CHARMM-GUI Input Generator for NAMD, GROMACS, AMBER, OpenMM, and CHARMM/OpenMM Simulations using the CHARMM36 Additive Force Field

Jumin Lee,[1] Xi Cheng,[1] Jason M. Swails,[2] Min Sun Yeom,[3] Peter K. Eastman,[4] Justin A. Lemkul,[5] Shuai Wei,[6] Joshua Buckner,[6] Jong Cheol Jeong,[7] Yifei Qi,[1] Sunhwan Jo,[8] Vijay S. Pande,[4] David A. Case,[2] Charles L. Brooks III,[6] Alexander D. MacKerell Jr.,[5] Jeffery B. Klauda,[9] and Wonpil Im[1]*

[1]Department of Molecular Biosciences and Center for Computational Biology, The University of Kansas, Lawrence, KS 66047, USA
[2]Department of Chemistry and Chemical Biology, Rutgers University, Piscataway, NJ 08854, USA
[3]Korean Institute of Science and Technology Information, Yuseong-gu, Daejeon 305-806, Korea
[4]Department of Bioengineering, Stanford University, Stanford, CA 94035, USA
[5]Department of Pharmaceutical Sciences, School of Pharmacy, University of Maryland, Baltimore, MD 21201, USA
[6]Department of Chemistry and the Biophysics Program, University of Michigan, Ann Arbor, MI 48109, USA
[7]Cancer Research Institute, Beth Israel Deaconess Cancer Center, Harvard Medical School, Boston, MA 02215, USA
[8]Leadership Computing Facility, Argonne National Laboratory, 9700 Cass Ave Bldg. 240, Argonne, IL 60439, USA
[9]Department of Chemical and Biomolecular Engineering and the Biophysics Program, University of Maryland, College Park, MD 20742, USA

*To whom correspondence should be addressed: Tel: +1-785-864-1993; Fax: +1-785-864-5558; e-mail: wonpil@ku.edu

Table S1. DPPC bilayer properties obtained from each program.

Programs	Abbreviations	SA/Lipid (Å^2)	Compressibility (dyn/cm)
NAMD	N-fsw-1	64.8 ± 0.1	222.5 ± 9.5
	N-fsw-2	62.9 ± 0.1	227.1 ± 7.1
	N-fsw-3	61.6 ± 0.1	242.4 ± 20.9
GROMACS Mixed precision	Gm-fsw-1	63.6 ± 0.1	212.6 ± 6.2
	Gm-fsw-2	61.2 ± 0.1	213.9 ± 7.6
	Gm-fsw-3	60.3 ± 0.1	212.4 ± 6.8
	Gm-sw-1	60.6 ± 0.1	212.2 ± 20.2
	Gm-sw-2	58.8 ± 0.2	167.7 ± 16.1
	Gm-sw-3	58.0 ± 0.3[a] 51.0 ± 1.7[b]	gel formation
GROMACS Double precision	Gd-fsw-1	63.4 ± 0.1	210.9 ± 8.4
	Gd-fsw-2	61.1 ± 0.1	212.1 ± 8.6
	Gd-fsw-3	60.4 ± 0.1	228.1 ± 16.6
	Gd-sw-1	60.4 ± 0.1	218.2 ± 13.5
	Gd-sw-2	59.1 ± 0.1	207.0 ± 12.2
	Gd-sw-3	58.4[a,c] 49.3 ± 0.4[b]	gel formation
AMBER	A-0.5-1	62.6 ± 0.1	234.5 ± 17.2
	A-0.5-2	60.2 ± 0.2	228.6 ± 18.3
	A-0.5-3	59.2 ± 0.1[a] 50.76[b,c]	gel formation
	A-1.0-1	62.7 ± 0.1	247.2 ± 11.8
	A-1.0-2	59.9 ± 0.1	272.0 ± 22.3
	A-1.0-3	58.7 ± 0.2	259.4 ± 33.8
OpenMM	O-fsw- 5	61.3 ± 0.2	250.3 ± 10.9
	O-fsw-10	61.6 ± 0.2	234.0 ± 21.7
	O-fsw-15	61.4 ± 0.2	248.6 ± 16.3
	O-fsw-100	61.6 ± 0.2	227.7 ± 12.4
CHARMM/OpenMM	CO-fsw-1	64.6 ± 0.2	227.8 ± 14.5
	CO-fsw-2	62.5 ± 0.1	238.3 ± 13.3
	CO-fsw-3	61.1 ± 0.2	240.0 ± 15.9
	CO-sw-1	61.4 ± 0.3	251.8 ± 17.5
	CO-sw-2	60.0 ± 0.2	213.2 ± 10.5
	CO-sw-3	58.9 ± 0.3	226.3 ± 25.2

