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Q9JLB5 ACH10 RAT 1 MGTRSHYLDLGFLLLLFLPA---ECLGAEGRLAHKLFRDLFANYTSALRPVADTDQTLNV 57 57 58 Q9GZZ6 ACH10 HUMAN 1 P43144 ACHA9 RAT 1 Q9UGM1 ACHA9\_HUMAN 1 58 TLEVTLSQIIDMDERNQVLTLYLWIRQEWTDAYLHWDPKAYGDLDAIRIPSRLVWRPDIV Q9JLB5 ACH10\_RAT 58 Q9GZZ6 ACH10 HUMAN 58 117 TLEVTLSQIIDMDERNQVLTLYLWIRQEWTDAYLRWDPNAYGGLDAIRIPSSLVWRPDIV 117 P43144 ACHA9 RAT 59 TLQVTLSQIKDMDERNQILTAYLWIRQTWHDAYLTWDRDQYDRLDSIRIPSDLVWRPDIV 118 Q9UGM1 ACHA9 HUMAN 59 118 LYNKADTQPPASASTNVVVRHDGAVRWDAPAITRSSCRVDVSAFPFDAQRCGLTFGSWTH Q9JLB5 ACH10 RAT 177 118 Q9GZZ6 ACH10\_HUMAN 118 P43144 ACHA9\_RAT 119 LYNKADAQPPGSASTNVVLRHDGAVRWDAPAITRSSCRVDVAAFPFDAQHCGLTFGSWTH LYNKADDESSEPVNTNVVLRYDGLITWDSPAITKSSCVVDVTYFPFDSOOCNLTFGSWTY 177 178 Q9UGM1 ACHA9 HUMAN 119 LYNKADDESSEPVNTNVVLRYDGLITWDAPAITKSSCVVDVTYFPFDNQQCNLTFGSWTY 178 Q9JLB5 ACH10 RAT 178 GGHQLDVRPRGTSASLADFVENVEWRVLGMPARRRVLTYGCCSEPYPDVTFTLLLRRRAA 237 Q9GZZ6 ACH10\_HUMAN 178 GGHQLDVRPRGAAASLADFVENVEWRVLGMPARRRVLTYGCCSEPYPDVTFTLLLRRRAA 237 P43144 ACHA9 RAT 179 NGNQVDIFNALDSGDLSDFIEDVEWEVHGMPAVKNVISYGCCSEPYPDVTFTLLLKRRSS 238 238 09JLB5 ACH10 RAT 238 AYVCNLLLPCVFISLLAPLAFHLPADSGEKVSLGVTVLLALTVFQLILAESMPPAESVPL 09GZZ6 ACH10-HUMAN 238 AYVCNLLLPCVLISLLAPLAFHLPADSGEKVSLGVTVLLALTVFQLLLAESMPPAESVPL 297 297 239 FYIVNLLIPCVLISFLAPLSFYLPAASGEKVSLGVTILLAMTVFQLMVAEIMPASENVPL Q9UGM1 ACHA9\_HUMAN 239 FYIVNLLIPCVLISFLAPLSFYLPAASGEKVSLGVTILLAMTVFQLMVAEIMPASENVPL 298 298 

 Q9JLB5
 ACH10
 RAT
 298
 IGKYYMATMTMVTFSTALTILIMNLHYCGPNAHPVPAWARVLLLGHLAKGLCVRERGEPC

 Q9GZZ6
 ACH10
 HUMAN
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 ACHA9\_RAT
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357 357 358 Q9UGM1 ACHA9<sup>-</sup>HUMAN 299 IGKYYIATMALITASTALTIMVMNIHFCGAEARPVPHWARVVILKYMSRVLFVYDVGESC 358 ·\*\*\*\*:\*\*\*<mark>:::\*</mark> \*\*\*\*\*\*::\*\*:\*\*\* ..:\*\*\* \*\*::::\* :::: \* \* : \*\* 386 389 418 418 

