

Two statins and cromolyn as possible drugs against the
cytotoxicity of $A\beta(31-35)$ and $A\beta(25-35)$ peptides: a
comparative study by advanced computer simulations
methods

Supporting Information

Fredrik Blomgren, Dawid Wojciech Pacut,
Wojciech Chrobak, Alexander Rodin, Jan Swenson, Inna Ermilova*

Department of Physics,
Chalmers University of Technology, SE 412 96, Gothenburg, Sweden

E-mail: inna.ermilova@chalmers.se; ina.ermilova@gmail.com

Content

1. Derived models

- 1.1. Partial atomic charges for cromolyn - Figure S1.
- 1.2. Partial atomic charges for atorvastatin - Figure S2.
- 1.3. Partial atomic charges for lovastatin - Figure S3.

2. Classical MD: convergence, dimensions, concentrations, sizes

- 2.1. Proof of convergence, shown using some simulations - Figures S4-S5.
- 2.2. Final sizes of simulation boxes - Table S1.
- 2.3. Concentrations of components for systems with cromolyn - Table S2.
- 2.4. Concentrations of components for systems with atorvastatin - Table S3.
- 2.5. Concentrations of components for systems with lovastatin - Table S4.

3. Classical MD: inter- and intramolecular interactions (radial distribution functions, contacts maps)

- 3.1. Radius of gyration of compounds (peptides and drugs) for systems with 6 molecules - Table S5.
- 3.2. Radius of gyration of compounds (peptides and drugs) for systems with 8 molecules - Table S6.
- 3.3. RDFs between molecular centers of mass of drugs - Figure S6.
- 3.4. RDFs between centers of mass of amino-acid residues and drugs - Figures S7-S16.
- 3.5. Contact maps for peptides in different simulations - Figures S17-S18.

4. Classical MD: secondary structures of peptides

- 4. Secondary structures of single peptides - Figures S19-S30.

5. Well-tempered metadynamics: potential of mean force profiles

- 5. Potential of mean force profiles for the binding between drug molecules and peptides - Figure S31.

1 Drug models: partial atomic charges

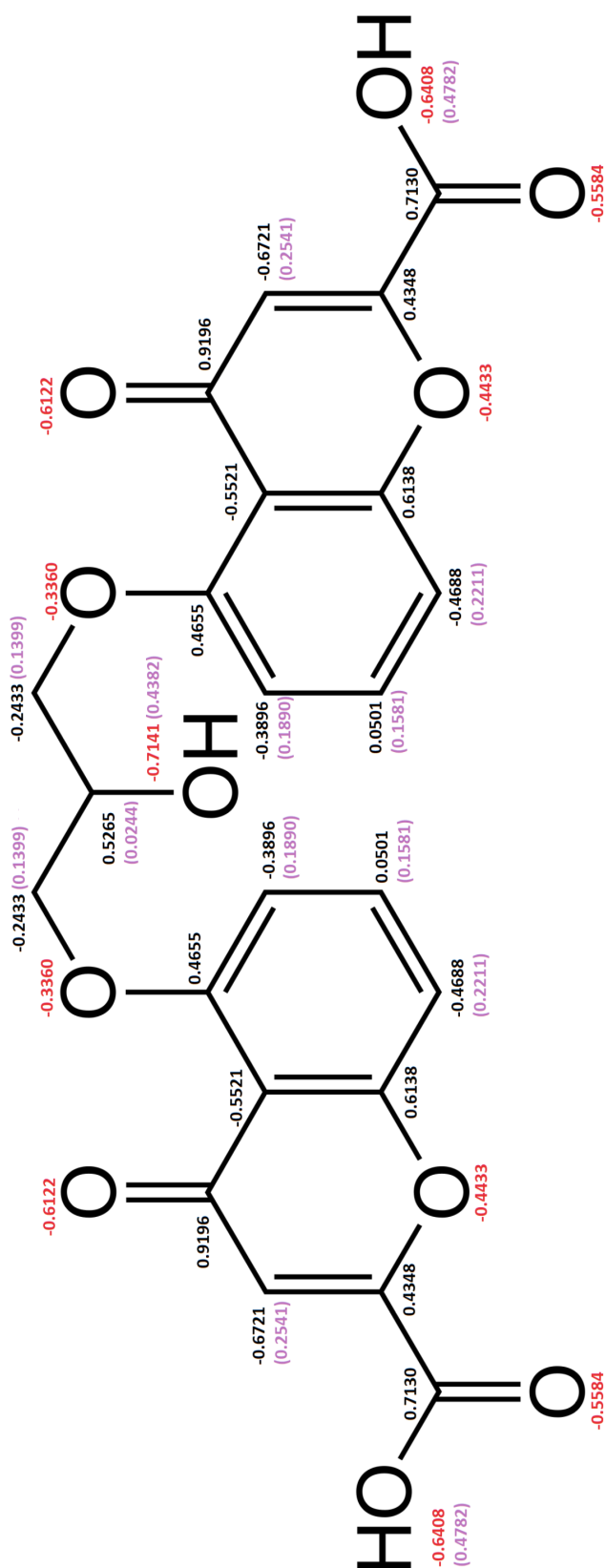


Figure S1: Partial atomic charges for cromolyn. Charges for hydrogen atoms are in parenthesis. Charge colors have the following meaning: red is for oxygen, black is for carbon, light violet is for hydrogen.

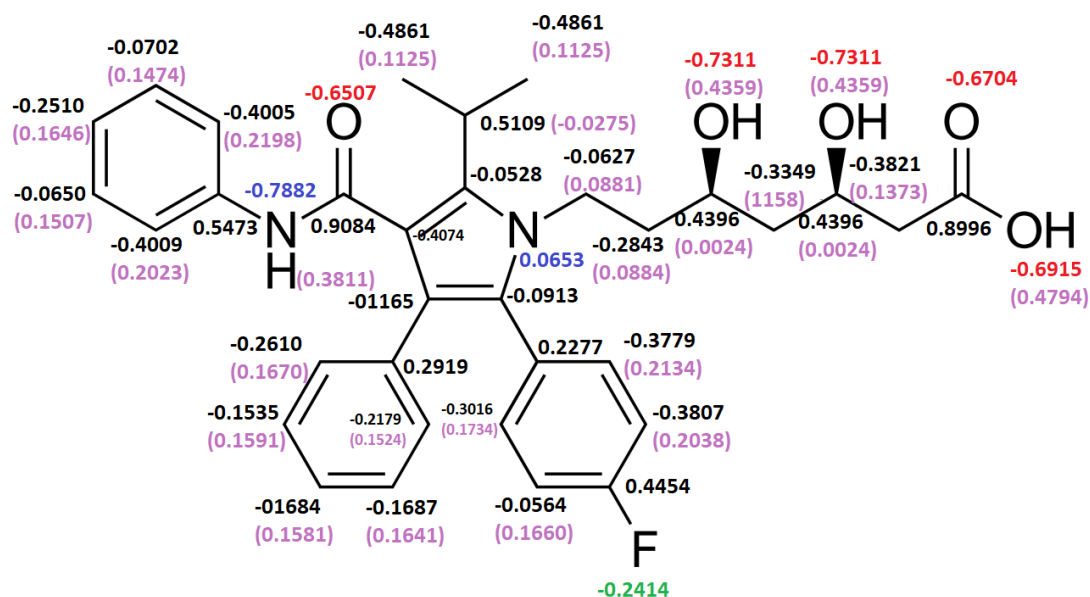


Figure S2: Partial atomic charges for atorvastatin. Charges for hydrogen atoms are in parenthesis. Charge colors have the following meaning: red is for oxygen, black is for carbon, light violet is for hydrogen, blue is for nitrogen, green is for fluor.

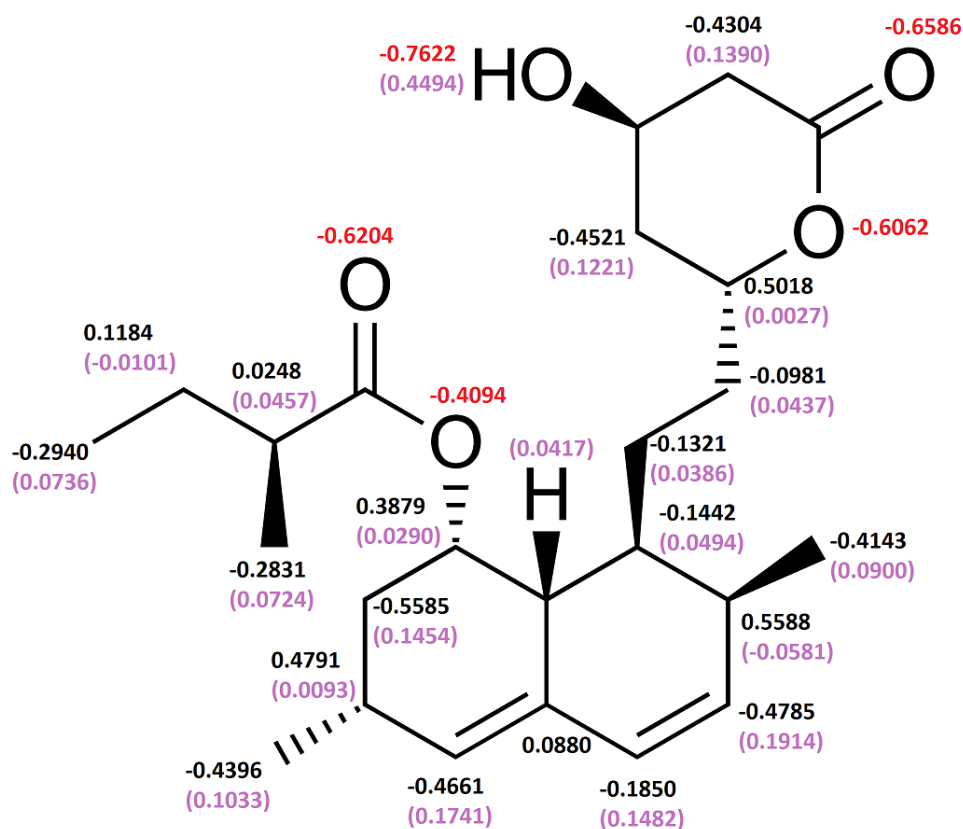


Figure S3: Partial atomic charges for lovastatin. Charges for hydrogen atoms are in parenthesis. Charge colors have the following meaning: red is for oxygen, black is for carbon, light violet is for hydrogen.

2 Classical MD: Final dimensions of simulation boxes and proofs of equilibration

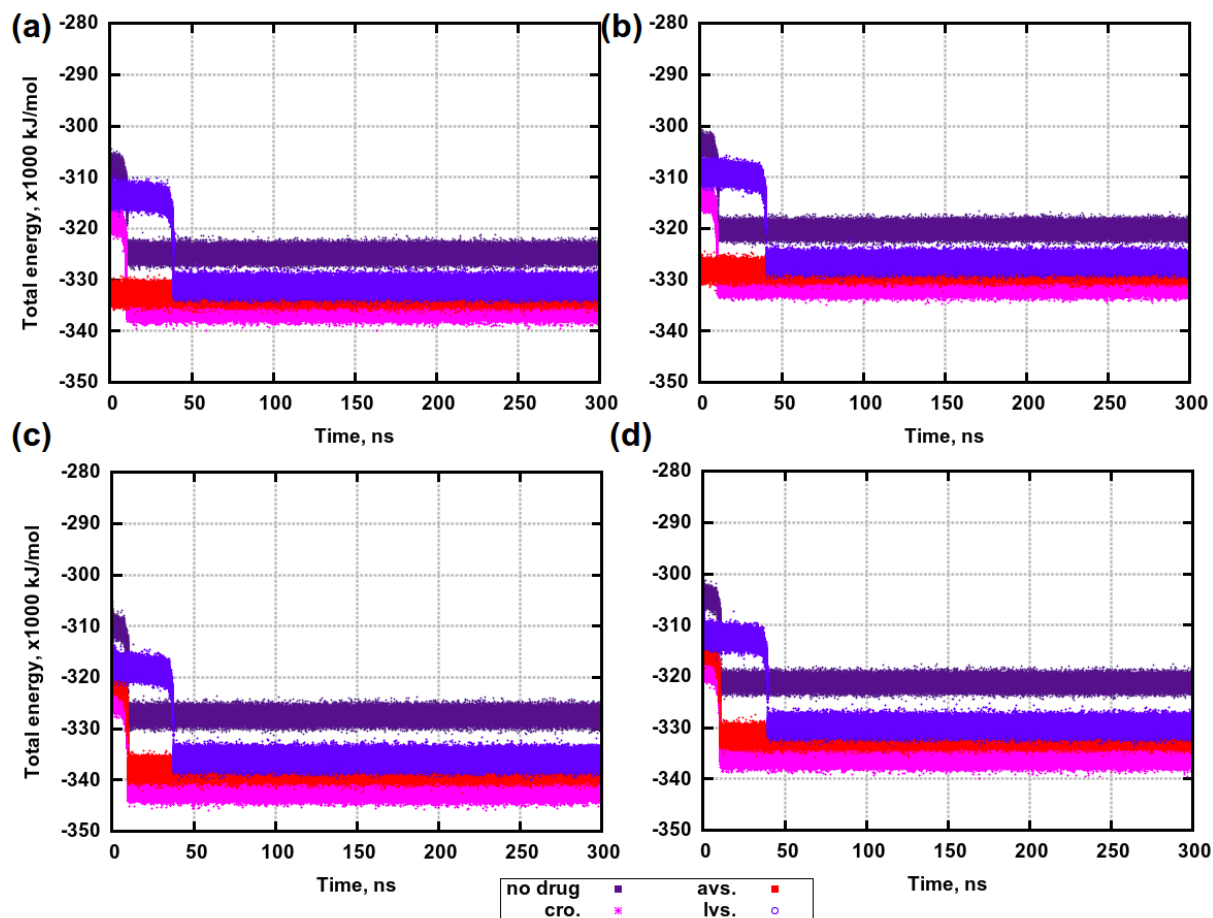


Figure S4: Convergence of total energy profiles for some simulated systems. (a) Systems containing 6 A β (25 – 35) (b) Systems containing 6 A β (31 – 35) (c) Systems containing 8 A β (25 – 35) (d) Systems containing 8 A β (31 – 35). Abbreviations mean the following: "no drug" - systems with no drugs, "cro." - systems containing cromolyn, "avs." - systems containing atorvastatin, "lvs." - systems containing lovastatin.