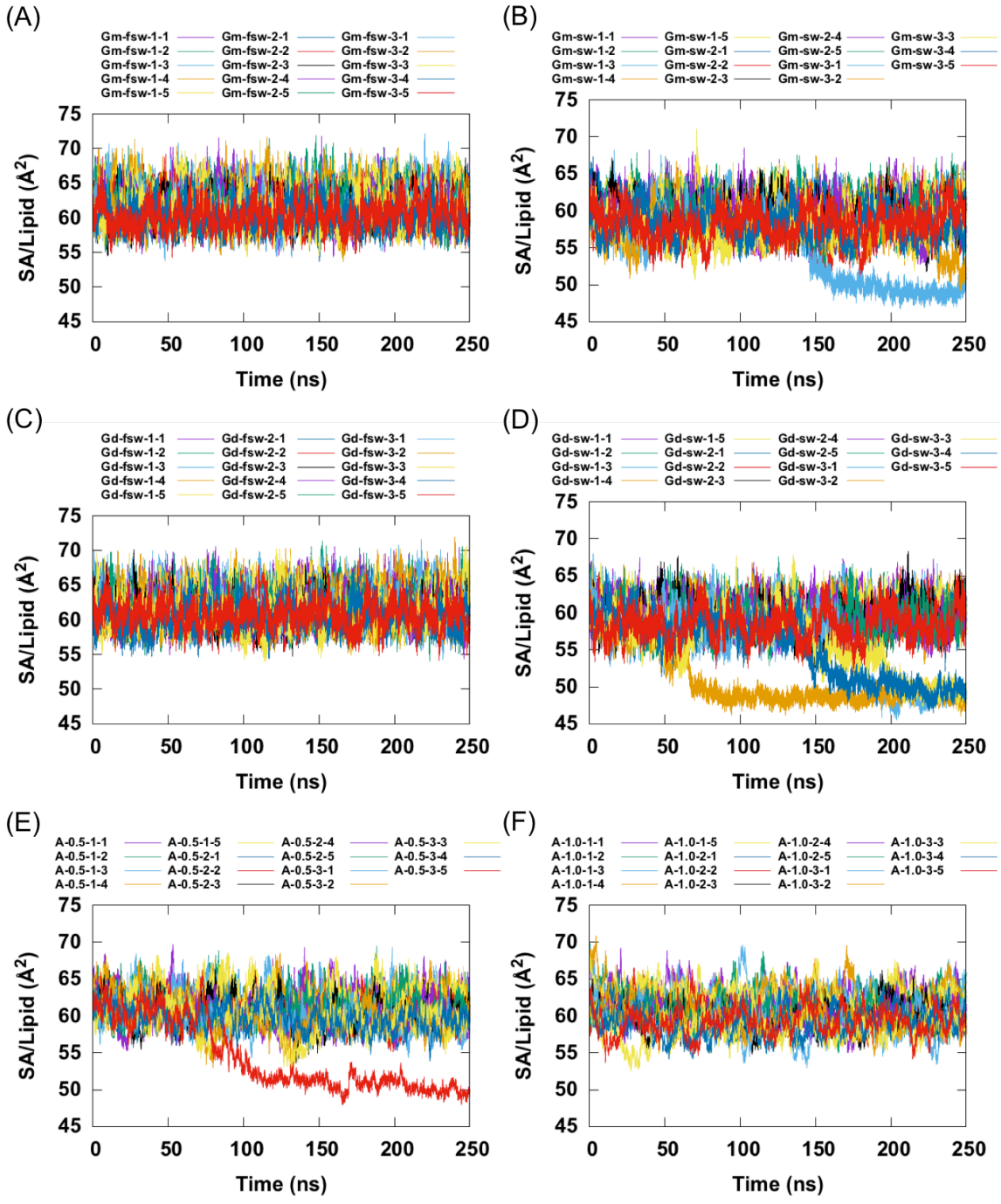
[a]liquid-phase property
[b]gel-phase property
[c]STE is not available because only one replica resulted in the particular phase among 5 replicas.