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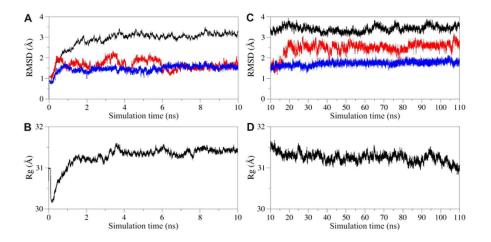
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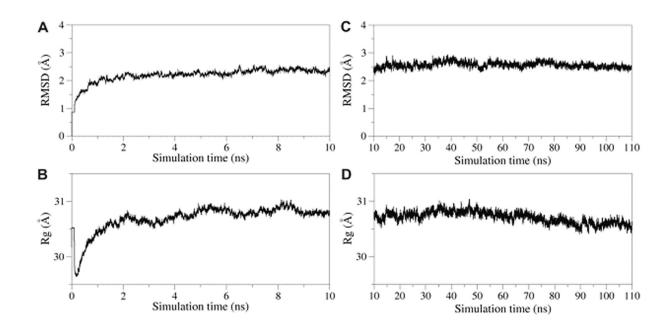
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**Figure S1.** Sequence alignment of human and rat  $\alpha$ 9 and  $\alpha$ 10 nAChR subunits color-coded by similarity and topological domain (red for signal peptide residues).

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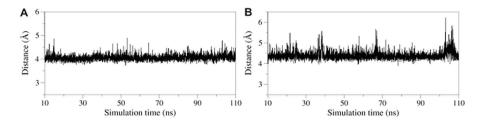
**Figure S2**. (A) Positional root-mean-square deviation (RMSD) from the initial model of rat  $(\alpha 9)_2(\alpha 10)_3$  ECD complex with RgIA during the equilibration phase, calculated for the backbone atoms of the receptor (black line) and the two bound  $\alpha$ -conotoxin ligands (red and blue lines). (B) Radius of gyration (Rg) of the receptor during the course of the equilibration phase of the MD simulations. (C) and (D) are the same as (A) and (B), respectively, during the course of the100-ns production MD runs.



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**Figure S3**. (A) Postitional root-mean-square deviation (RMSD) of the backbone atoms of the receptor from the initial model of rat  $(\alpha 9)_2(\alpha 10)_3$  ECD complex with ACh during the equilibration phase. (B) Radius of gyration (Rg) of the receptor during the course of the MD simulations. (C) and (D) are the same as (A) and (B), respectively, during the course of the 100-ns production MD runs.

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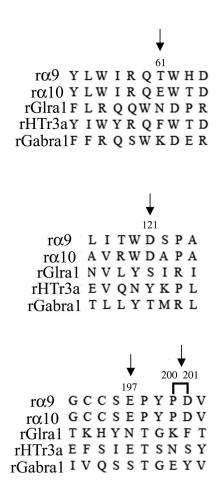


**Figure S4.** Distance between D201-C<sup> $\gamma$ </sup> of  $\alpha$ 10(+) subunit and R7-C<sup> $\zeta$ </sup> of RgIA as a function of simulation time taken from : (A) the MDs of the native receptor, and (B) the MDs of the  $\alpha$ 9 $\alpha$ 10P200Q mutant.

Molecular interaction of  $\alpha$ -conotoxin RgIA with the rat  $\alpha 9\alpha 10$  nAChR

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**Figure S5**. Alignment of critical  $\alpha$ -CTx RgIA binding residues in ECDs of the rat  $\alpha$ 9 and  $\alpha$ 10 nAChR subunits with other rat Cys-loop ligand-gated ion channels. These other pentameric channels include glycine (Glra1), 5-HT<sub>3</sub> (HTr3a) and GABA<sub>A</sub> (Gabra1). The sequence alignment among the rat ECDs was performed with MacVector 10.5.1 ClustalW alignment, using the UNIPROT accession codes P43144 for rat  $\alpha$ 9, Q9JLB5 for rat  $\alpha$ 10, P35563 for 5HT3A, P62813 for GABA<sub>A</sub> alpha1 subunit and P07727 for Glycine receptor alpha1 subunit. Note that few of the residues are conserved in the non-nicotinic receptors. Numbering is for the  $\alpha$ 9 and  $\alpha$ 10 nAChR subunits.