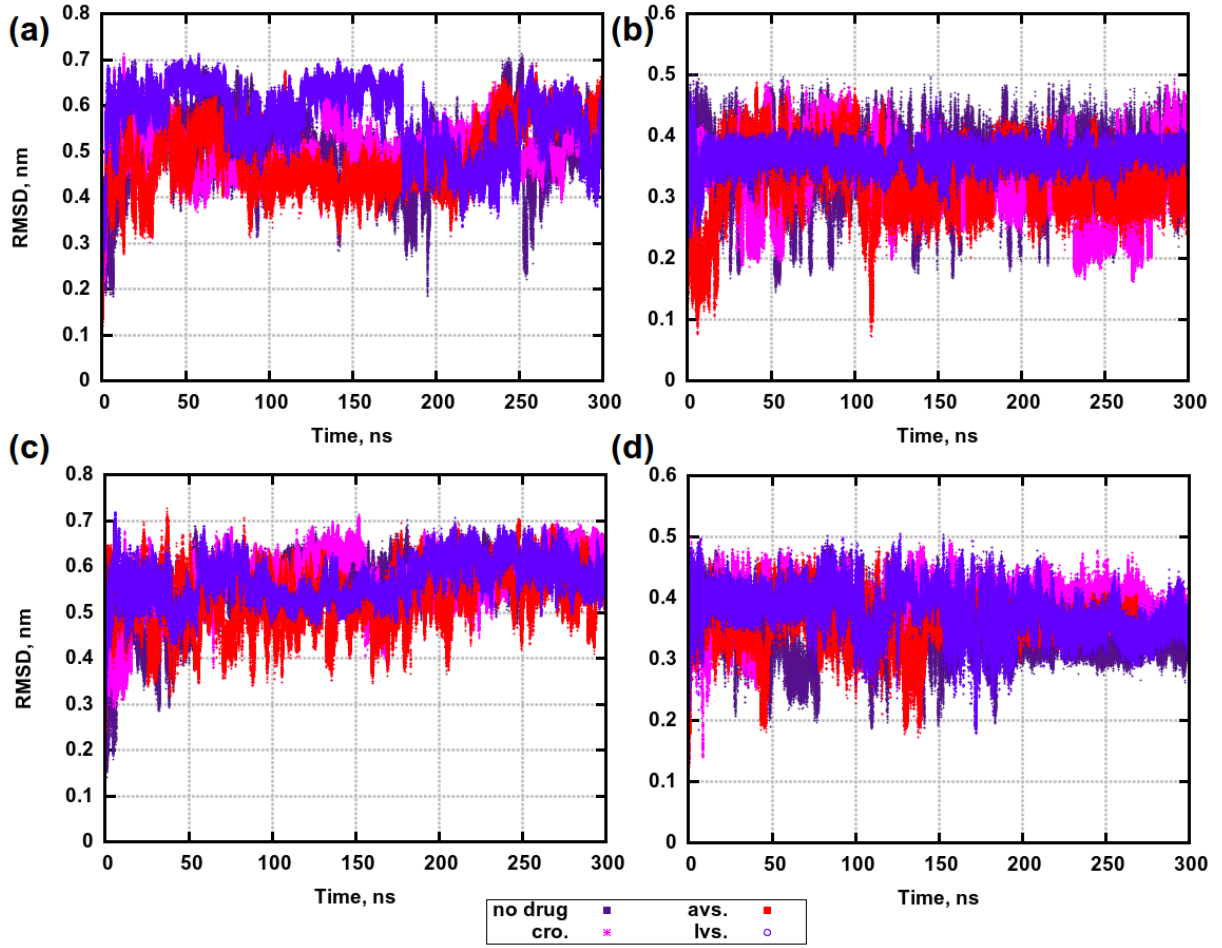


Figure S5: Root mean square deviation (RMSD) for selected single peptides in some simulated systems. (a) Systems containing 6 A β (25 – 35) (b) Systems containing 6 A β (31 – 35) (c) Systems containing 8 A β (25 – 35) (d) Systems containing 8 A β (31 – 35). Abbreviations mean the following: "no drug" - systems with no drugs, "cro." - systems containing cromolyn, "avs." - systems containing atorvastatin, "lvs." - systems containing lovastatin.

Table S1: Dimensions of simulation boxes (in *nm*) after the equilibration (classical MD).

System	Cromolyn	Atorvastatin	Lovastatin
	x=y=z	x=y=z	x=y=z
6 Drug	6.77	6.78	6.77
8 Drug	6.77	6.79	6.78
6 A β (25 – 35)+ 6 Drug	6.82	6.83	6.82
8 A β (25 – 35)+ 8 Drug	6.84	6.86	6.85
6 A β (31 – 35)+ 6 Drug	6.80	6.81	6.80
8 A β (31 – 35)+ 8 Drug	6.82	6.83	6.82

For calculations of molar concentrations the following equation was applied:

$$c = \frac{N}{N_A V} \quad (\text{S1})$$

In this formula: N is the number of molecules of a component, $N_A = 6.02214076 \cdot 10^{23} \text{ mol}^{-1}$ is the Avogadro's number, V is the volume of the simulation box after the equilibration.

Table S2: Concentrations (c) of components (in mol/m^3) for systems with Cromolyn. "counter" represents Cl counter ions.

System	c($A\beta$)	c(Drug)	c(counter)
6 Drug	none	32.11	none
8 Drug	none	42.81	none
6 $A\beta(25 - 35)$ +6 Drug	31.41	31.41	31.41
8 $A\beta(25 - 35)$ +8 Drug	41.51	41.51	41.51
6 $A\beta(31 - 35)$ +6 Drug	31.69	31.69	none
8 $A\beta(31 - 35)$ +8 Drug	41.88	41.88	none

Table S3: Concentrations (c) of components (in mol/m^3) for systems with Atorvastatin. "counter" represents Cl counter ions.

System	c($A\beta$)	c(Drug)	c(counter)
6 Drug	none	31.97	none
8 Drug	none	42.44	none
6 $A\beta(25 - 35)$ +6 Drug	31.27	31.27	31.27
8 $A\beta(25 - 35)$ +8 Drug	41.15	41.15	41.15
6 $A\beta(31 - 35)$ +6 Drug	31.55	31.55	none
8 $A\beta(31 - 35)$ +8 Drug	41.69	41.69	none

Table S4: Concentrations (c) of components (in mol/m^3) for systems with Lovastatin. "counter" represents Cl counter ions.

System	c($A\beta$)	c(Drug)	c(counter)
6 Drug	none	32.11	none
8 Drug	none	42.62	none
6 $A\beta(25 - 35)$ +6 Drug	31.41	31.41	31.41
8 $A\beta(25 - 35)$ +8 Drug	41.33	41.33	41.33
6 $A\beta(31 - 35)$ +6 Drug	31.69	31.69	none
8 $A\beta(31 - 35)$ +8 Drug	41.88	41.88	none

3 Classical MD: RDFs, radius of gyration and contact maps

Table S5: Radius of gyration in nm (systems with 6 molecules).

System	Peptide	Drug
pure cro.	–	1.59
pure avs.	–	2.05
pure lvs.	–	2.17
$A\beta(25 - 35)$ & cro.	3.06	2.16
$A\beta(25 - 35)$ & avs.	2.82	1.62
$A\beta(25 - 35)$ & lvs.	3.15	2.14
$A\beta(25 - 35)$ (pure)	2.94	–
$A\beta(31 - 35)$ & cro.	2.82	1.99
$A\beta(31 - 35)$ & avs.	2.61	1.83
$A\beta(31 - 35)$ & lvs.	2.29	1.93
$A\beta(31 - 35)$ (pure)	3.00	–

Table S6: Radius of gyration in nm (systems with 8 molecules).

System	Peptide	Drug
pure cro.	–	1.94
pure avs.	–	2.17
pure lvs.	–	1.94
$A\beta(25 - 35)$ & cro.	2.92	2.17
$A\beta(25 - 35)$ & avs.	3.06	2.08
$A\beta(25 - 35)$ & lvs.	3.30	2.75
$A\beta(25 - 35)$ (pure)	3.01	–
$A\beta(31 - 35)$ & cro.	2.42	1.94
$A\beta(31 - 35)$ & avs.	2.84	2.52
$A\beta(31 - 35)$ & lvs.	2.61	2.20
$A\beta(31 - 35)$ (pure)	2.73	–

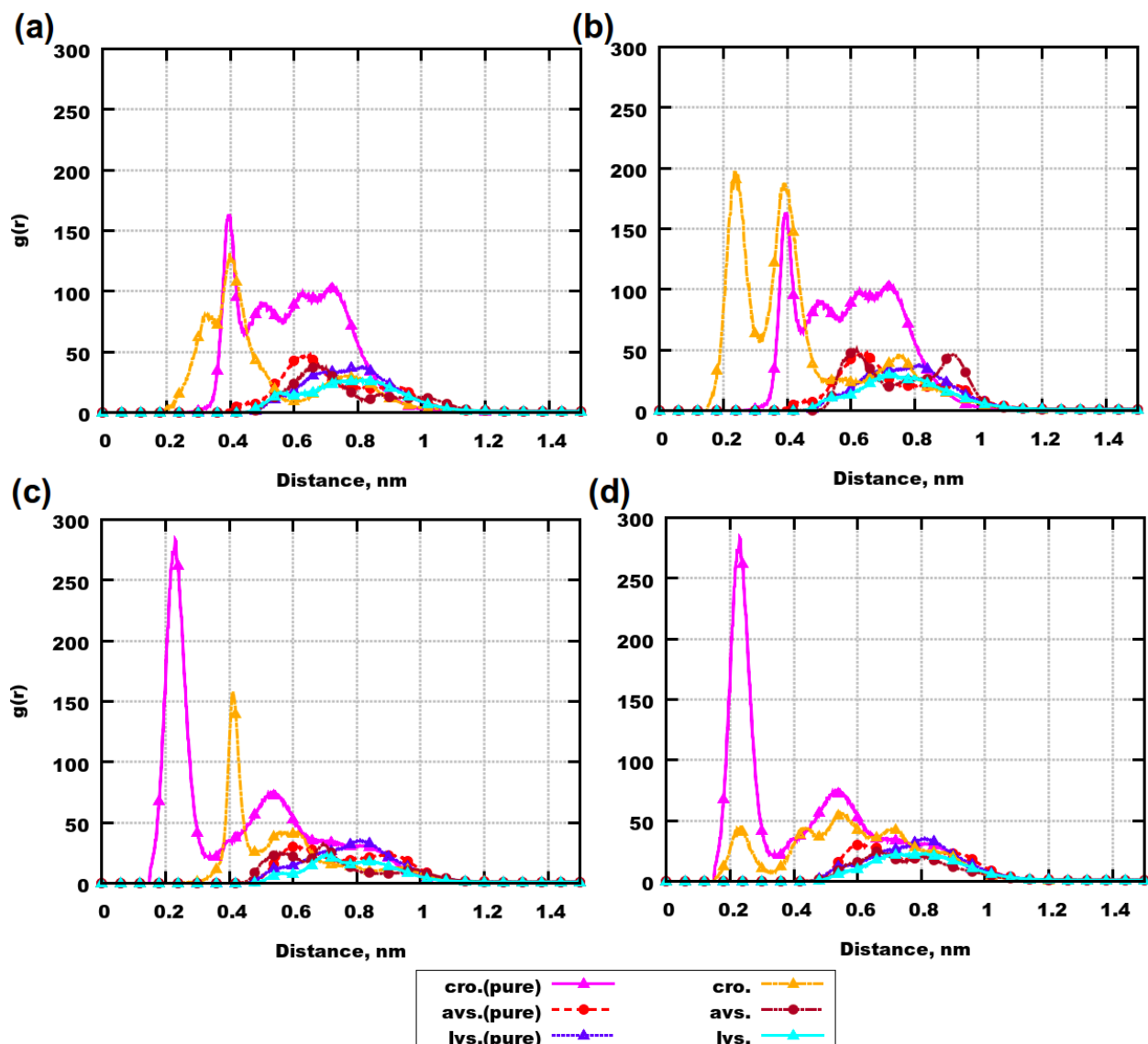


Figure S6: Radial distribution functions between molecular centers of mass of drugs. (a) Systems without (pure) and with 6 $A\beta(25 - 35)$. (b) Systems without (pure) and with 6 $A\beta(31 - 35)$. (c) Systems without (pure) and with 8 $A\beta(25 - 35)$. (d) Systems without (pure) and with 8 $A\beta(31 - 35)$. Abbreviations mean the following: "cro." - systems containing cromolyn, "avs." - systems containing atorvastatin, "lvs." - systems containing lovastatin. Here curves for systems without peptides were plotted for a comparison.

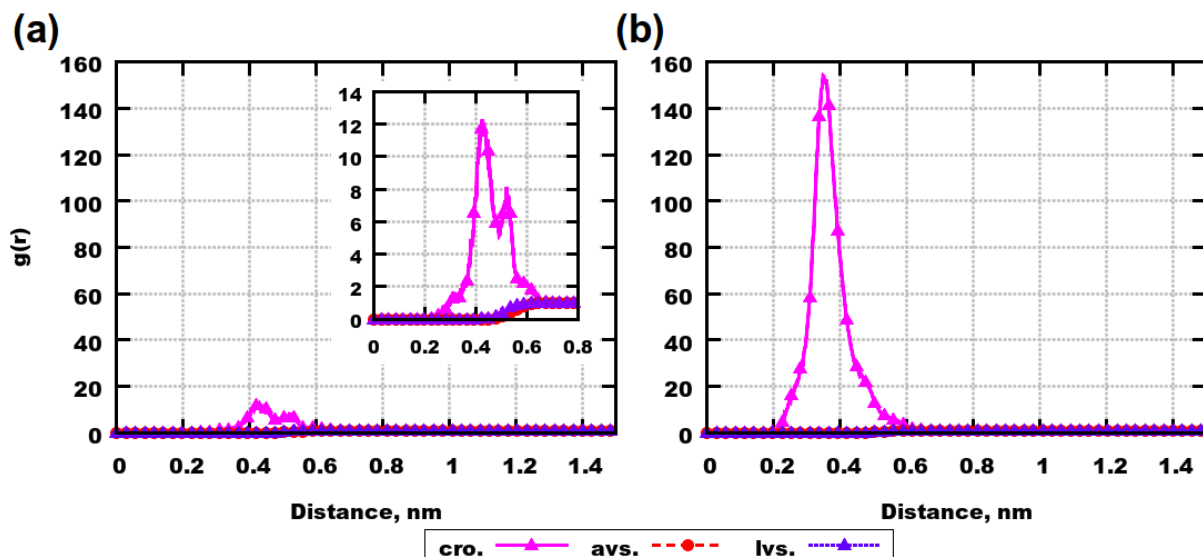


Figure S7: Radial distribution functions between molecular centers of mass of glycine (GLY_{25}) and drugs. (a) Systems containing 6 $A\beta(25-35)$ with and without drugs. (b) Systems containing 8 $A\beta(25-35)$ with and without drugs. Abbreviations mean the following: "cro." - systems containing cromolyn, "avs." - systems containing atorvastatin, "lvs." - systems containing lovastatin.