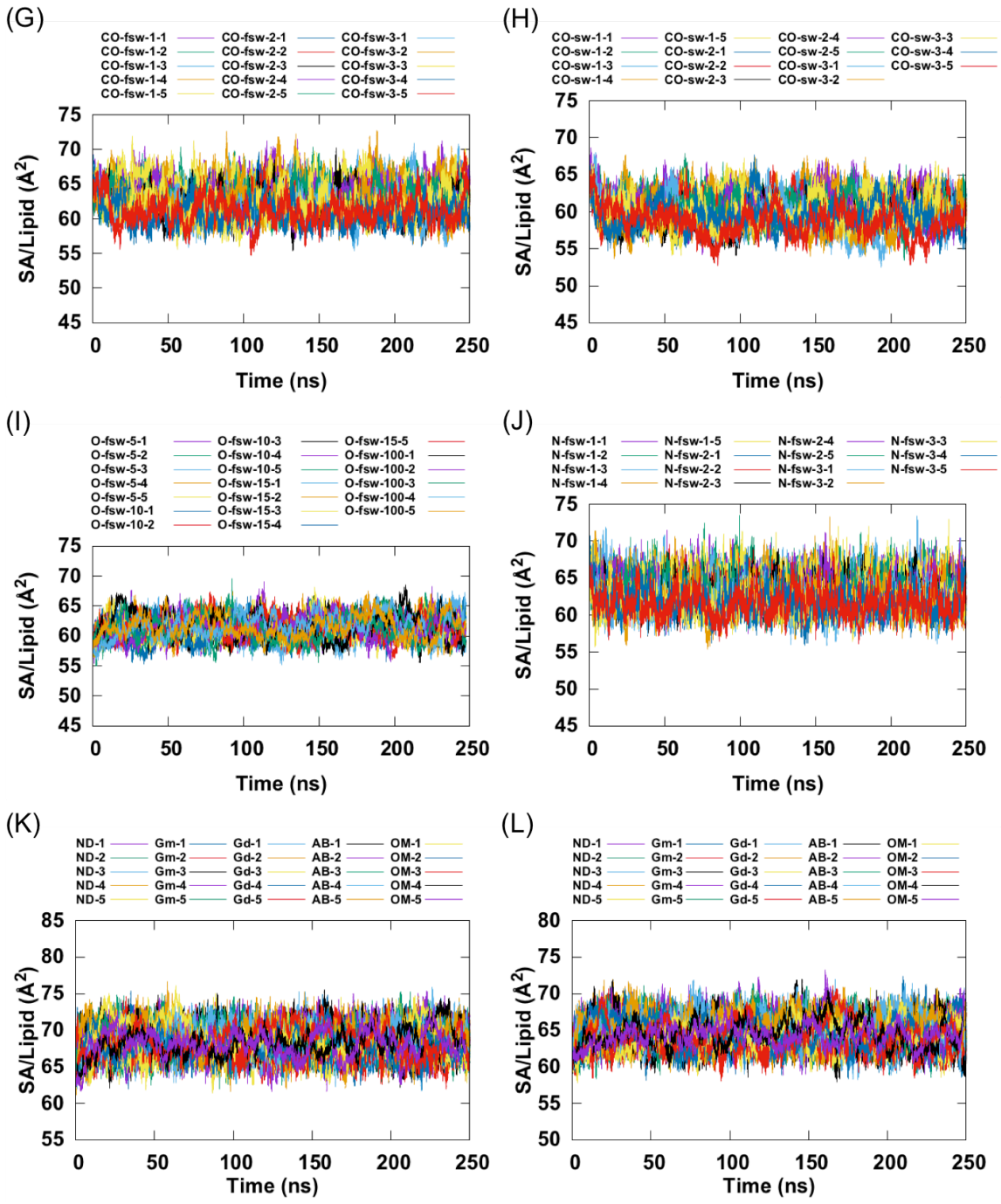
Table S2. Other lipid properties obtained from each program with the optimal protocols.

