94	38.38	3.44	29.89
32	C ₁₃ H ₁₅ N ₈ O ₃ F ₃	388.31	40.21	3.89	28.86	40.09	3.70	28.73
33	C ₁₅ H ₁₉ N ₈ O ₃ F ₃	416.36	43.27	4.60	26.91	43.11	4.63	26.87
20	C ₁₅ H ₂₂ N ₈ O ₅ F ₃	450.37	40.00	4.70	24.88	39.78	4.55	24.57
15	C ₁₉ H ₂₀ N ₈ O	376.42	60.63	5.36	29.77	60.74	5.37	29.83
16	C ₁₉ H ₁₉ N ₈ OCl	410.86	55.54	4.66	27.27	55.31	4.72	27.40
17	C ₁₉ H ₁₉ N ₈ OF	394.41	57.86	4.86	28.41	57.55	4.83	28.65
18	C ₁₉ H ₁₉ N ₈ OCl	410.86	55.54	4.66	27.27	55.28	4.66	27.18
19	C ₁₉ H ₁₉ N ₈ OBr	455.31	50.12	4.21	24.61	49.97	4.14	24.48
20	C ₁₇ H ₂₂ N ₈ O ₂	370.41	55.12	5.99	30.25	55.20	6.03	30.31

Figure 1: Hypothetical binding mode of compound **28** obtained after docking simulations inside the hA_{2A} AR binding site. The pose is viewed from the membrane side facing TM6, TM7 and TM1. The view of TM7 is partially omitted. Side chains of some amino acids important for ligand recognition and H-bonding interactions are highlighted. Hydrogen atoms are not displayed.