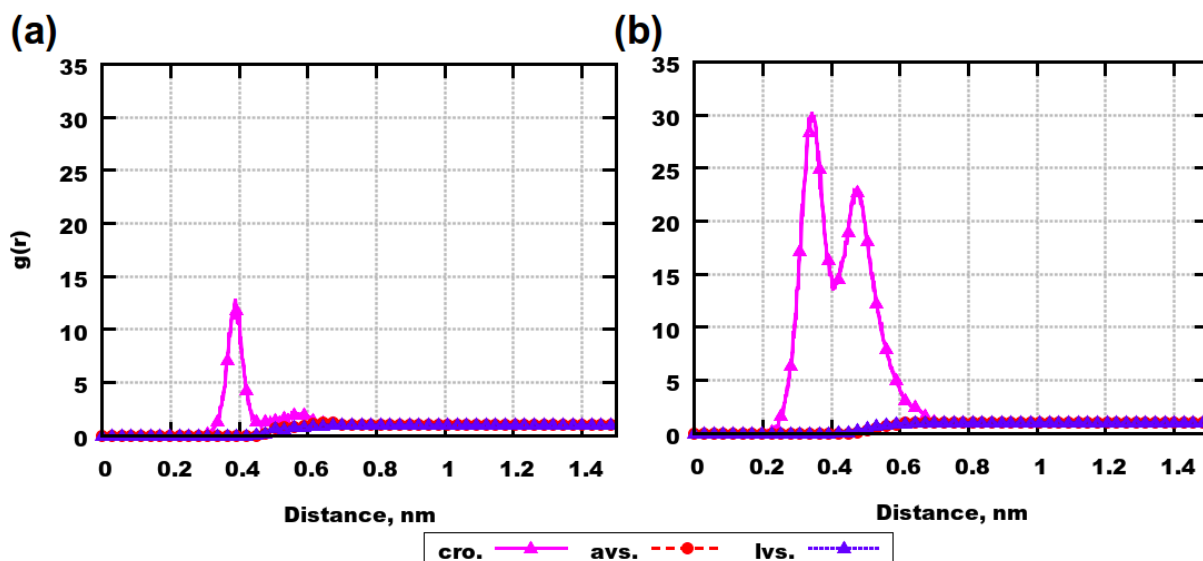


Figure S8: Radial distribution functions between molecular centers of mass of serine (SER_{26}) and drugs. (a) Systems containing 6 $A\beta(25-35)$ with and without drugs. (b) Systems containing 8 $A\beta(25-35)$ with and without drugs. Abbreviations mean the following: "cro." - systems containing cromolyn, "avs." - systems containing atorvastatin, "lvs." - systems containing lovastatin.

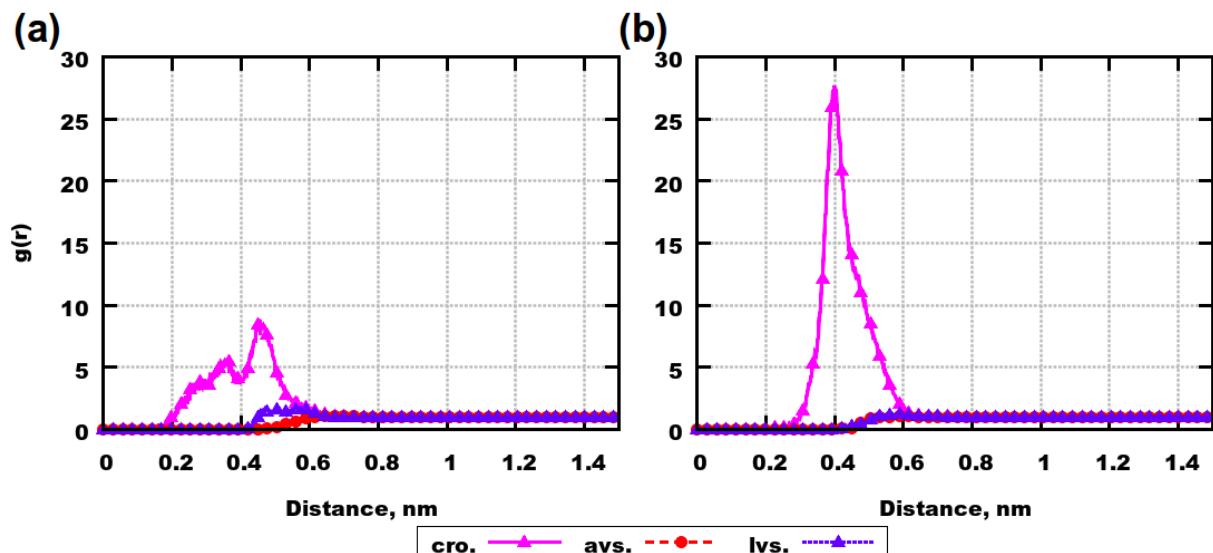


Figure S9: Radial distribution functions between molecular centers of mass of asparagine (ASN_{27}) and drugs. (a) Systems containing 6 $A\beta(25-35)$ with and without drugs. (b) Systems containing 8 $A\beta(25-35)$ with and without drugs. Abbreviations mean the following: "cro." - systems containing cromolyn, "avs." - systems containing atorvastatin, "lvs." - systems containing lovastatin.

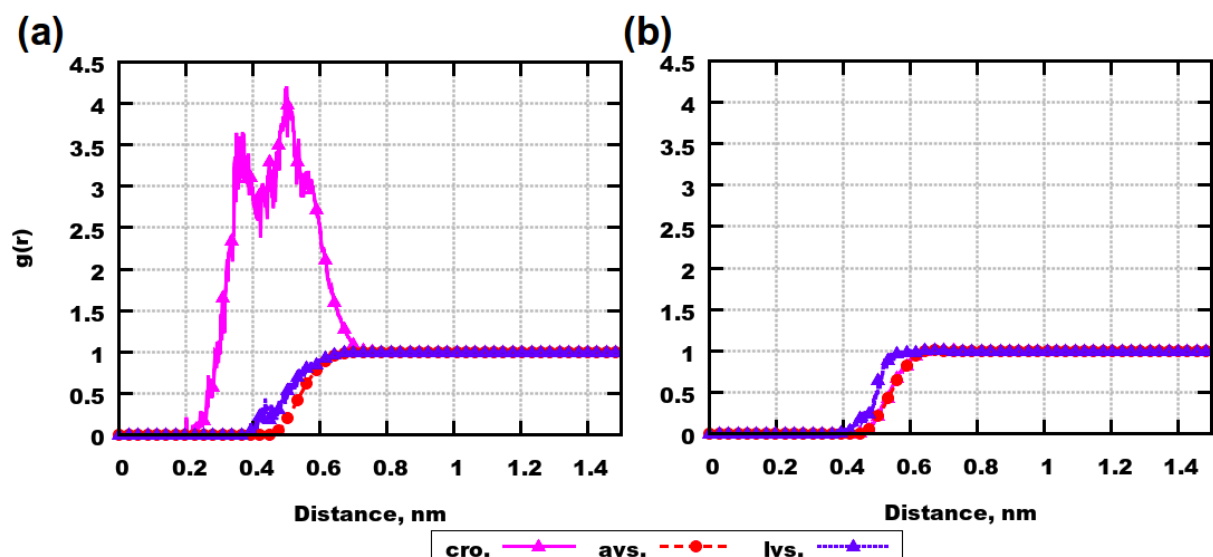


Figure S10: Radial distribution functions between molecular centers of mass of lysine (LYS_{28}) and drugs. (a) Systems containing 6 $A\beta(25-35)$ with and without drugs. (b) Systems containing 8 $A\beta(25-35)$ with and without drugs. Abbreviations mean the following: "cro." - systems containing cromolyn, "avs." - systems containing atorvastatin, "lvs." - systems containing lovastatin.

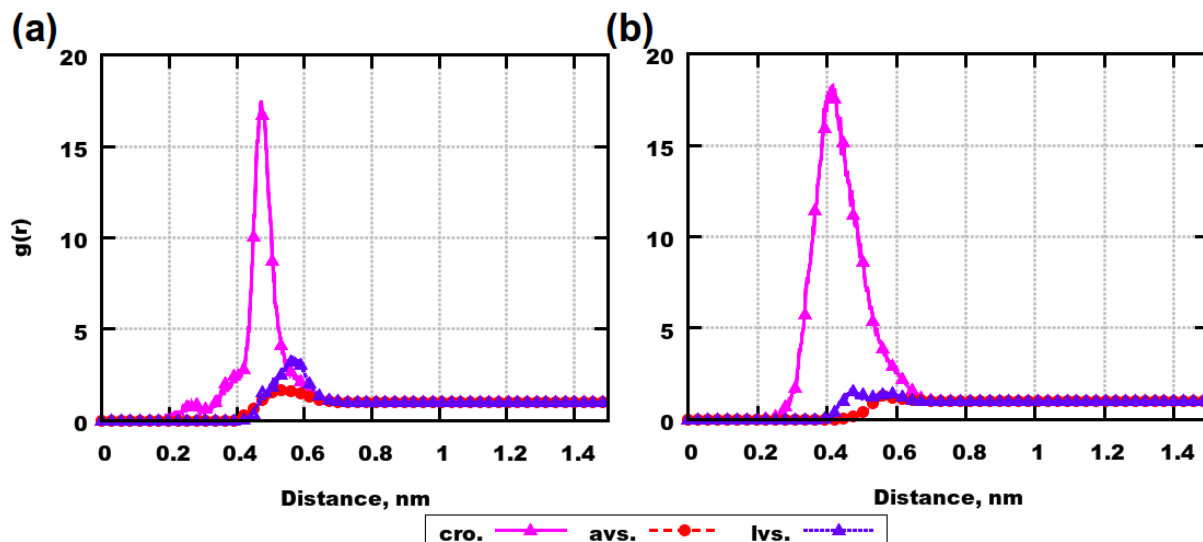


Figure S11: Radial distribution functions between molecular centers of mass of glycine (GLY_{29}) and drugs. (a) Systems containing 6 $A\beta(25-35)$ with and without drugs. (b) Systems containing 8 $A\beta(25-35)$ with and without drugs. Abbreviations mean the following: "cro." - systems containing cromolyn, "avs." - systems containing atorvastatin, "lvs." - systems containing lovastatin.

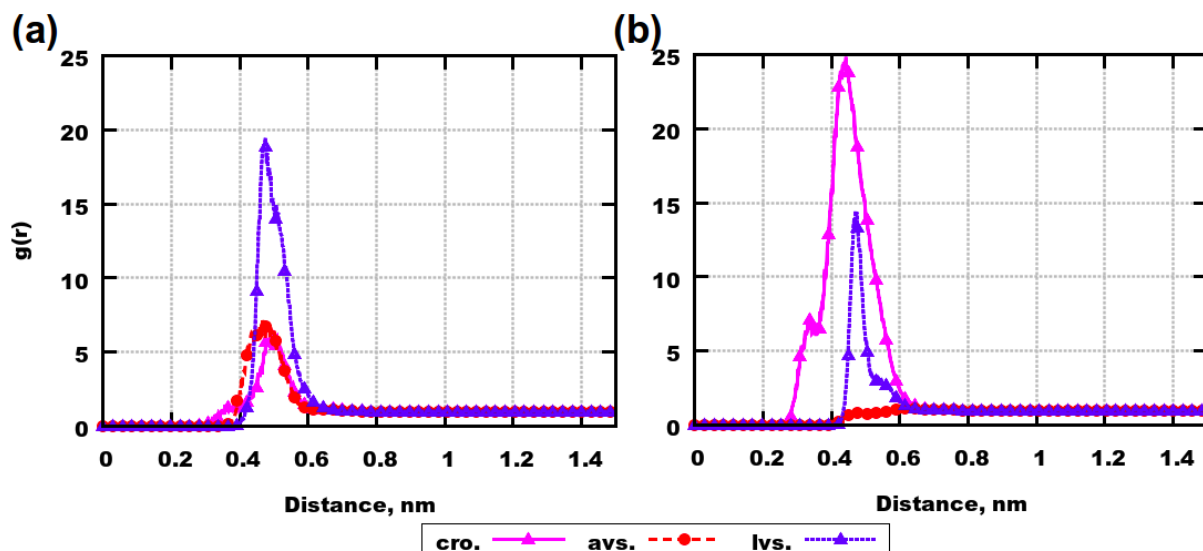


Figure S12: Radial distribution functions between molecular centers of mass of alanine (ALA_{30}) and drugs. (a) Systems containing 6 $A\beta(25-35)$ with and without drugs. (b) Systems containing 8 $A\beta(25-35)$ with and without drugs. Abbreviations mean the following: "cro." - systems containing cromolyn, "avs." - systems containing atorvastatin, "lvs." - systems containing lovastatin.

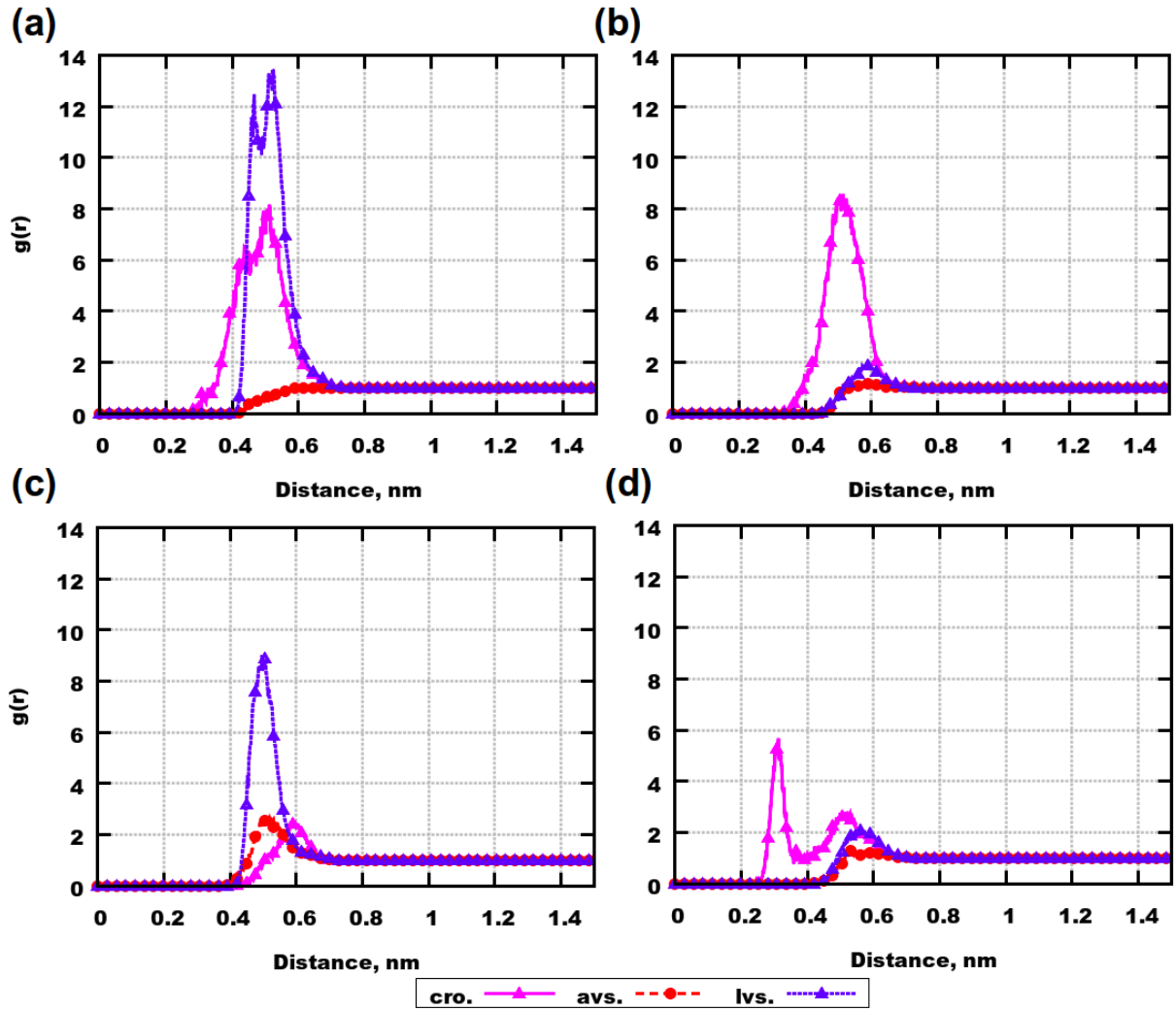


Figure S13: Radial distribution functions between molecular centers of mass of isoleucine (ILE_{31}) and drugs. (a) Systems containing 6 A β (25–35) with and without drugs. (b) Systems containing 6 A β (31–35) with and without drugs. (c) Systems containing 8 A β (25–35) with and without drugs. (d) Systems containing 8 A β (31–35) with and without drugs. Abbreviations mean the following: "cro." - systems containing cromolyn, "avs." - systems containing atorvastatin, "lvs." - systems containing lovastatin.

