Electronic Supplementary Material (ESI) for Molecular BioSystems.

Supporting Information

Table S1. Binding free energy contributions of key binding-site residues calculated by the binding energy decomposition for three representative compounds(kcal/mol).

	(*S*)-amlodipine					(*R*)-amlodipine				
	ΔE_{vdw}	ΔE_{ele}	ΔG_{GB}	ΔG_{SA}	ΔG_{bind}	ΔE_{vdw}	ΔE_{ele}	ΔG_{GB}	ΔG_{SA}	ΔG_{bind}
Ile1049	-0.64	0.34	-0.30	-0.12	-0.72	-1.26	-0.10	0.18	-0.16	-0.68
Val1053	-1.72	0.38	-0.14	-0.14	-1.60	-1.28	-0.04	0.24	-0.28	-0.68
Thr1056	-3.80	-5.66	3.94	-0.36	-5.90	0.18	-9.42	3.26	-0.22	-3.10
Gln1060	-1.30	1.30	2.50	-0.04	0.14	-0.20	-3.80	3.62	-0.12	-0.25
Phe1129	-2.32	-1.60	2.08	-0.14	-2.00	-2.92	-0.40	1.16	-0.44	-1.30
Ser1132	-4.50	-1.66	4.34	-0.46	-2.28	-1.84	0.28	2.00	-0.22	0.12
Ile1173	-3.74	-5.12	3.82	-0.26	-5.30	-0.32	0.24	-0.20	-0.00	-0.14
Phe1176	-2.28	2.10	-1.20	-0.04	-1.42	-0.44	0.42	-0.38	0.00	-0.20
Met1177	-5.84	1.56	-0.96	-0.70	-5.94	-4.18	-0.48	1.40	-0.66	-1.97
Ile1180	-1.78	-0.02	0.06	-0.18	-1.92	-3.76	-0.26	0.36	-0.48	-2.06
Tyr1508	-2.96	-6.20	4.40	-0.56	-5.32	-1.94	0.30	1.20	-0.32	-0.38
Met1509	-4.98	-0.80	1.48	-0.54	-4.82	-3.96	-0.50	1.44	-0.66	-1.84

	nifedipine					(*S*)-felodipine				
	ΔE_{vdw}	ΔE_{ele}	ΔG_{GB}	ΔG_{SA}	ΔG_{bind}	ΔE_{vdw}	ΔE_{ele}	ΔG_{GB}	ΔG_{SA}	ΔG_{bind}
Ile1049	-0.66	0.22	-0.18	-0.04	-0.68	-0.68	-0.08	-0.04	-0.06	-0.70
Val1053	-2.16	-0.74	0.70	-0.24	-2.44	-1.74	-0.34	0.48	-0.18	-1.78
Thr1056	-1.96	-1.88	2.08	-0.22	-2.00	-2.80	-1.48	1.72	-0.40	-2.96
Gln1060	-1.44	-1.52	3.60	-0.24	0.42	-2.22	-6.58	7.60	-0.42	-1.60
Phe1129	-6.08	0.04	1.60	-0.76	-2.00	-5.80	0.24	0.98	-0.50	-5.08
Ser1132	-2.06	-0.92	2.02	-0.15	-1.28	-1.76	0.40	0.40	-0.22	-1.18
Ile1173	-1.46	0.40	-0.34	-0.14	-1.54	-2.44	-0.22	0.30	-0.20	-2.56
Phe1176	-0.30	0.24	-0.24	-0.04	-0.30	-1.10	0.46	-0.06	0.04	-0.74
Met1177	-3.52	0.26	0.50	-0.68	-3.46	-2.96	-0.06	0.54	-0.42	-2.88
Ile1180	-1.76	-0.22	0.24	-0.14	-1.88	-2.04	-0.02	0.06	-0.32	-2.32
Tyr1508	-0.76	0.14	-0.02	0.01	-0.66	-2.82	-1.66	1.82	-0.24	-2.92
Met1509	-6.40	-2.94	2.70	-0.84	-7.48	-5.58	-2.42	2.72	-0.70	-2.92