Lipids	Programs	SA/Lipid ($Å^2$)	Compressibility (dyn/cm)
DOPC	NAMD	68.7 ± 0.1	278.0 ± 13.4
	GROMACS-mixed	68.0 ± 0.1	255.5 ± 14.8
	GROMACS-double	68.0 ± 0.1	262.1 ± 18.5
	AMBER	69.7 ± 0.1	301.2 ± 12.3
	OpenMM	68.6 ± 0.2	259.5 ± 26.9
POPC	NAMD	65.0 ± 0.1	249.6 ± 19.7
	GROMACS-mixed	64.1 ± 0.2	262.5 ± 18.2
	GROMACS-double	64.1 ± 0.1	242.0 ± 9.30
	AMBER	66.0 ± 0.1	270.3 ± 18.3
	OpenMM	64.7 ± 0.1	274.6 ± 31.5
POPE	NAMD	57.8 ± 0.1	270.0 ± 15.8
	GROMACS-mixed	56.7 ± 0.1	270.1 ± 8.8
	GROMACS-double	56.6 ± 0.2	258.7 ± 18.2
	AMBER	58.1 ± 0.1	254.8 ± 4.4
	OpenMM	57.7 ± 0.1	266.4 ± 24.5
POPS	NAMD	56.9 ± 0.2	261.1 ± 22.8
	GROMACS-mixed	56.0 ± 0.4	262.1 ± 33.2
	GROMACS-double	56.2 ± 0.2	291.6 ± 41.4
	AMBER	59.0 ± 0.1	270.5 ± 28.5
	OpenMM	56.9 ± 0.5	274.0 ± 28.9
PSM	NAMD	55.2 ± 0.2	456.4 ± 64.8
	GROMACS-mixed	54.3 ± 0.2	445.4 ± 13.3
	GROMACS-double	54.6 ± 0.1	417.8 ± 43.0
	AMBER	56.6 ± 0.3	392.3 ± 49.9
	OpenMM	55.7 ± 0.2	403.2 ± 49.9

Table S3. The bilayer property comparison between each program and NAMD.

Lipids	GROMACS/NAMD		AMBER/NAMD		OpenMM/NAMD	
	A_L (%)	K_A (%)	A_L (%)	K_A (%)	A_L (%)	K_A (%)
DOPC	99.0	91.9	101.5	108.3	99.9	93.3
POPC	98.6	105.2	101.5	108.3	99.5	110.0
POPE	98.1	100.0	100.5	94.4	99.8	98.7
POPS	98.4	100.4	103.7	103.6	100.0	104.9
PSM	98.4	97.6	102.5	86.0	100.9	88.3