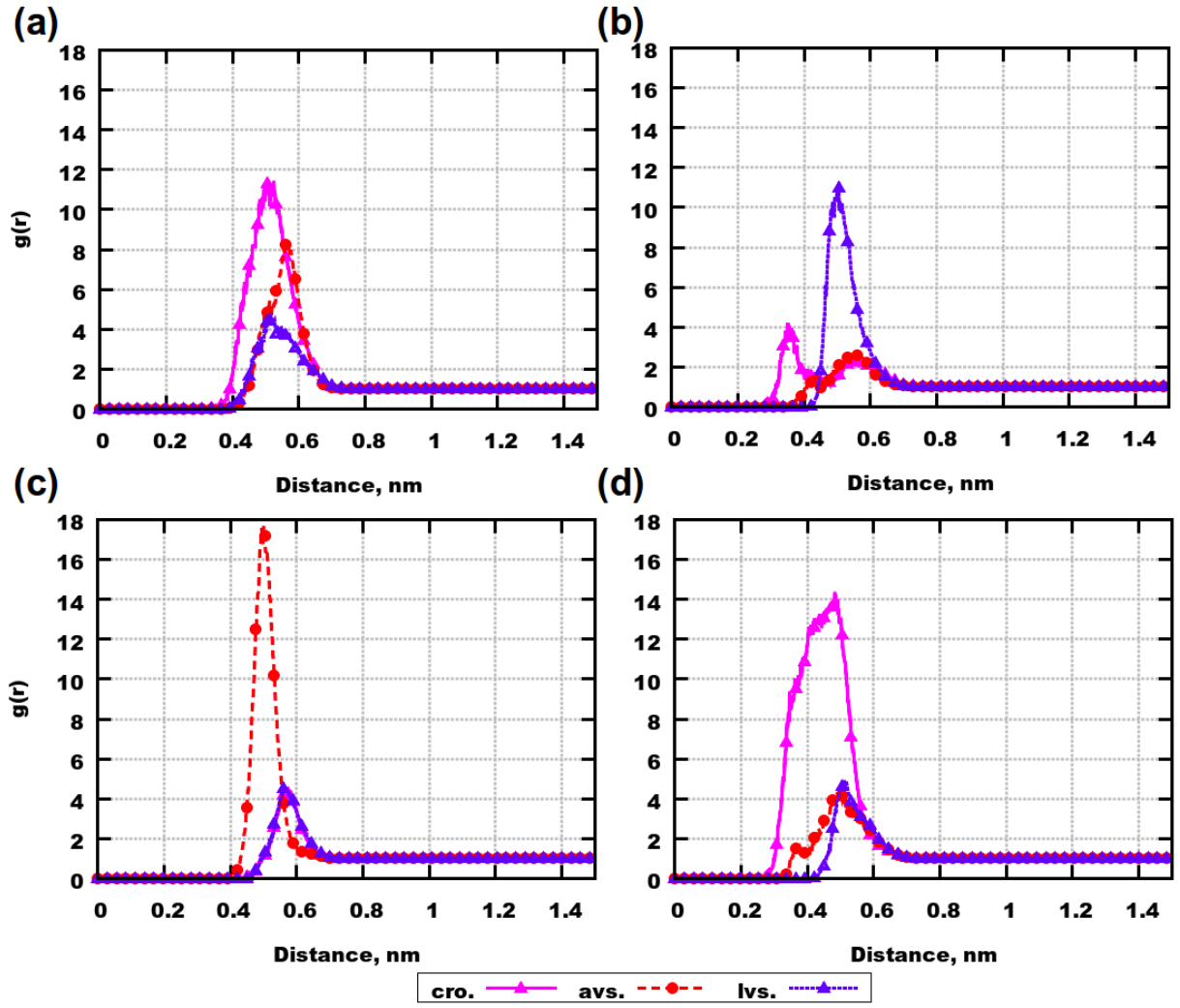


Figure S14: Radial distribution functions between molecular centers of mass of isoleucine (ILE_{32}) and drugs. (a) Systems containing 6 $A\beta(25-35)$ with and without drugs. (b) Systems containing 6 $A\beta(31-35)$ with and without drugs. (c) Systems containing 8 $A\beta(25-35)$ with and without drugs. (d) Systems containing 8 $A\beta(31-35)$ with and without drugs. Abbreviations mean the following: "cro." - systems containing cromolyn, "avs." - systems containing atorvastatin, "lvs." - systems containing lovastatin.

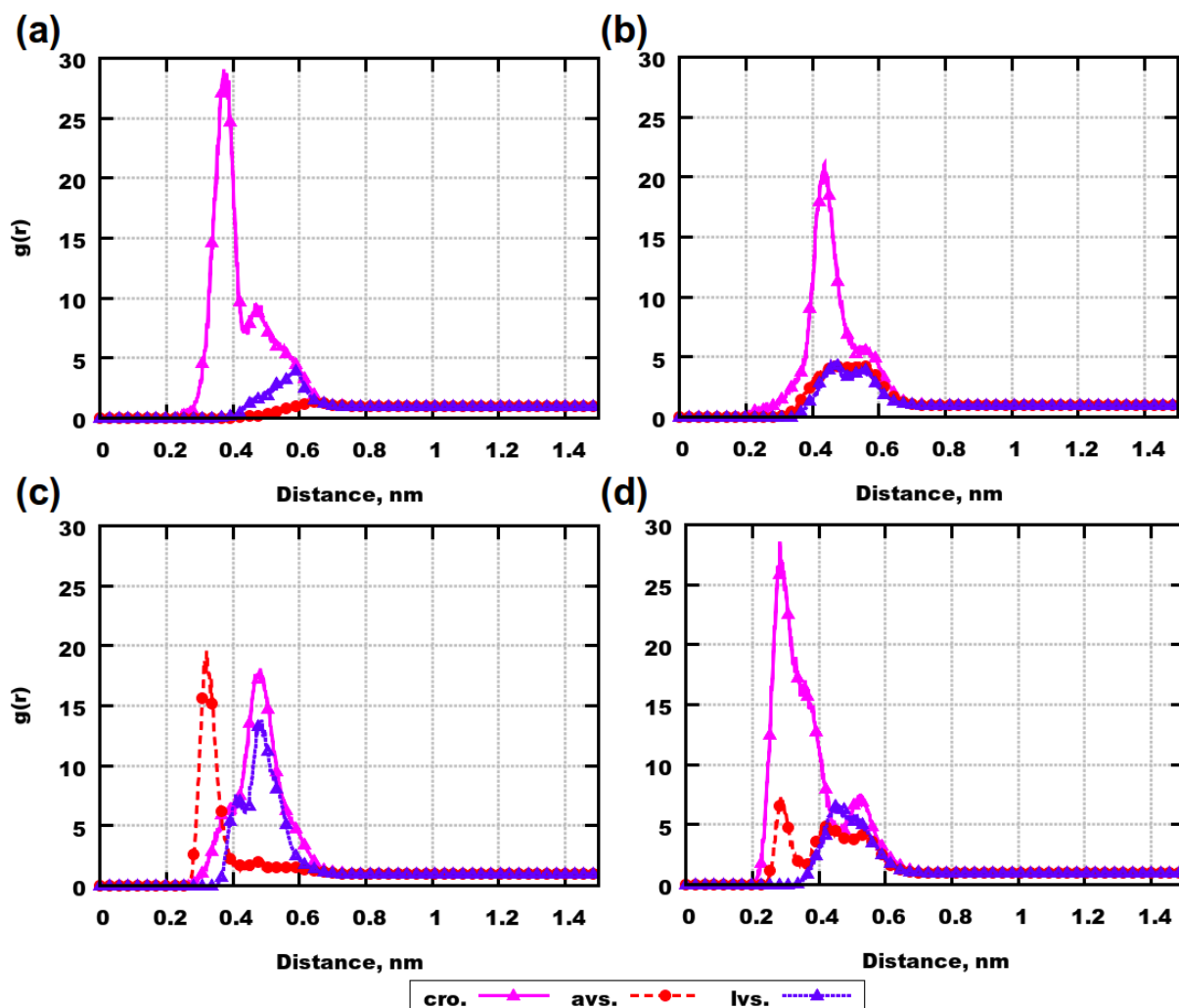


Figure S15: Radial distribution functions between molecular centers of mass of glycine (GLY_{33}) and drugs. (a) Systems containing 6 $A\beta(25-35)$ with and without drugs. (b) Systems containing 6 $A\beta(31-35)$ with and without drugs. (c) Systems containing 8 $A\beta(25-35)$ with and without drugs. (d) Systems containing 8 $A\beta(31-35)$ with and without drugs. Abbreviations mean the following: "cro." - systems containing cromolyn, "avs." - systems containing atorvastatin, "lvs." - systems containing lovastatin.

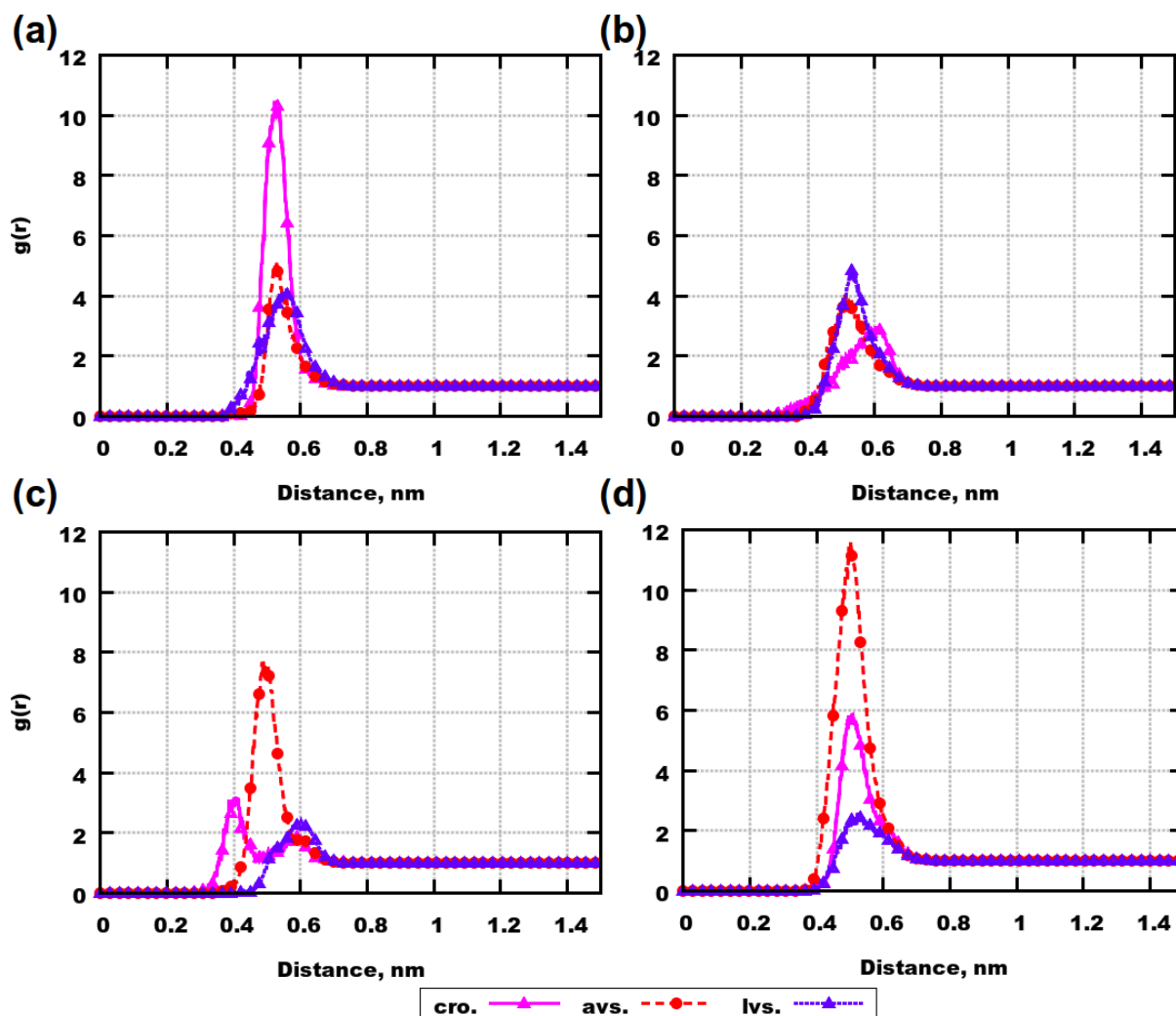


Figure S16: Radial distribution functions between molecular centers of mass of leucine (LEU_{34}) and drugs. (a) Systems containing 6 $A\beta(25-35)$ with and without drugs. (b) Systems containing 6 $A\beta(31-35)$ with and without drugs. (c) Systems containing 8 $A\beta(25-35)$ with and without drugs. (d) Systems containing 8 $A\beta(31-35)$ with and without drugs. Abbreviations mean the following: "cro." - systems containing cromolyn, "avs." - systems containing atorvastatin, "lvs." - systems containing lovastatin.