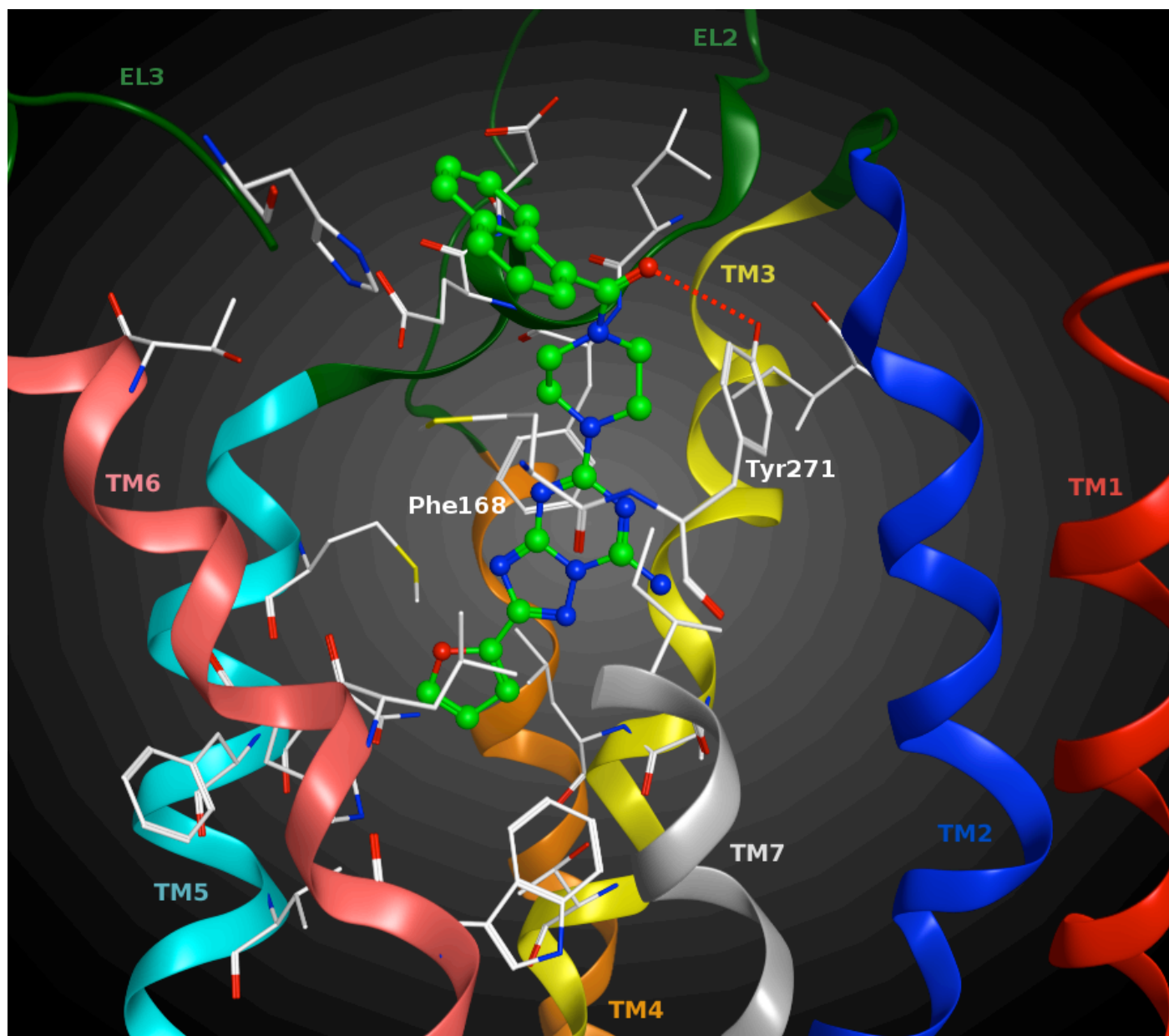


Figure 2: Hypothetical binding mode of compound **37** obtained after docking simulations inside the hA_{2A} AR binding site. The pose is viewed from the membrane side facing TM6, TM7 and TM1. The view of TM7 is partially omitted. Side chains of some amino acids important for ligand recognition and H-bonding interactions are highlighted. Hydrogen atoms are not displayed.

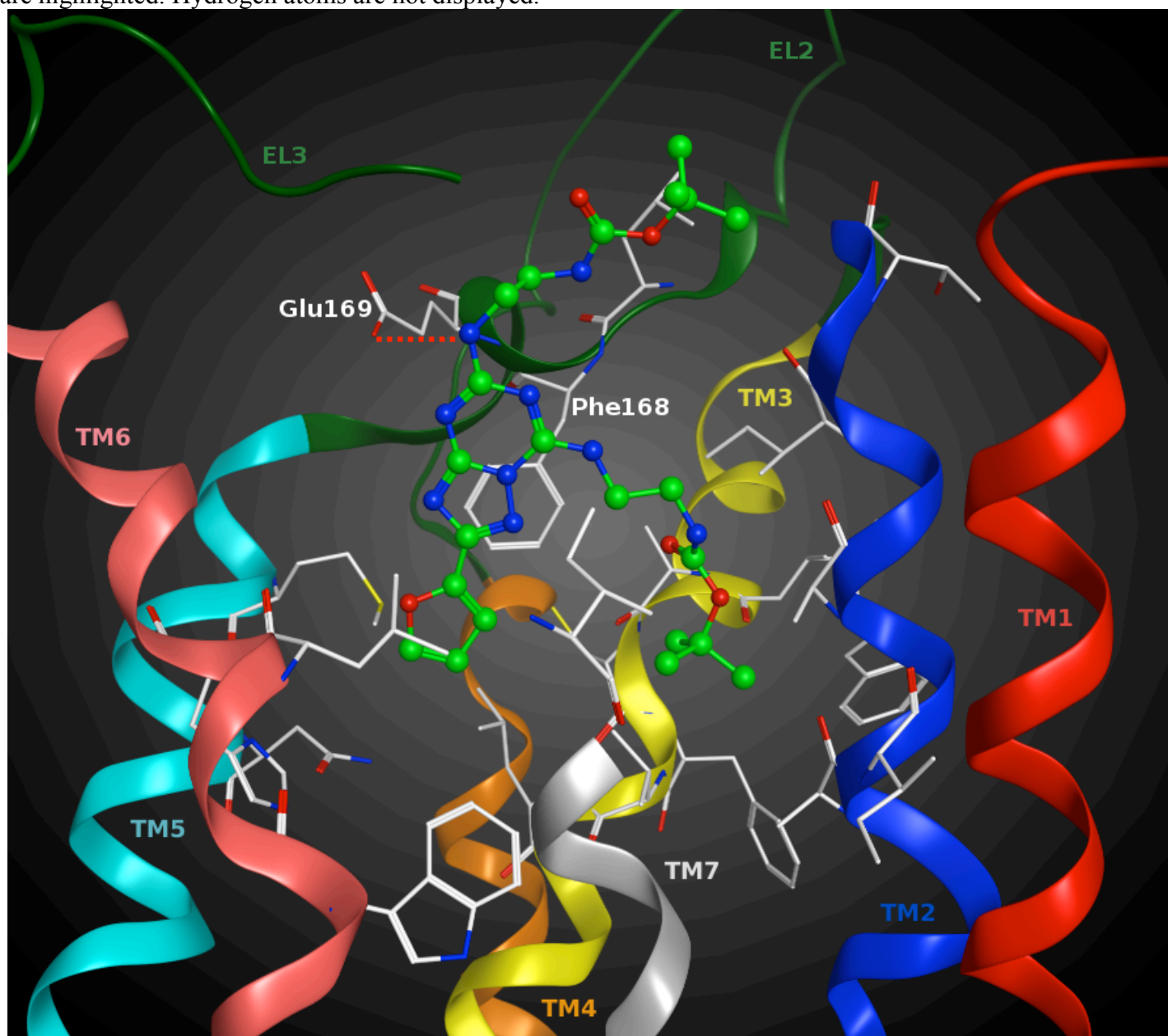


Figure 3: Hypothetical binding mode of compound **43** obtained after docking simulations inside the hA_{2A} AR binding site. The pose is viewed from the membrane side facing TM6, TM7 and TM1. The view of TM7 is partially omitted. Side chains of some amino acids important for ligand recognition and H-bonding interactions are highlighted. Hydrogen atoms are not displayed.

