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Title Key role of the TM2-TM3 loop in calcium potentiation of the α9α10 nicotinic acetylcholine receptor

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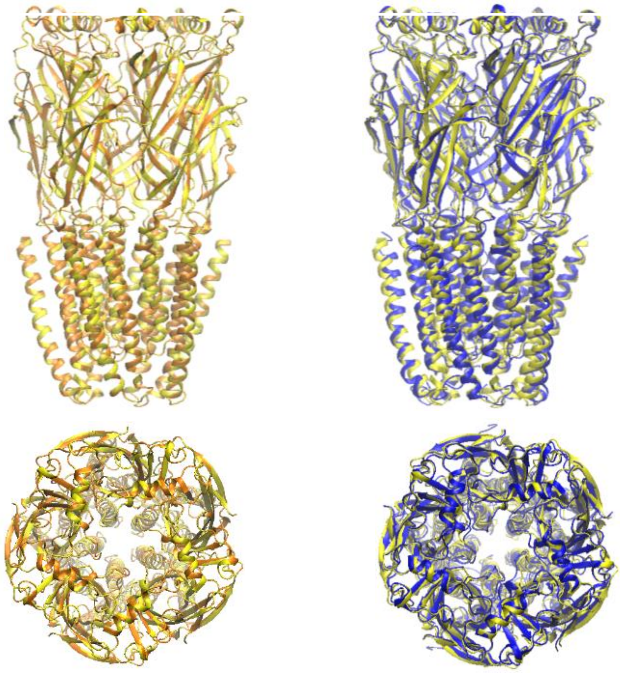
a

Receptors	RMSD (Å) α9	α9α10	a9α10*
α9	0.03	1.07	1.30
α9α10		1.10	0.98
a9α10*			0.61

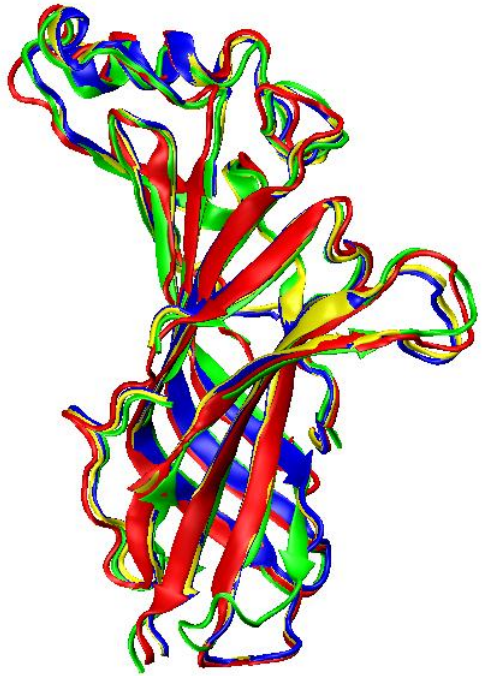
a9α10* = a9α10$^{\alpha 9TM2TM3loop}$

α9 (r1) vs α9 (r2) **α9 (r1) vs α9α10 (r2)**



b

Receptors	RMSD (Å) α9	α10	4uy2	α7 (D)
α9		0.6	1.9	1.3
α10			2.0	1.4
4uy2				2.0
α7 (D)				

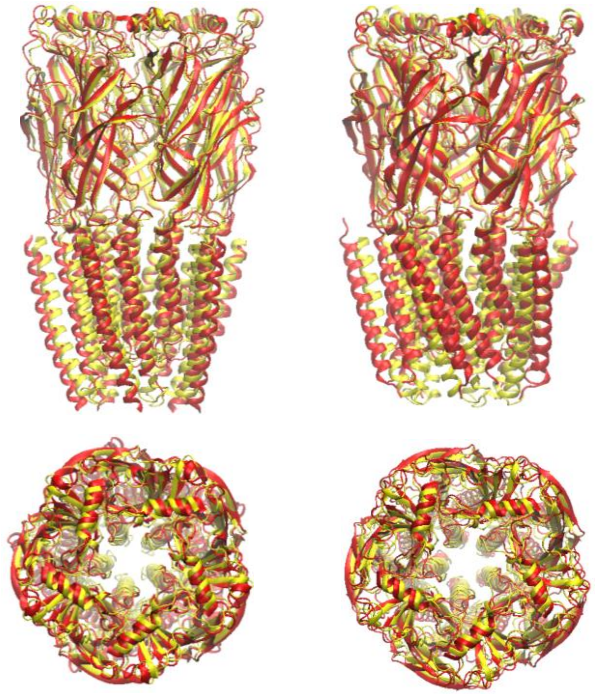


c

α7 State	RMSD (Å) α9	α9α10	α9α10*
D	2.2	2.6	2.7
R	2.9	3.2	3.2
A	3.6	3.7	3.7

a9α10* = a9α10$^{\alpha 9TM2TM3loop}$

α9 (r1) vs α7-D **α9 (r1) vs α7-A**



Structural comparison of α9, α9α10, and α9α10$^{\alpha 9TM2TM3loop}$ AlphaFold models with reference nAChR structures. Panel a: Comparison between the receptor models used in this study. The table data correspond to the average RMSD after whole structure fitting of the model replicas (r1 and r2) generated. Panel b: Comparison of the extracellular domain (ECD) of the α9 (yellow) and α10 (blue) chains of the AlphaFold models with the ECD of the human α9 CRX structure (PDB ID: 4UY2, green) and the cryo-EM structure of human α7 in the desensitized conformation (red). Panel c: Comparison between the α9 and α9α10 structural models and the cryo-EM structures of human α7 in the desensitized (D), resting (R), and active (A) conformations (pdb Ids= 7koq, 7koo and 7kox, respectively). The superposition of selected structures from the comparisons in Panels A, B, and C are presented.