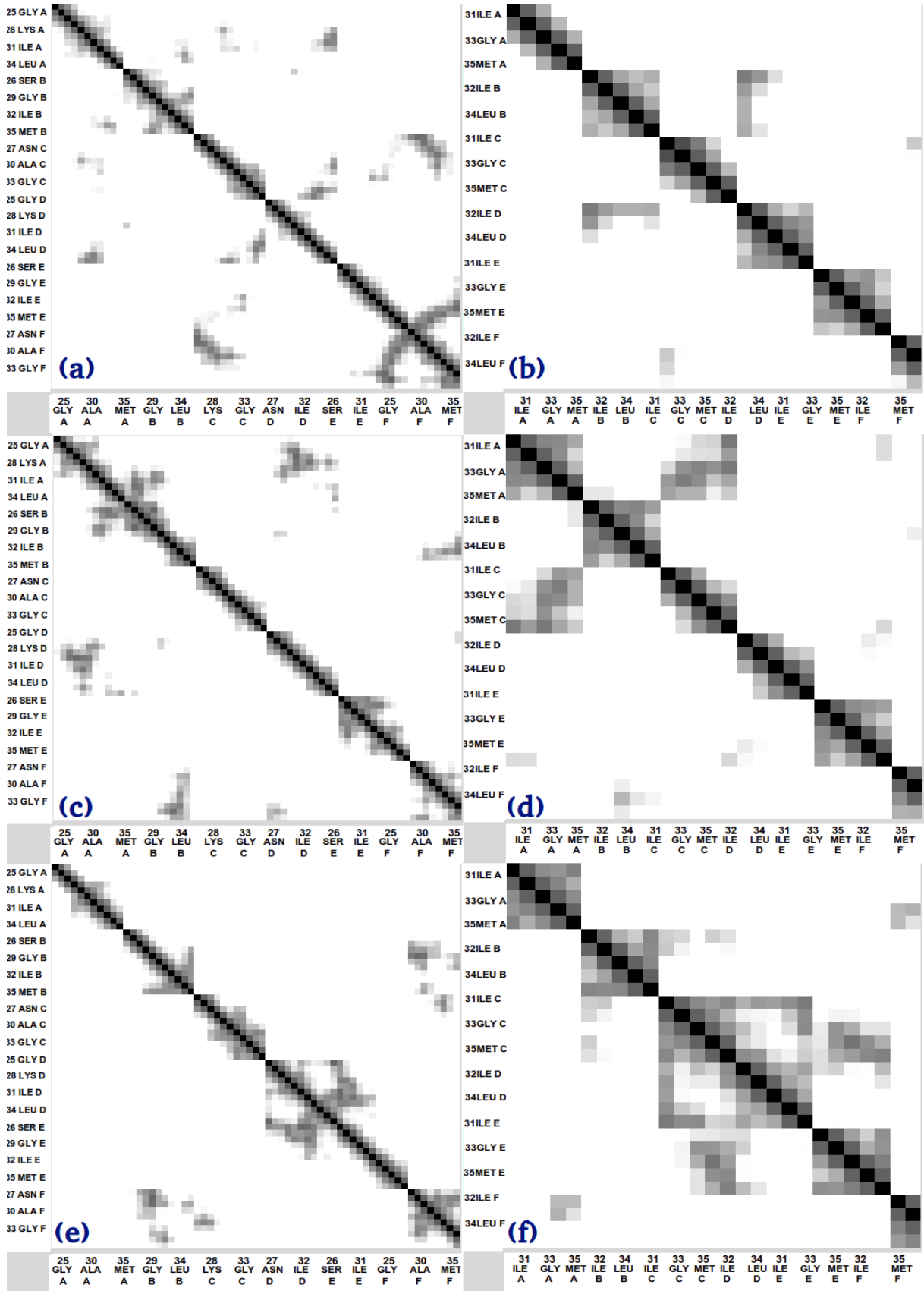


Figure S17: Contact maps for systems with 6 molecules, computed during the last 50 ns. (a) Aβ(25 – 35) and cromolyn. (b) Aβ(31 – 35) and cromolyn. (c) Aβ(25 – 35) and atorvastatin. (d) Aβ(31 – 35) and atorvastatin. (e) Aβ(25 – 35) and lovastatin. (f) Aβ(31 – 35) and lovastatin.

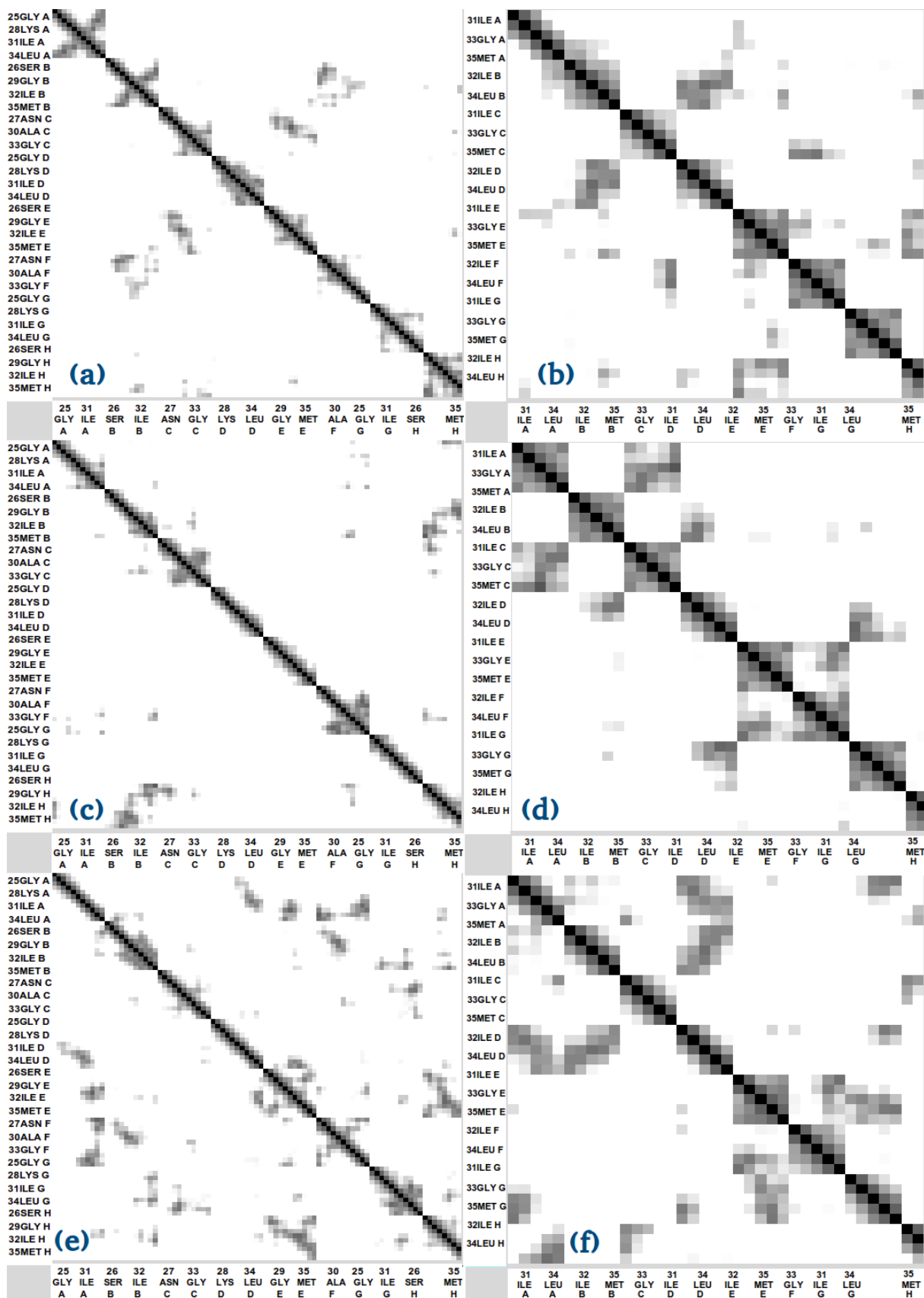


Figure S18: Contact maps for systems with 8 molecules, computed during the last 50 ns. (a) Aβ(25 – 35) and cromolyn. (b) Aβ(31 – 35) and cromolyn. (c) Aβ(25 – 35) and atorvastatin. (d) Aβ(31 – 35) and atorvastatin. (e) Aβ(25 – 35) and lovastatin. (f) Aβ(31 – 35) and lovastatin.

4 Classical MD: secondary structures of peptides

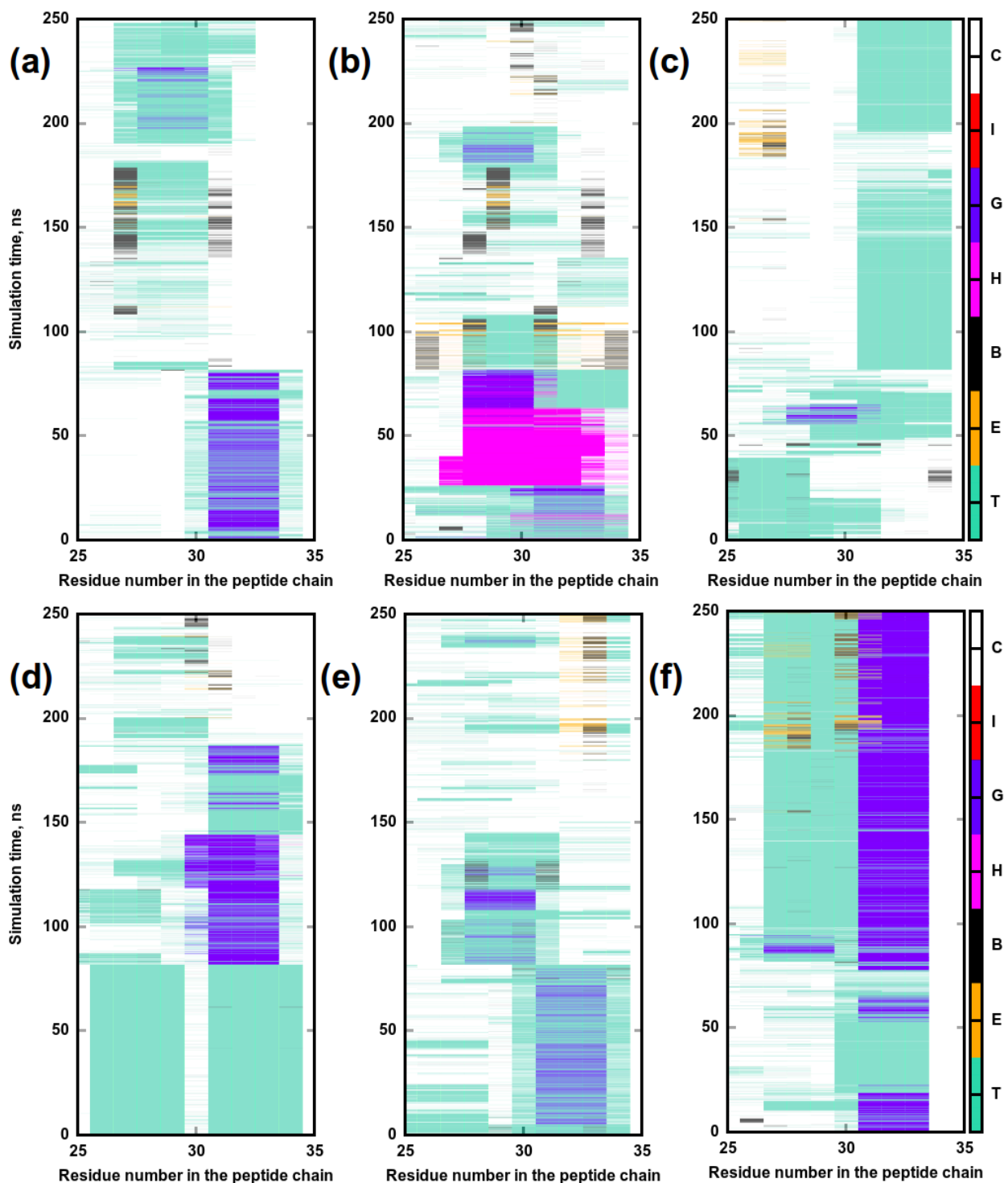


Figure S19: Secondary structures of A β (25 – 35) for the system containing 6 peptides and 6 molecules of cromolyn. Secondary structures are coded as the following: *T* - turn, *E* - extended conformation, *B* - isolated β -bridge, *H* - α -helix, *G* - 3_{10} -helix, *I* - π -helix, *C* - coil. Letters (a)-(f) are denoting separate peptides.

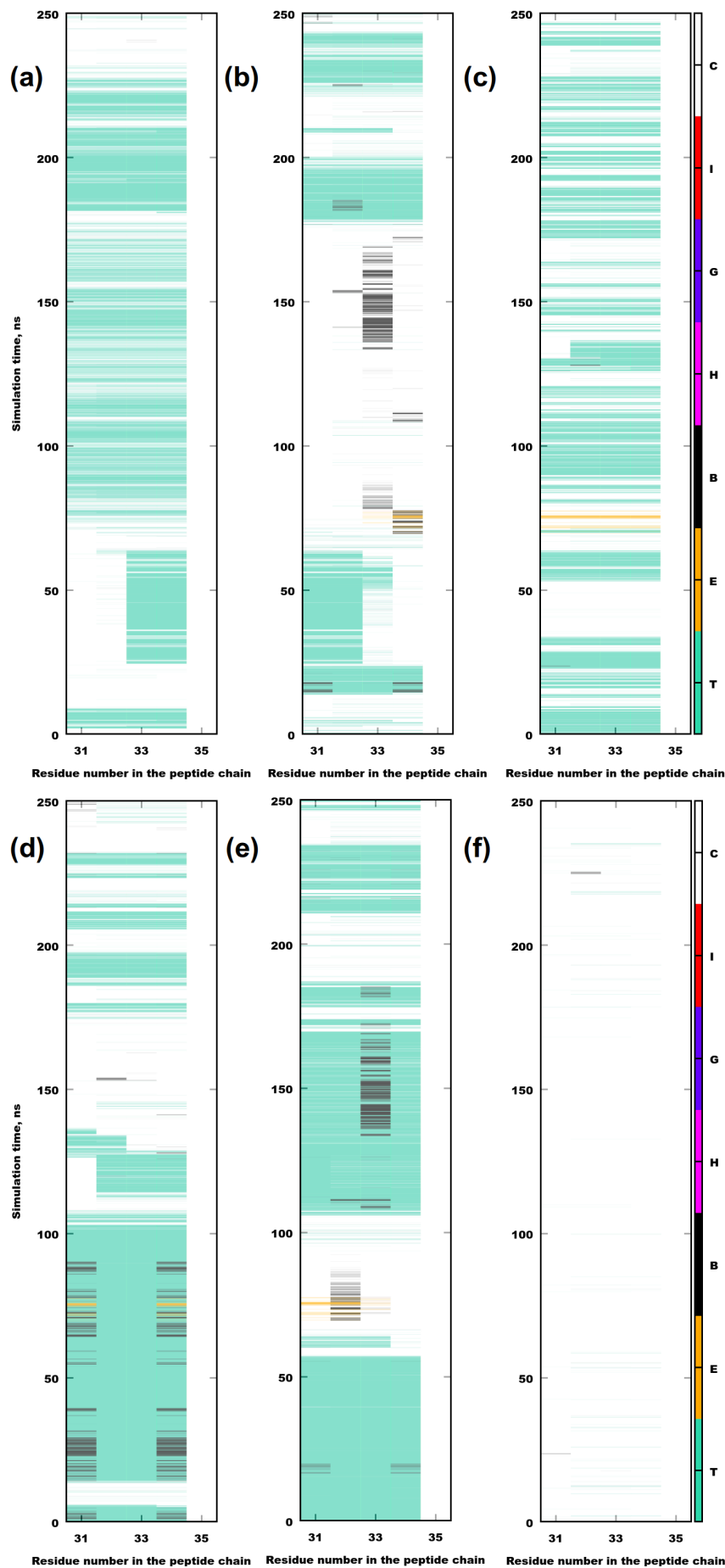


Figure S20: Secondary structures of A β (31 – 35) for the system containing 6 peptides and 6 molecules of cromolyn. Secondary structures are coded as the following: *T* - turn, *E* - extended conformation, *B* - isolated β -bridge, *H* - α -helix, *G* - 3_{10} -helix, *I* - π -helix, *C* - coil. Letters (a)-(f) are denoting separate peptides.