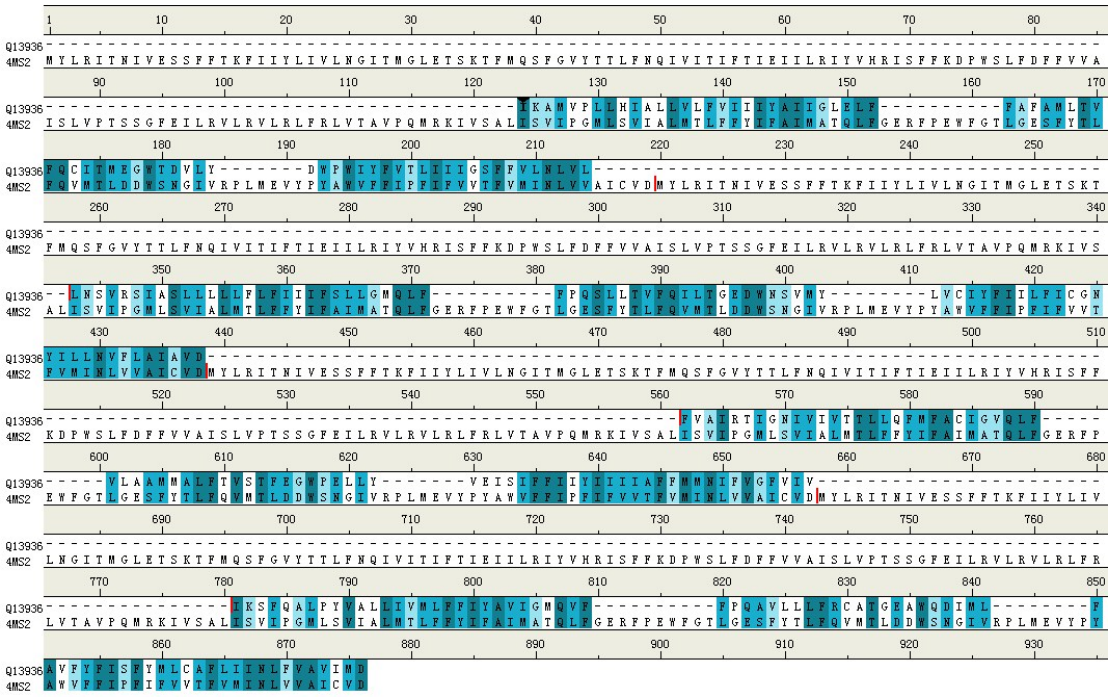

Figure S1. Sequence alignment of LTCC (human $Ca_v1.2$: residues 1-309) and bacterium Ca_vAb (PDB entry: 4MS2) used for homology modeling.