(A)
Gm-fsw-1-1 Gm-fsw-2-1 Gm-fsw-3-1
Gm-fsw-1-2 Gm-fsw-2-2 Gm-fsw-3-2
Gm-fsw-1-3 Gm-fsw-2-3 Gm-fsw-3-3
Gm-fsw-1-4 Gm-fsw-2-4 Gm-fsw-3-4
Gm-fsw-1-5 Gm-fsw-2-5 Gm-fsw-3-5
SA/Lipid (Å2)
Time (ns)
(B)
Gm-sw-1-1 Gm-sw-1-5 Gm-sw-2-4 Gm-sw-3-3
Gm-sw-1-2 Gm-sw-2-1 Gm-sw-2-5 Gm-sw-3-4
Gm-sw-1-3 Gm-sw-2-2 Gm-sw-3-1 Gm-sw-3-5
Gm-sw-1-4 Gm-sw-2-3 Gm-sw-3-2
SA/Lipid (Å2)
Time (ns)
(C)
Gd-fsw-1-1 Gd-fsw-2-1 Gd-fsw-3-1
Gd-fsw-1-2 Gd-fsw-2-2 Gd-fsw-3-2
Gd-fsw-1-3 Gd-fsw-2-3 Gd-fsw-3-3
Gd-fsw-1-4 Gd-fsw-2-4 Gd-fsw-3-4
Gd-fsw-1-5 Gd-fsw-2-5 Gd-fsw-3-5
SA/Lipid (Å2)
Time (ns)
(D)
Gd-sw-1-1 Gd-sw-1-5 Gd-sw-2-4 Gd-sw-3-3
Gd-sw-1-2 Gd-sw-2-1 Gd-sw-2-5 Gd-sw-3-4
Gd-sw-1-3 Gd-sw-2-2 Gd-sw-3-1 Gd-sw-3-5
Gd-sw-1-4 Gd-sw-2-3 Gd-sw-3-2
SA/Lipid (Å2)
Time (ns)
(E)
A-0.5-1-1 A-0.5-1-5 A-0.5-2-4 A-0.5-3-3
A-0.5-1-2 A-0.5-2-1 A-0.5-2-5 A-0.5-3-4
A-0.5-1-3 A-0.5-2-2 A-0.5-3-1 A-0.5-3-5
A-0.5-1-4 A-0.5-2-3 A-0.5-3-2
SA/Lipid (Å2)
Time (ns)
(F)
A-1.0-1-1 A-1.0-1-5 A-1.0-2-4 A-1.0-3-3
A-1.0-1-2 A-1.0-2-1 A-1.0-2-5 A-1.0-3-4
A-1.0-1-3 A-1.0-2-2 A-1.0-3-1 A-1.0-3-5
A-1.0-1-4 A-1.0-2-3 A-1.0-3-2
SA/Lipid (Å2)
Time (ns)


(G)
CO-fsw-1-1
CO-fsw-1-2
CO-fsw-1-3
CO-fsw-1-4
CO-fsw-1-5
CO-fsw-2-1
CO-fsw-2-2
CO-fsw-2-3
CO-fsw-2-4
CO-fsw-2-5
CO-fsw-3-1
CO-fsw-3-2
CO-fsw-3-3
CO-fsw-3-4
CO-fsw-3-5
SA/Lipid (Å2)
Time (ns)
(H)
CO-sw-1-1
CO-sw-1-2
CO-sw-1-3
CO-sw-1-4
CO-sw-1-5
CO-sw-2-1
CO-sw-2-2
CO-sw-2-3
CO-sw-2-4
CO-sw-2-5
CO-sw-3-1
CO-sw-3-2
CO-sw-3-3
CO-sw-3-4
CO-sw-3-5
SA/Lipid (Å2)
Time (ns)
(I)
O-fsw-5-1
O-fsw-5-2
O-fsw-5-3
O-fsw-5-4
O-fsw-5-5
O-fsw-10-1
O-fsw-10-2
O-fsw-10-3
O-fsw-10-4
O-fsw-10-5
O-fsw-15-1
O-fsw-15-2
O-fsw-15-3
O-fsw-15-4
O-fsw-15-5
O-fsw-100-1
O-fsw-100-2
O-fsw-100-3
O-fsw-100-4
O-fsw-100-5
SA/Lipid (Å2)
Time (ns)
(J)
N-fsw-1-1
N-fsw-1-2
N-fsw-1-3
N-fsw-1-4
N-fsw-1-5
N-fsw-2-1
N-fsw-2-2
N-fsw-2-3
N-fsw-2-4
N-fsw-2-5
N-fsw-3-1
N-fsw-3-2
N-fsw-3-3
N-fsw-3-4
N-fsw-3-5
SA/Lipid (Å2)
Time (ns)
(K)
ND-1
ND-2
ND-3
ND-4
ND-5
Gm-1
Gm-2
Gm-3
Gm-4
Gm-5
Gd-1
Gd-2
Gd-3
Gd-4
Gd-5
AB-1
AB-2
AB-3
AB-4
AB-5
OM-1
OM-2
OM-3
OM-4
OM-5
SA/Lipid (Å2)
Time (ns)
(L)
ND-1
ND-2
ND-3
ND-4
ND-5
Gm-1
Gm-2
Gm-3
Gm-4
Gm-5
Gd-1
Gd-2
Gd-3
Gd-4
Gd-5
AB-1
AB-2
AB-3
AB-4
AB-5
OM-1
OM-2
OM-3
OM-4
OM-5
SA/Lipid (Å2)
Time (ns)