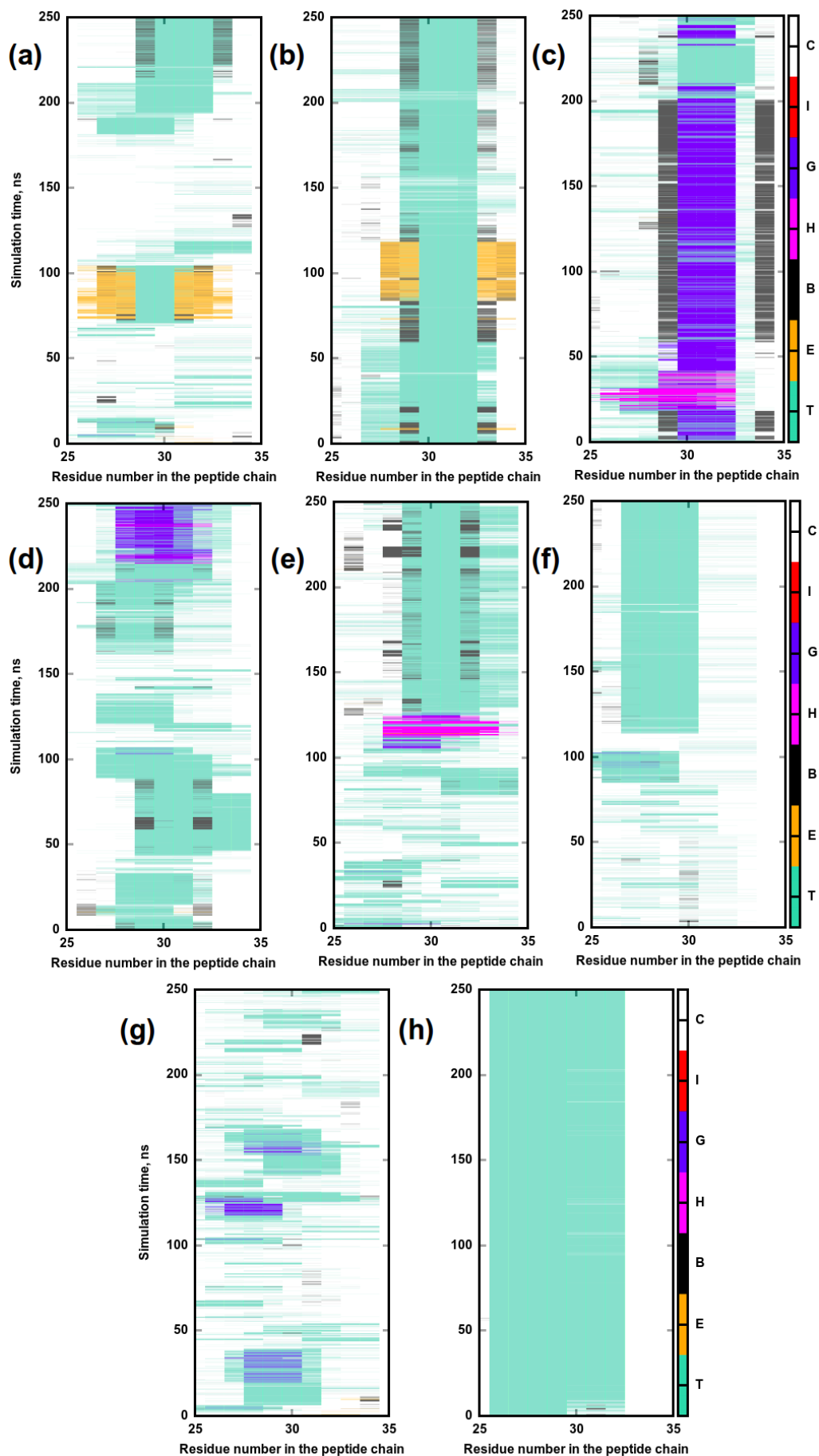


Figure S21: Secondary structures of Aβ(25 – 35) for the system containing 8 peptides and 8 molecules of cromolyn. Secondary structures are coded as the following: *T* - turn, *E* - extended conformation, *B* - isolated β-bridge, *H* - α-helix, *G* - 3₁₀-helix, *I* - π-helix, *C* - coil. Letters (a)-(h) are denoting separate peptides.

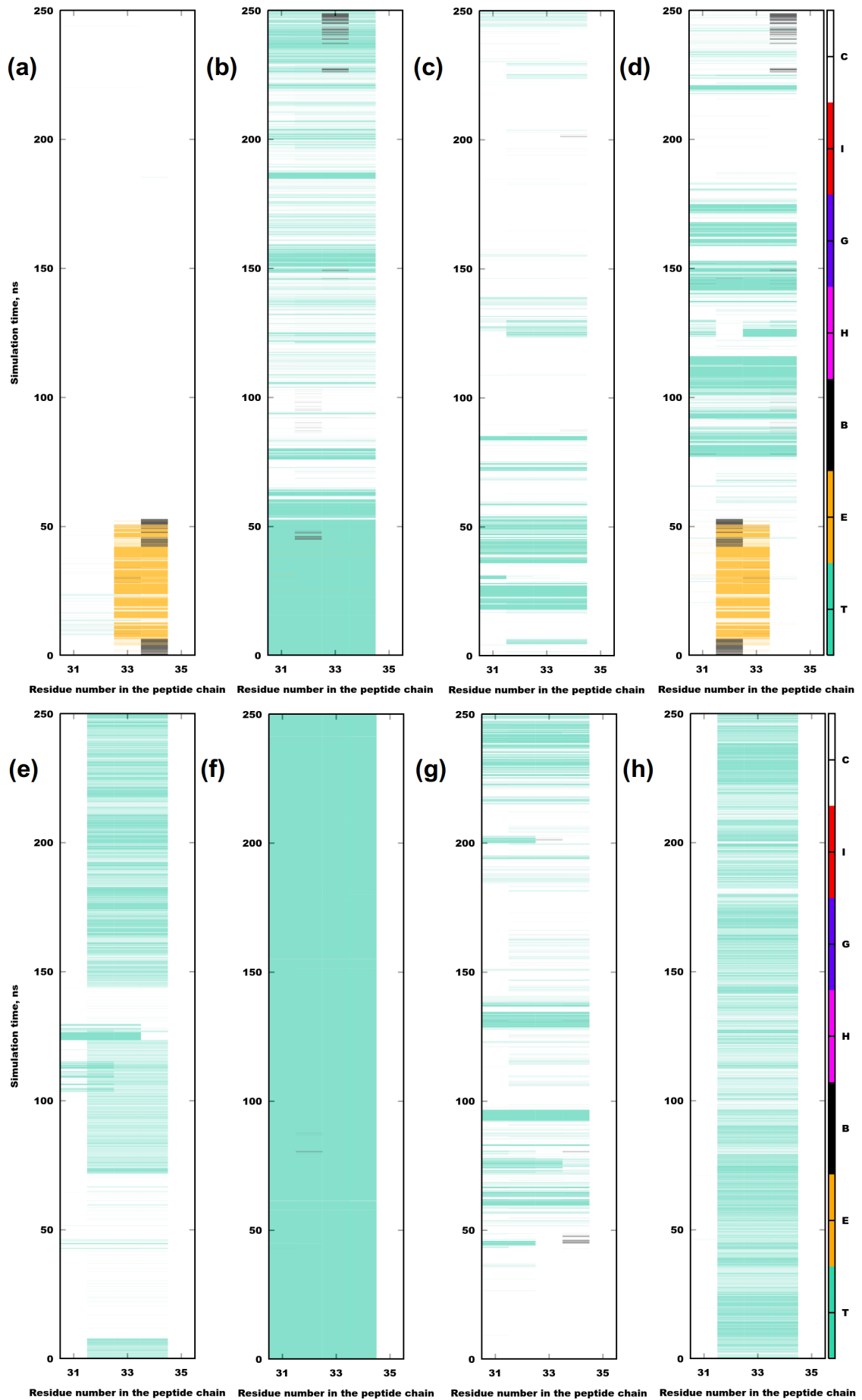


Figure S22: Secondary structures of A β (31-35) for the system containing 8 peptides and 8 molecules of cromolyn. Secondary structures are coded as the following: *T* - turn, *E* - extended conformation, *B* - isolated β -bridge, *H* - α -helix, *G* - 3_{10} -helix, *I* - π -helix, *C* - coil. Letters (a)-(h) are denoting separate peptides.

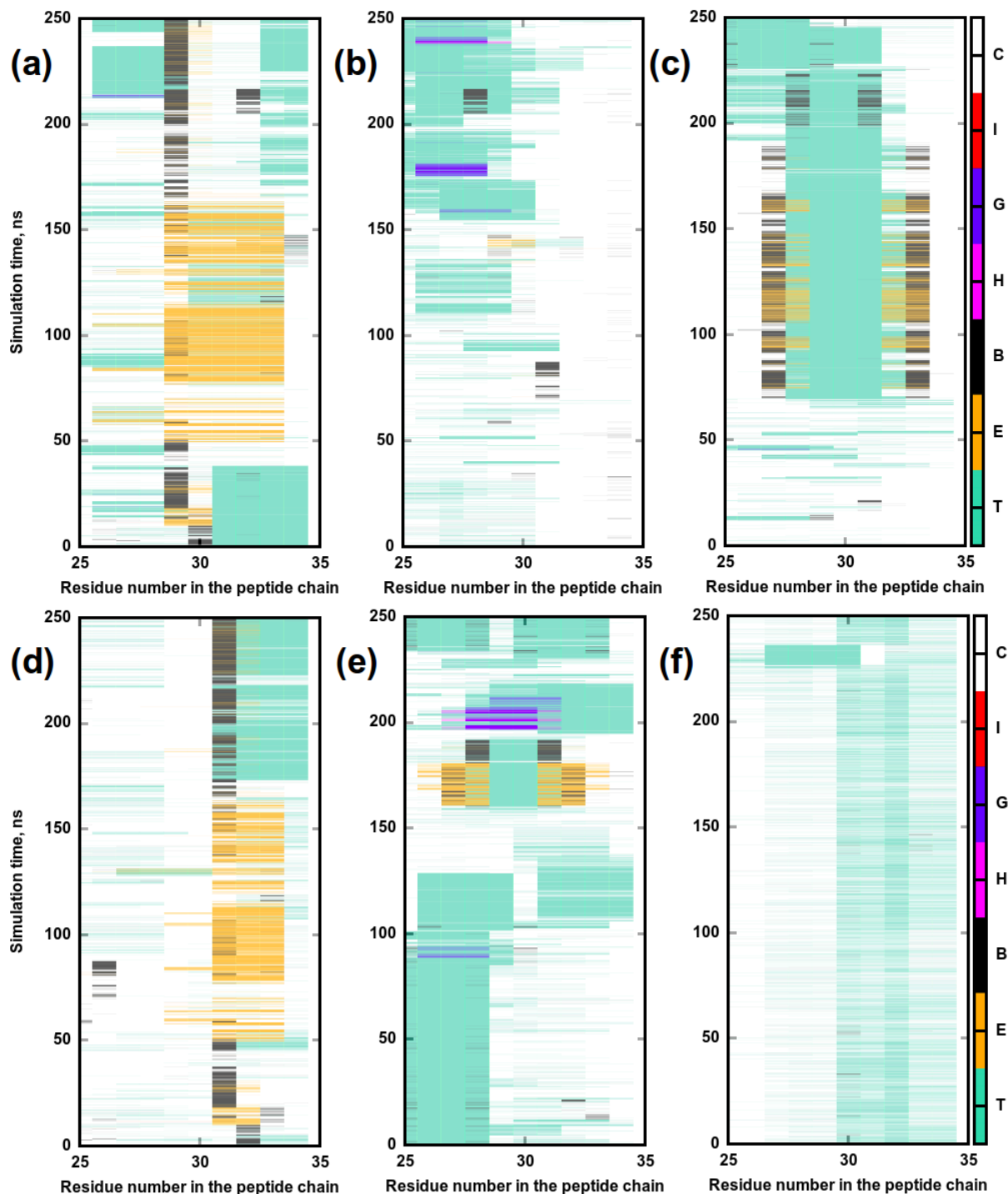


Figure S23: Secondary structures of A β (25 – 35) for the system containing 6 peptides and 6 molecules of atorvastatin. Secondary structures are coded as the following: *T* - turn, *E* - extended conformation, *B* - isolated β -bridge, *H* - α -helix, *G* - 3_{10} -helix, *I* - π -helix, *C* - coil. Letters (a)-(f) are denoting separate peptides.