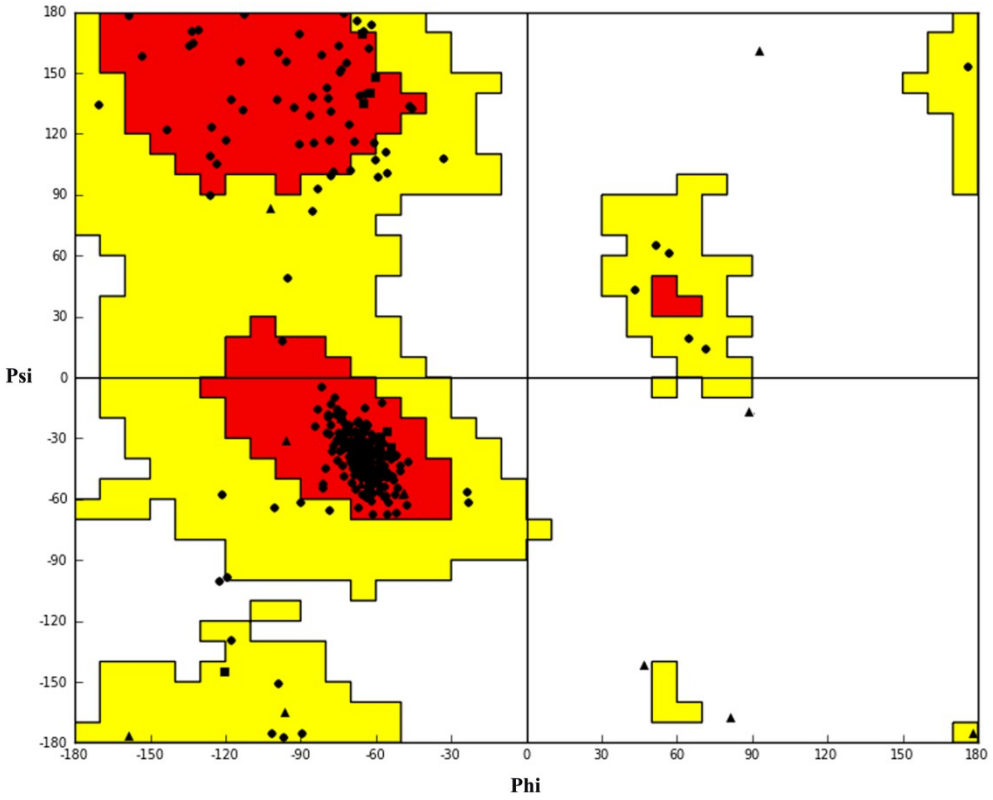

Figure S2. Ramachandran plot of $Ca_v1.2$ constructed by homology modeling.

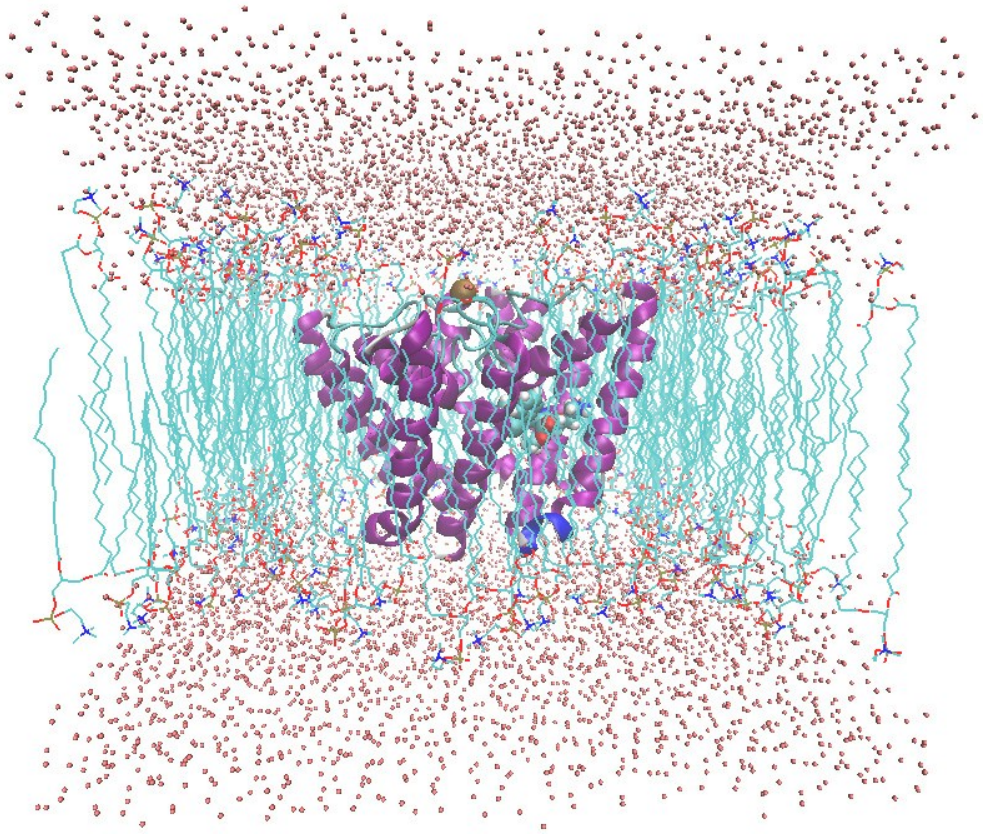

Figure S3. MD simulation box of $Ca_v1.2$ in complex with (*S*)-amlodipine, the lipid and water molecules.

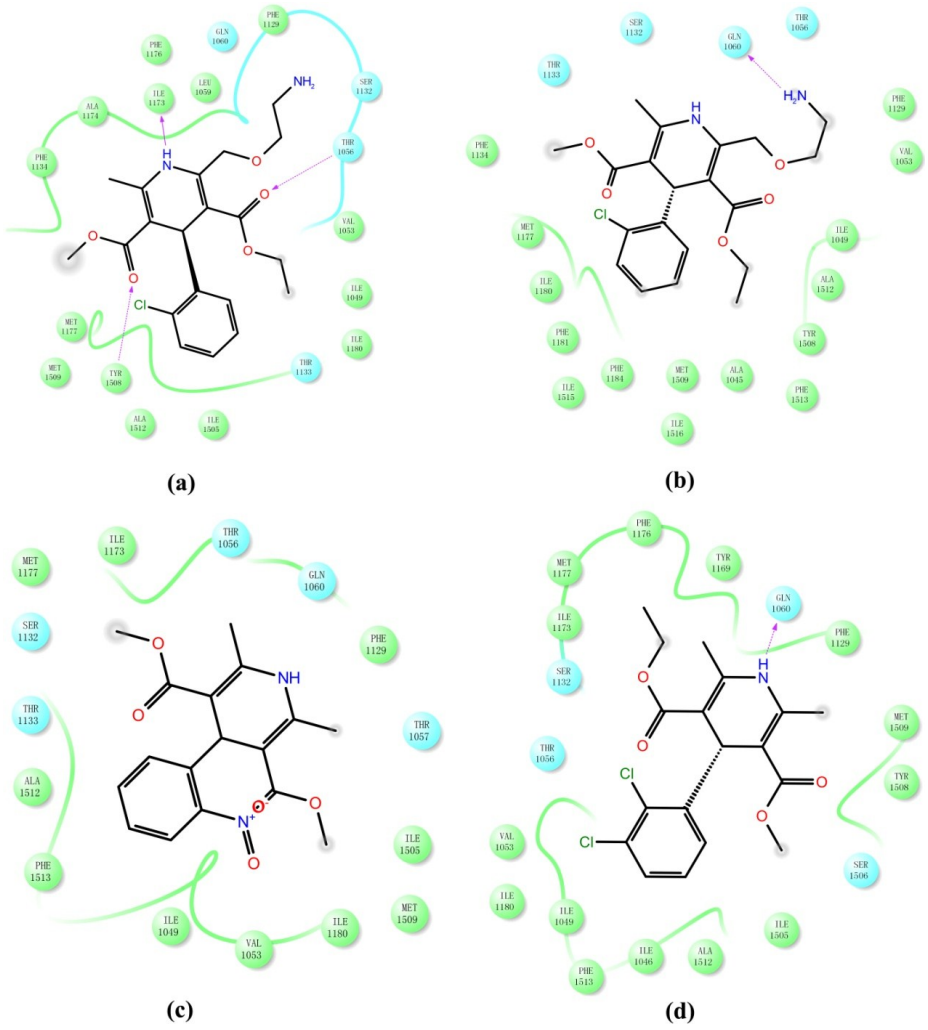

Figure S4. Schematic representation of the interactions between $Ca_v1.2$ and (a) (*S*)-amlodipine, (b) (*R*)-amlodipine, (c) nifedipine or (d) (*S*)-felodipine.