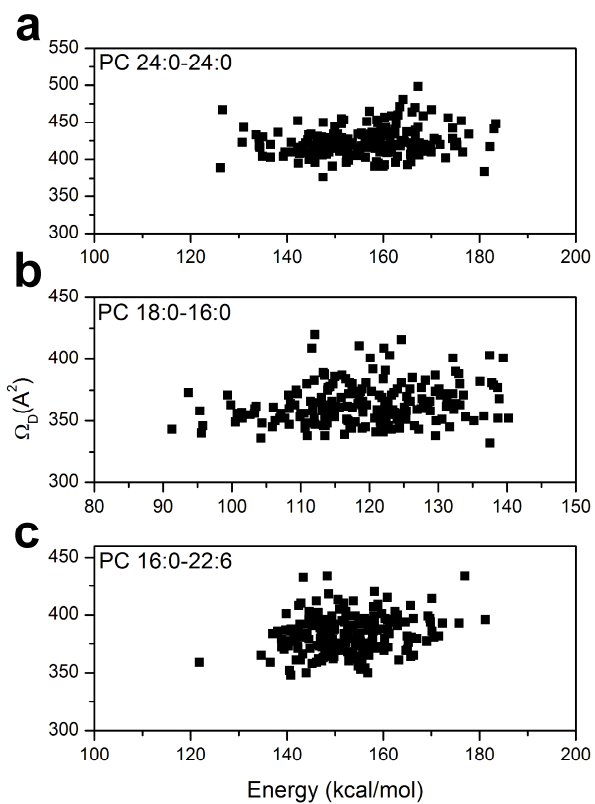


**Figure S1.** Scatter plots of collision cross sections vs. energy for 200 conformations sampled from MD simulations. a) 24:0-24:0 PC, b) 18:0-16:0 PC, and c) 16:0-22:6 PC

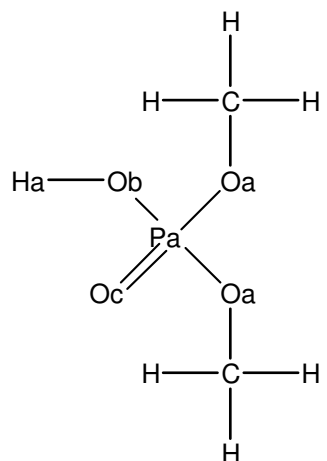


**Table S1.** Mass, drift time, and corrected drift time of ion molecule used in this study.

Name	cationization	<sup>c</sup> mass	<i>t<sub>d</sub></i> (ms)	<sup>d</sup> <i>t<sub>d</sub>'</i> (ms)
<sup>a</sup> 5:0-5:0 PC	H <sup>+</sup>	426	3.58	3.39
	Na <sup>+</sup>	448	3.97	3.77
<sup>a</sup> 8:0-8:0 PC	H <sup>+</sup>	510	4.99	4.78
	Na <sup>+</sup>	532	5.50	5.29
<sup>a</sup> 11:0-11:0 PC	H <sup>+</sup>	594	6.40	6.18
	Na <sup>+</sup>	616	6.85	6.62
<sup>a</sup> 14:0-16:0 PC	H <sup>+</sup>	706	8.06	7.82
	Na <sup>+</sup>	728	8.32	8.07
<sup>a</sup> 16:0-16:0 PC	H <sup>+</sup>	734	8.64	8.39
	Na <sup>+</sup>	756	8.77	8.51
<sup>a</sup> 18:0-14:0 PC	H <sup>+</sup>	734	8.58	8.33
	Na <sup>+</sup>	756	8.77	8.51
<sup>a,b</sup> 16:0-18:2 PC	H <sup>+</sup>	758	8.51	8.26
<sup>a</sup> 18:0-16:0 PC	H <sup>+</sup>	762	8.96	8.71
	Na <sup>+</sup>	784	9.15	8.89
<sup>a</sup> 16:0-20:4 PC	H <sup>+</sup>	782	8.58	8.32
<sup>a,b</sup> 18:0-18:2 PC	H <sup>+</sup>	786	8.90	8.64
<sup>a</sup> 18:0-18:1 PC	H <sup>+</sup>	788	8.96	8.70
<sup>a</sup> 18:0-18:0 PC	H <sup>+</sup>	790	9.41	9.15
<sup>a</sup> 16:0-22:6 PC	H <sup>+</sup>	806	8.83	8.57
<sup>a</sup> 24:0-24:0 PC	H <sup>+</sup>	958	12.2	11.9
<sup>b</sup> KK (cytC)	H <sup>+</sup>	275	1.86	1.70
<sup>b</sup> HK (cytC)	H <sup>+</sup>	284	1.86	1.70
<sup>b</sup> GKK (cytC)	H <sup>+</sup>	332	2.37	2.20
<sup>b</sup> GGGGGG	H <sup>+</sup>	362	2.18	2.00
<sup>b</sup> ATNE (cytC)	H <sup>+</sup>	434	3.20	3.01
<sup>b</sup> AAAAAA	H <sup>+</sup>	446	3.14	2.94
<sup>b</sup> KATNE (cytC)	H <sup>+</sup>	563	4.29	4.07
<sup>b</sup> Ac-GDVEK (cytC)	H <sup>+</sup>	590	4.80	4.58
<sup>b</sup> GITWK (cytC)	H <sup>+</sup>	605	5.12	4.89
<sup>b</sup> IFVQK (cytC)	H <sup>+</sup>	635	5.70	5.46
<sup>b</sup> YIPGTK (cytC)	H <sup>+</sup>	679	6.02	5.78
<sup>b</sup> MIFAGIK (cytC)	H <sup>+</sup>	780	7.36	7.10
<sup>b</sup> