Supporting Information: Cholesterol Dependence of the Conformational Changes in Metabotropic Glutamate Receptor 1

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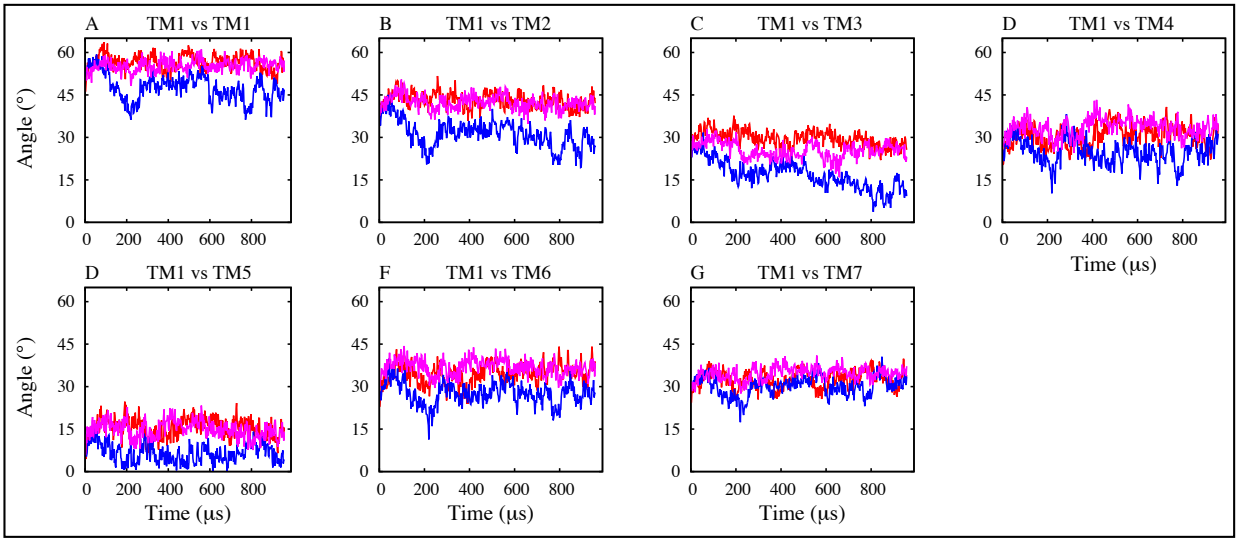

Fig. S1. Time series plot showing the interhelical angle throughout the simulations for simulation set 1. The interhelical angle between TM1 and TM2-TM7 has been calculated for each frame of the simulation.

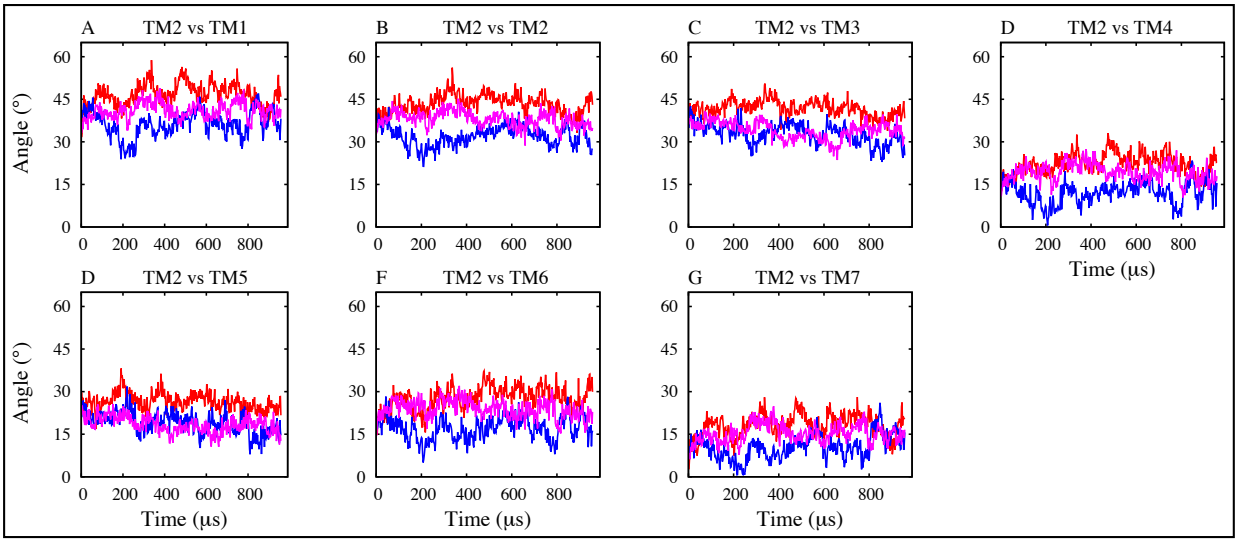

Fig. S2. Time series plot showing the interhelical angle throughout the simulations for simulation set 1. The interhelical angle between TM2 and TM1, TM3-TM7 has been calculated for each frame of the simulation.

Tables

Table S1: Occupancy (%) of Hydrogen Bond Interactions of All Protomers from Simulation Set 1

	0 % CHOL		**10 % CHOL**		**25 % CHOL**	
System	**A**	**B**	**A**	**B**	**A**	**B**
Y672-T794	3	12	13	8	**98**	6
T768-Y792	0	0	0	0	**51**	0
S627-K678	**19**	59	**35**	61	68	73
M791-T768	94	95	96	95	**34**	95
Y770-N680	95	96	96	**51**	98	**33**
R661-E728	3	46	**84**	13	14	8
E783-K834	74	98	97	97	94	73