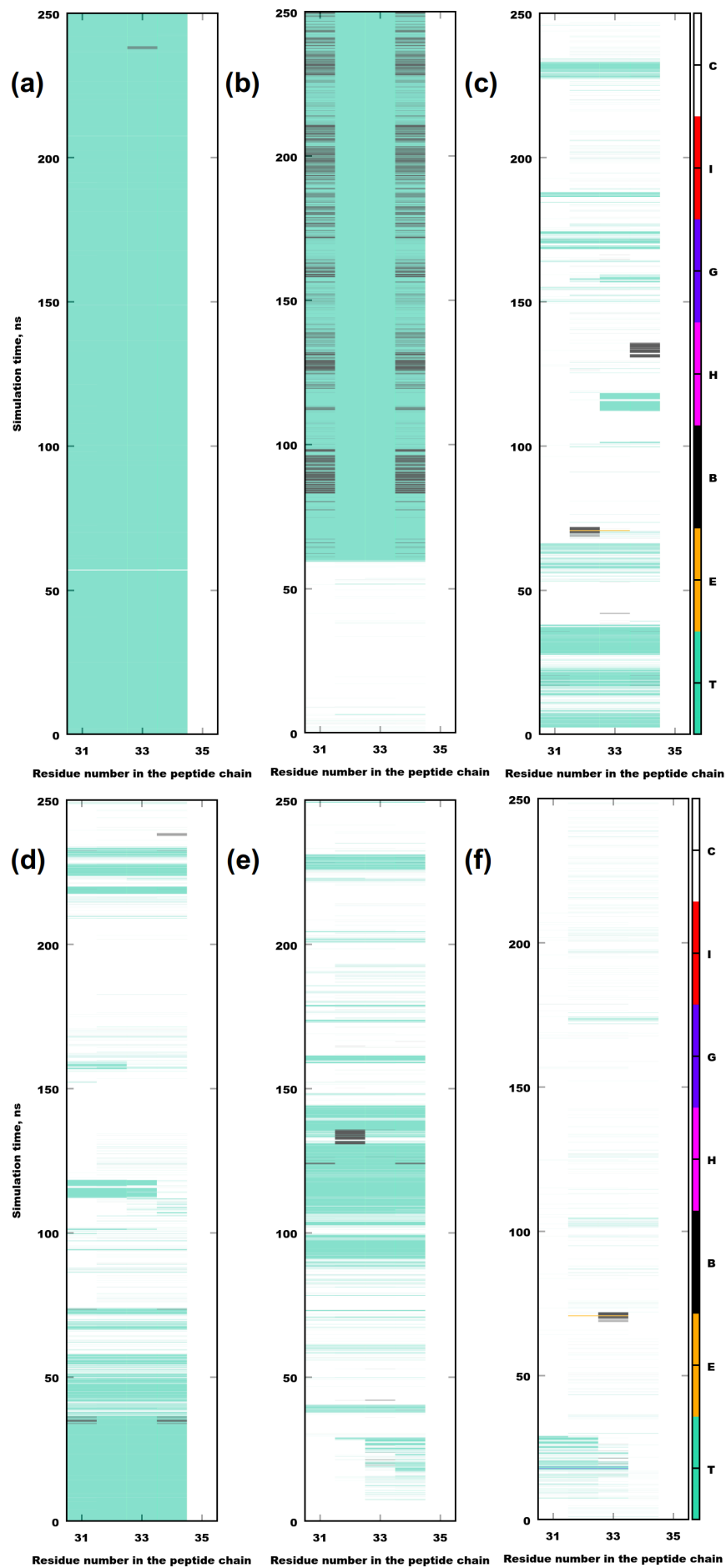


Figure S24: Secondary structures of A β (31 – 35) for the system containing 6 peptides and 6 molecules of atorvastatin. Secondary structures are coded as the following: *T* - turn, *E* - extended conformation, *B* - isolated β -bridge, *H* - α -helix, *G* - 3_{10} -helix, *I* - π -helix, *C* - coil. Letters (a)-(f) are denoting separate peptides.

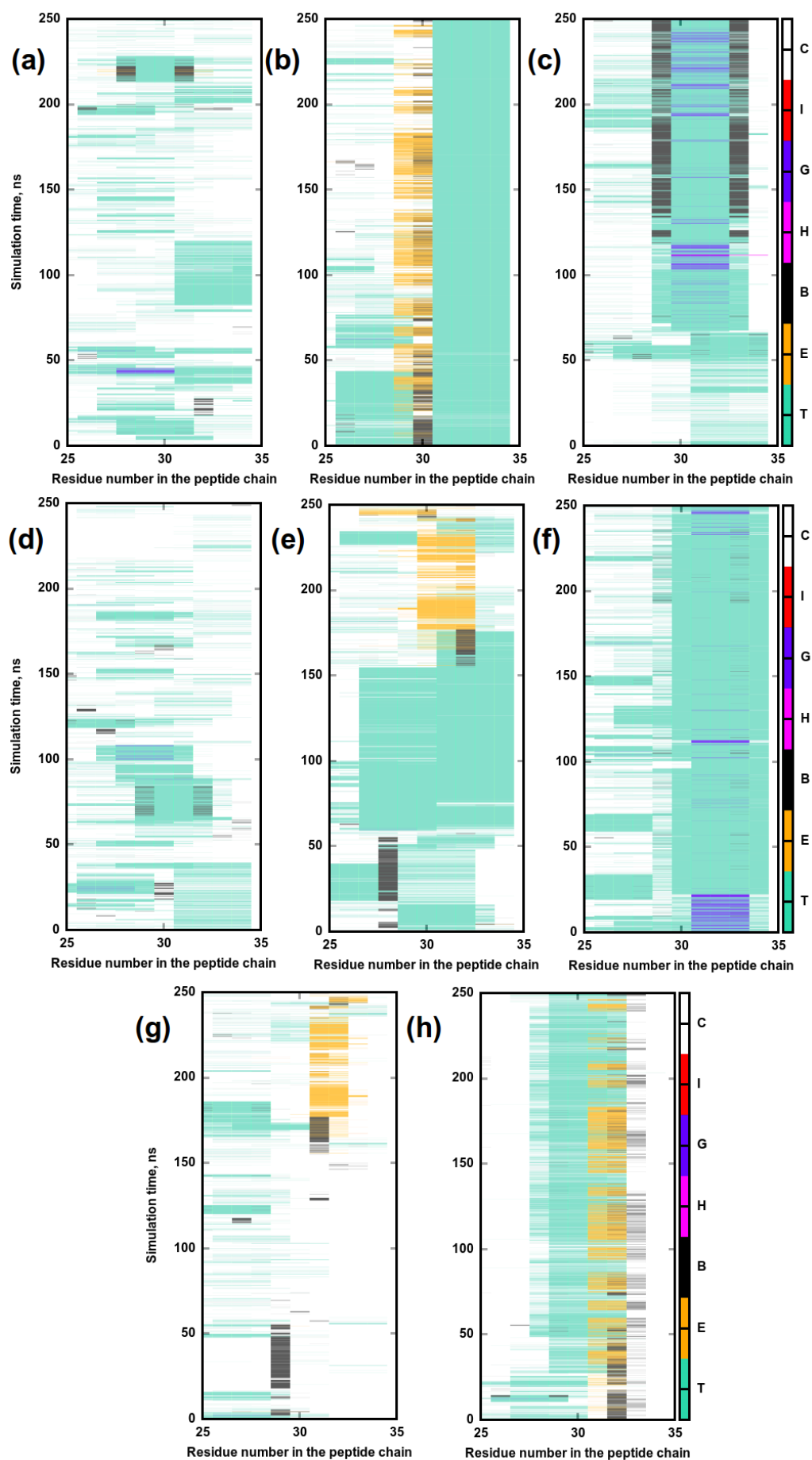


Figure S25: Secondary structures of A β (25 – 35) for the system containing 8 peptides and 8 molecules of atorvastatin. Secondary structures are coded as the following: *T* - turn, *E* - extended conformation, *B* - isolated β -bridge, *H* - α -helix, *G* - 3_{10} -helix, *I* - π -helix, *C* - coil. Letters (a)-(h) are denoting separate peptides.

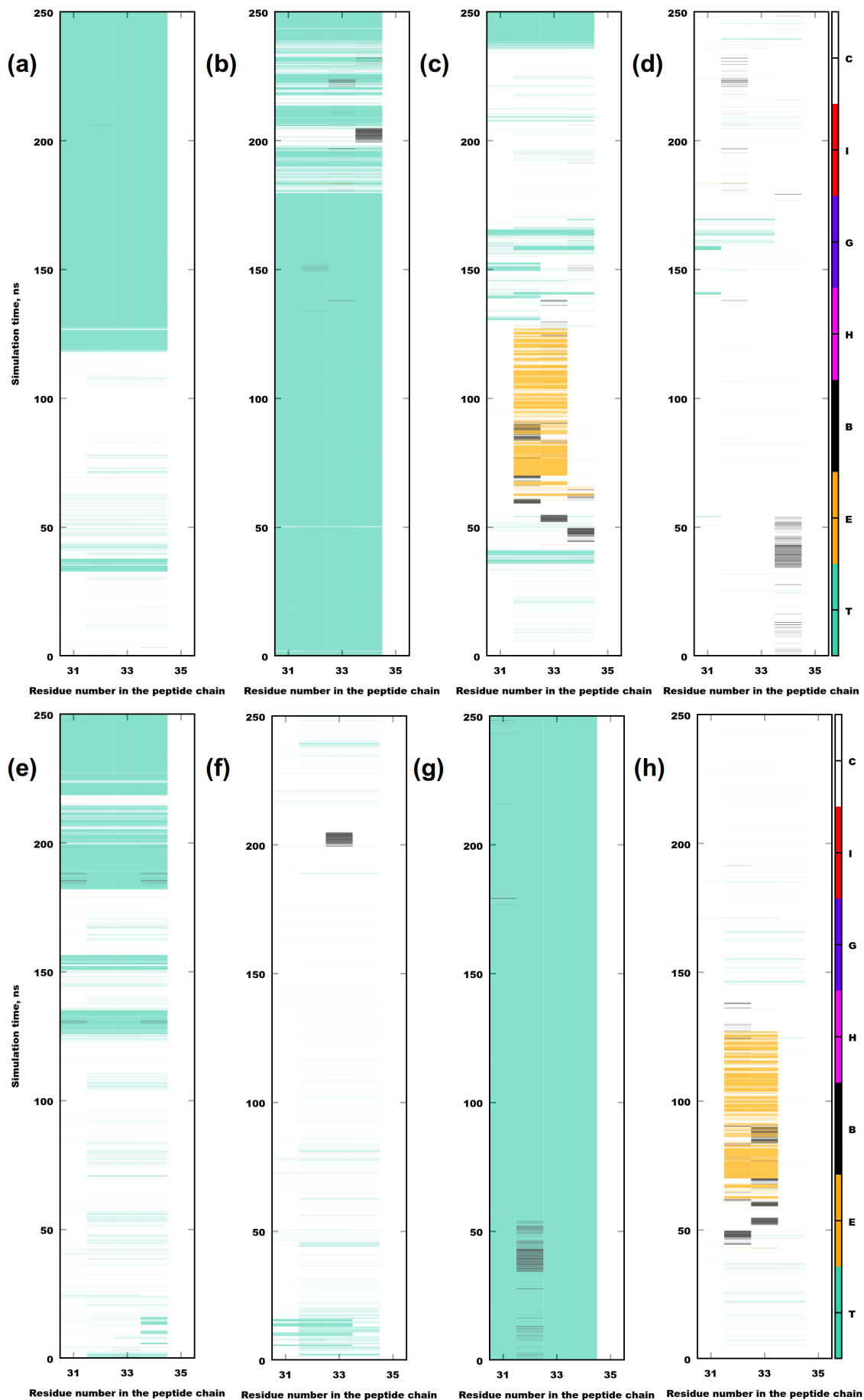


Figure S26: Secondary structures of A β (31 – 35) for the system containing 8 peptides and 8 molecules of atorvastatin. Secondary structures are coded as the following: *T* - turn, *E* - extended conformation, *B* - isolated β -bridge, *H* - α -helix, *G* - 3_{10} -helix, *I* - π -helix, *C* - coil. Letters (a)-(h) are denoting separate peptides.

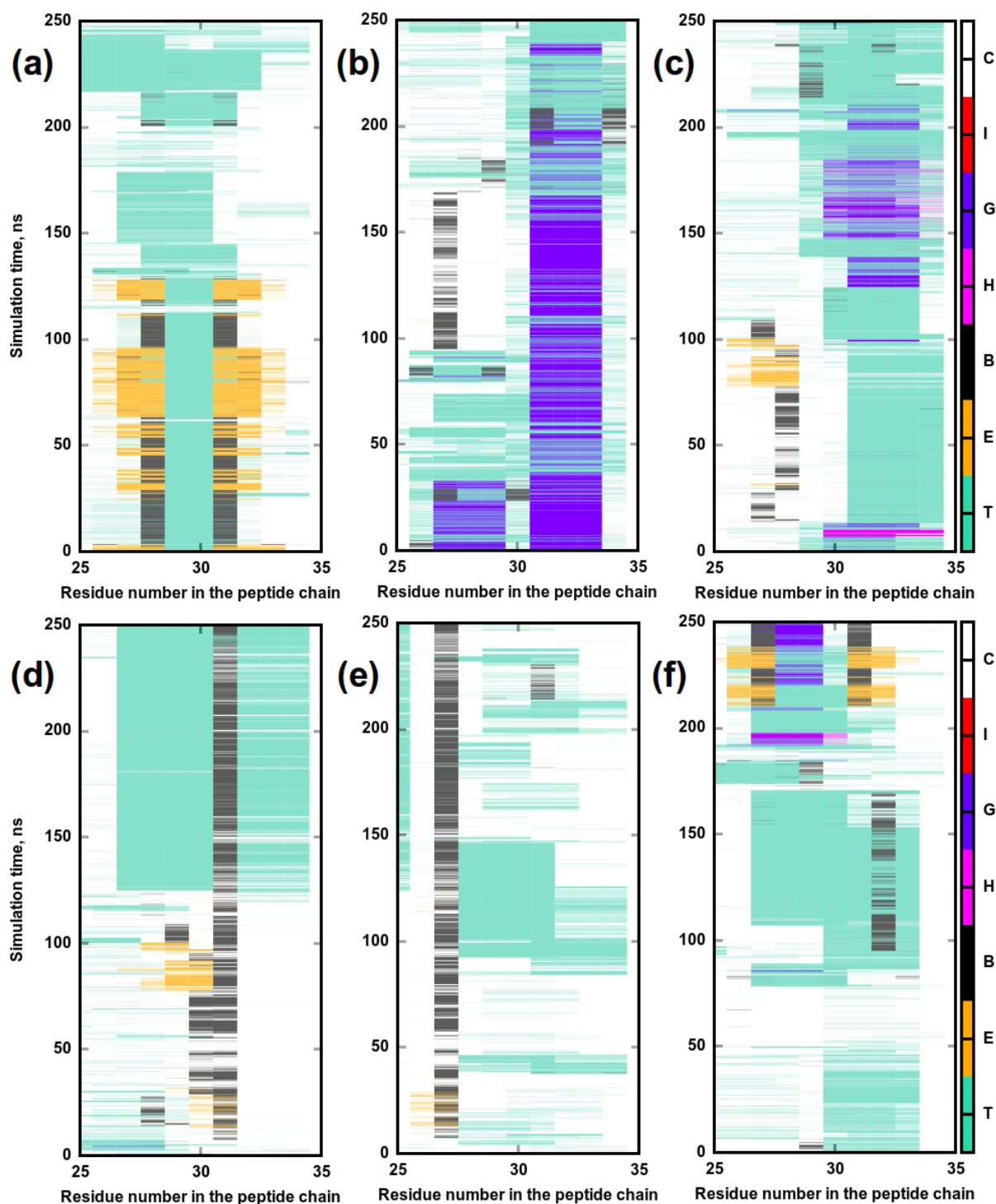


Figure S27: Secondary structures of A β (25 – 35) for the system containing 6 peptides and 6 molecules of lovastatin. Secondary structures are coded as the following: *T* - turn, *E* - extended conformation, *B* - isolated β -bridge, *H* - α -helix, *G* - 3_{10} -helix, *I* - π -helix, *C* - coil. Letters (a)-(f) are denoting separate peptides.