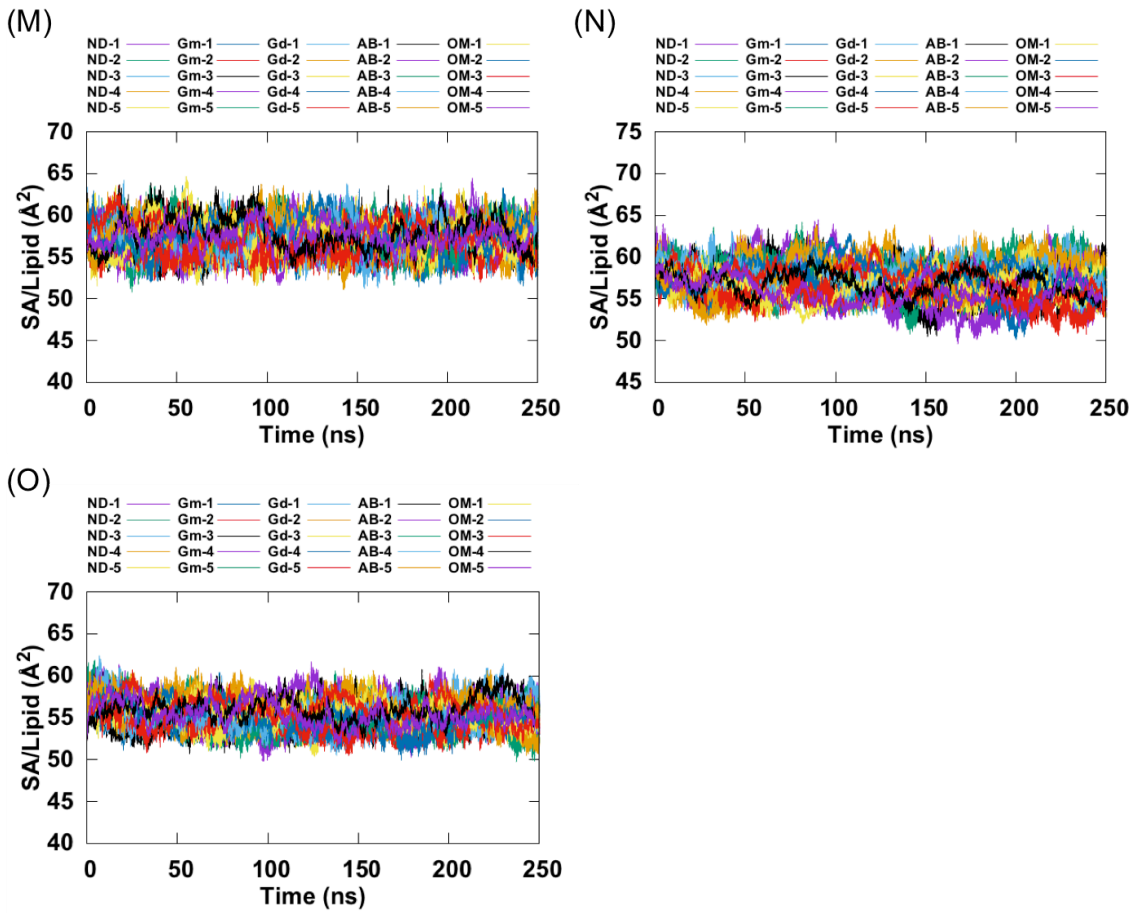
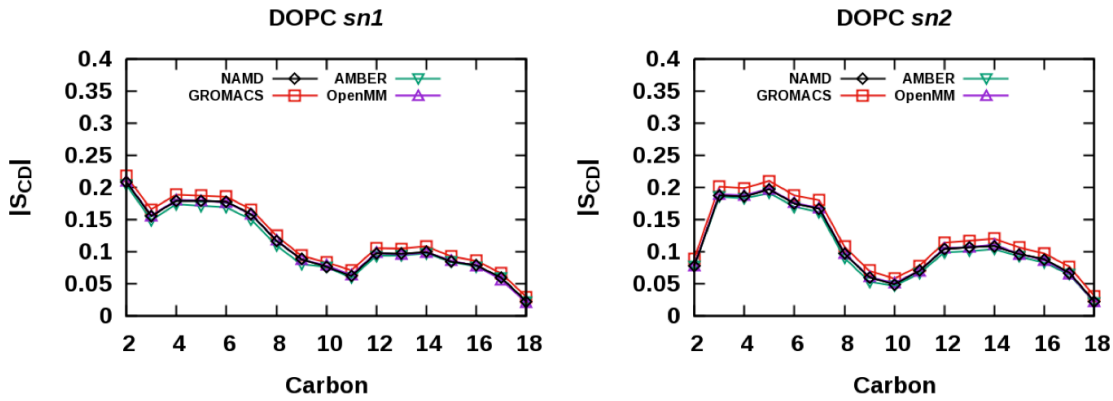
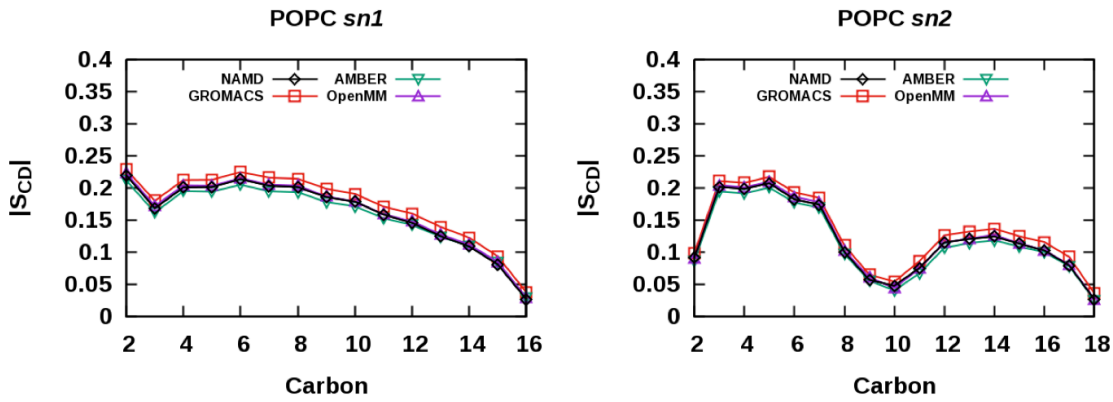


Figure S1. The time-series of surface area per lipid properties of (A-J) DPPC bilayer, (A) GROMACS mixed precision simulations with the force-based switching function, (B) GROMACS mixed precision simulations with the potential-based switching function, (C) GROMACS double precision simulations with the force-based switching function, (D) GROMACS double precision simulations with the potential-based switching function, (E) AMBER simulations with tau-p of 0.5 ps, (F) AMBER simulations with tau-p of 1.0 ps, (G) CHARMM/OpenMM simulations with the force-based switching function, (H) CHARMM/OpenMM simulations with the potential-based switching function, (I) OpenMM simulations, (J) NAMD simulations, (K) DOPC, (L) POPC, (M) POPE, (N) POPS, and (O) PSM bilayers.

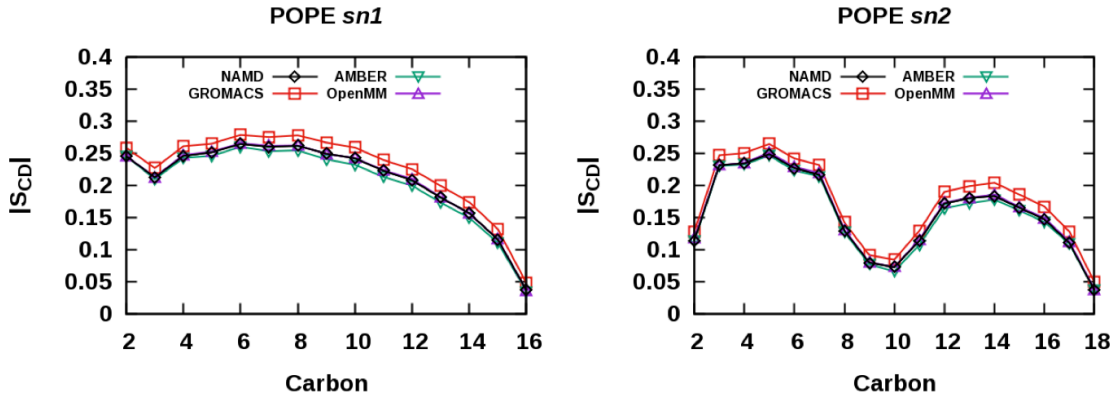
(A)


DOPC sn1
DOPC sn2
NAMD
AMBER
GROMACS
OpenMM
|SCD|
Carbon

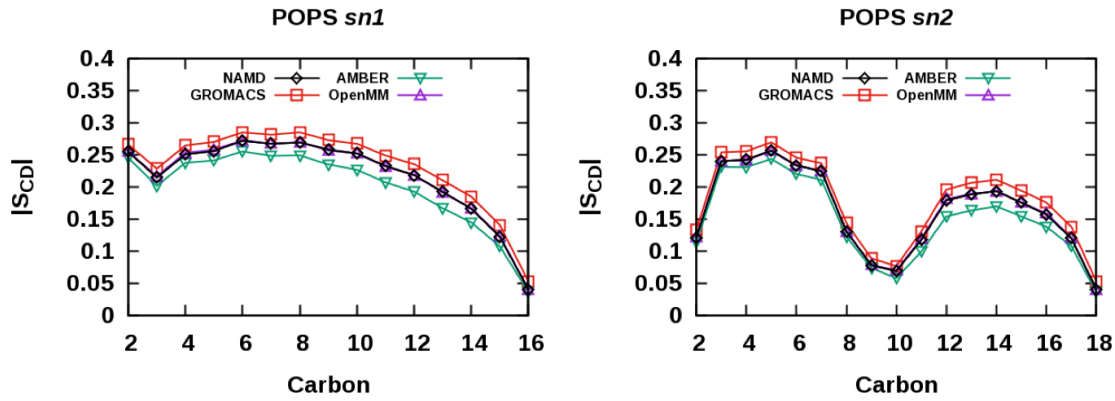
(B)


POPC sn1
POPC sn2
NAMD
AMBER
GROMACS
OpenMM
|SCD|
Carbon

(C)


POPE sn1
POPE sn2
NAMD
AMBER
GROMACS
OpenMM
|SCD|
Carbon

(D)



(E)

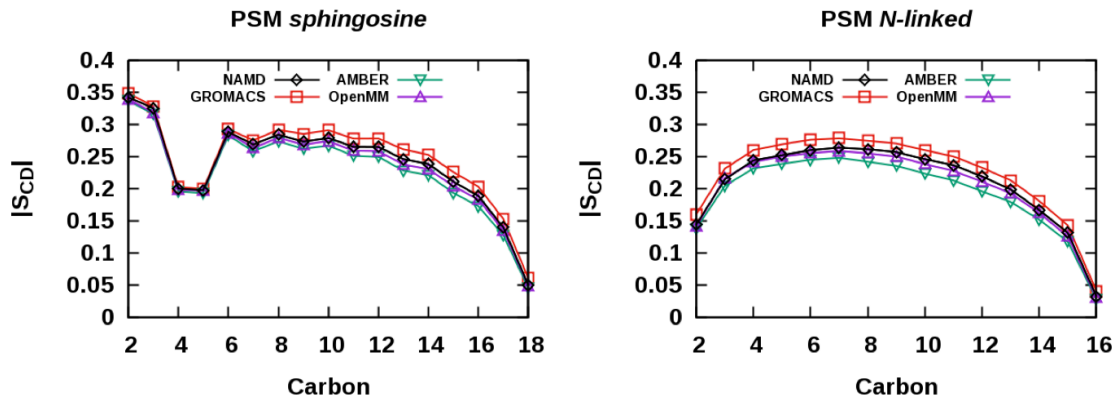


Figure S2. The S_{CD} order parameters of lipids derived from each program. (A) DOPC. (B) POPC. (C) POPE. (D) POPS. (E) PSM.