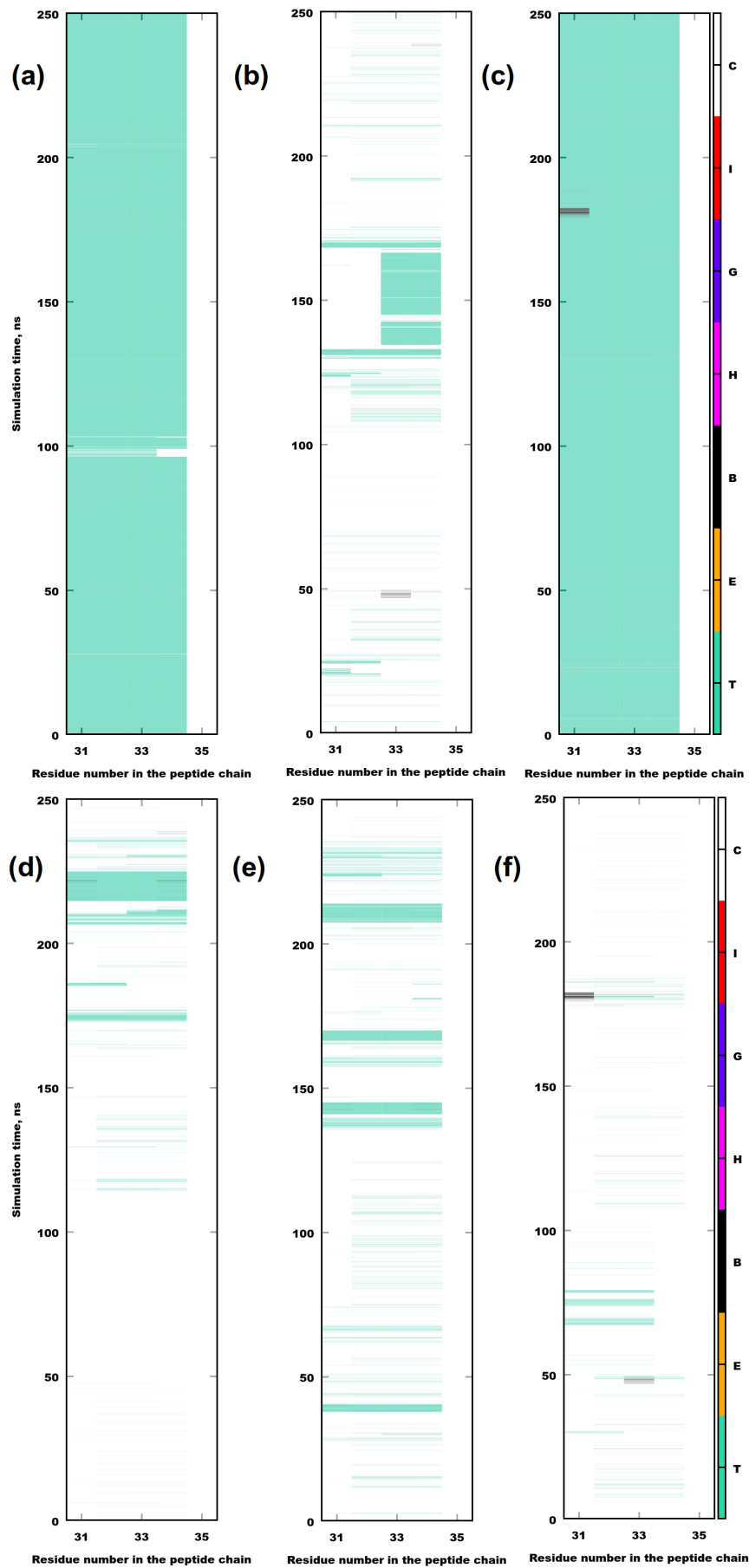


Figure S28: Secondary structures of A β (31 – 35) for the system containing 6 peptides and 6 molecules of lovastatin. Secondary structures are coded as the following: *T* - turn, *E* - extended conformation, *B* - isolated β -bridge, *H* - α -helix, *G* - 3_{10} -helix, *I* - π -helix, *C* - coil. Letters (a)-(f) are denoting separate peptides.

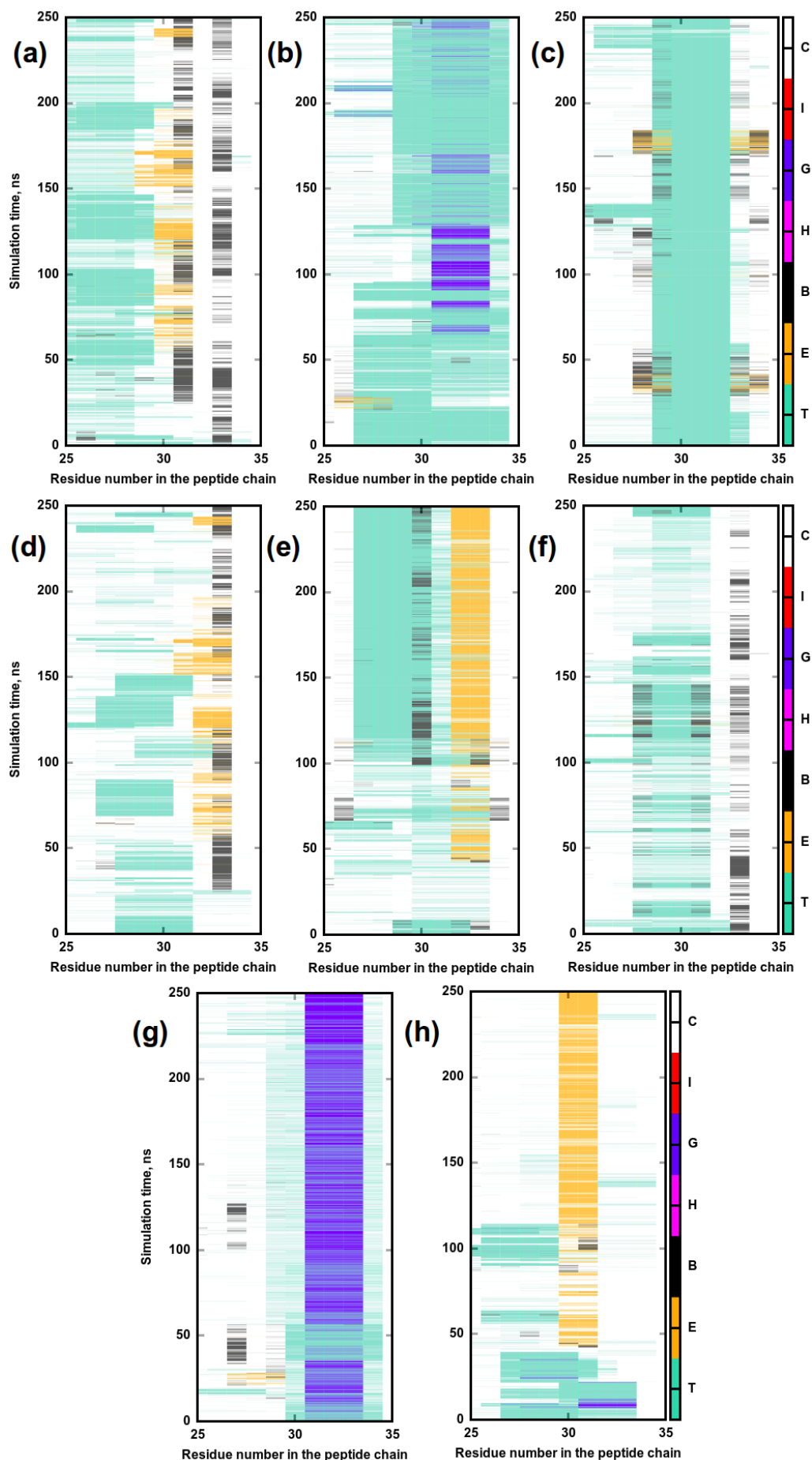


Figure S29: Secondary structures of A β (25 – 35) for the system containing 8 peptides and 8 molecules of lovastatin. Secondary structures are coded as the following: *T* - turn, *E* - extended conformation, *B* - isolated β -bridge, *H* - α -helix, *G* - 3_{10} -helix, *I* - π -helix, *C* - coil. Letters (a)-(h) are denoting separate peptides.

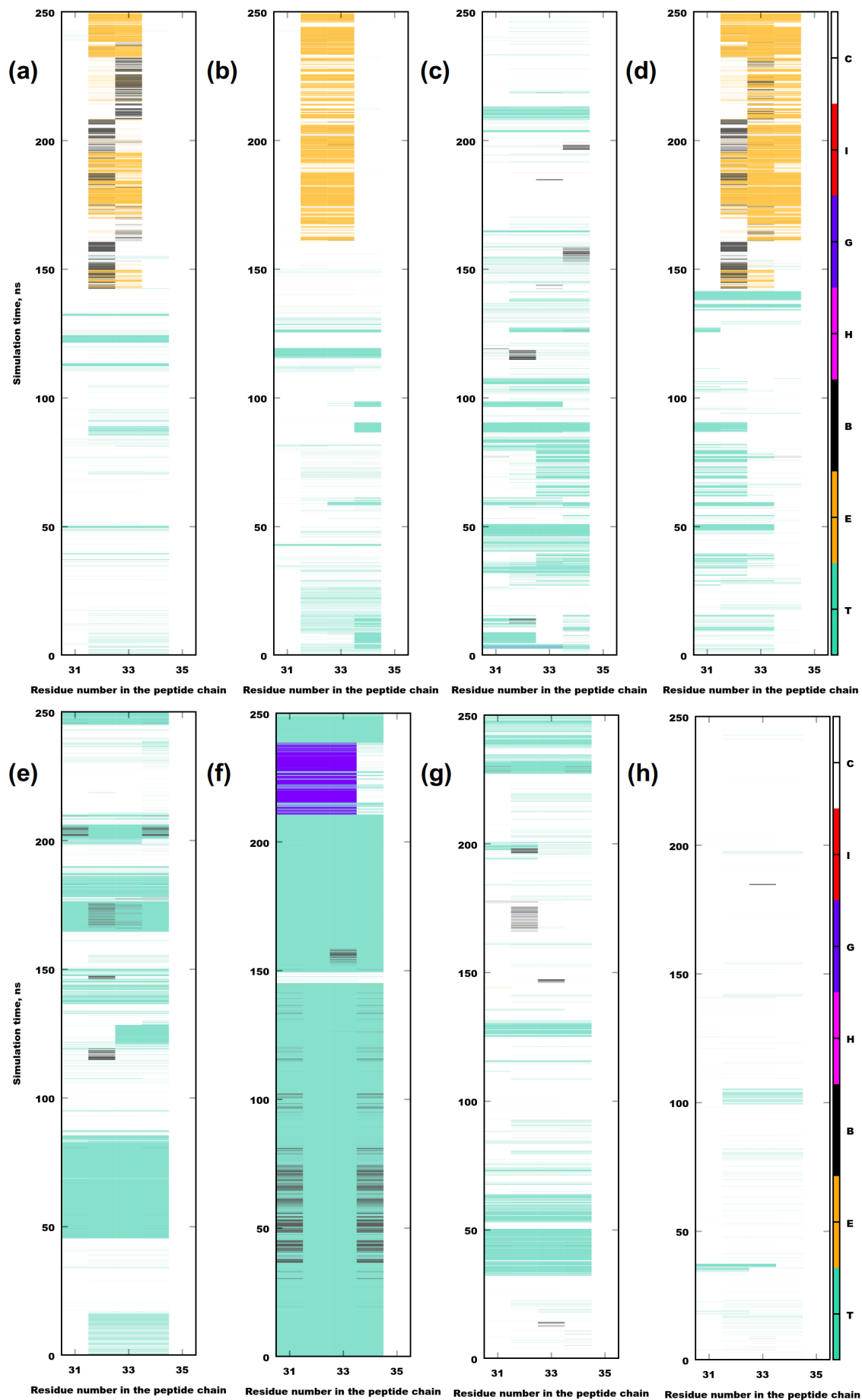


Figure S30: Secondary structures of A β (31-35) for the system containing 8 peptides and 8 molecules of lovastatin. Secondary structures are coded as the following: *T* - turn, *E* - extended conformation, *B* - isolated β -bridge, *H* - α -helix, *G* - 3_{10} -helix, *I* - π -helix, *C* - coil. Letters (a)-(h) are denoting separate peptides.

5 Well-tempered metadynamics: potential of mean force profiles

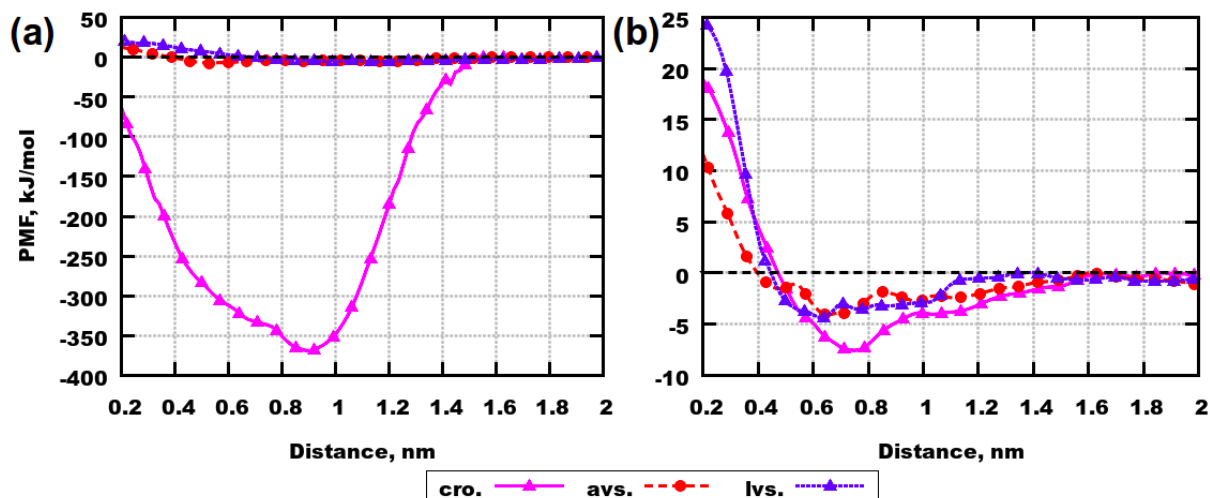


Figure S31: Potential of mean force profiles for CV2. (a) Systems with A β (25–35). (b) Systems with A β (31–35). Abbreviations mean the following: "cro." - systems containing cromolyn, "avs." - systems containing atorvastatin, "lvs." - systems containing lovastatin.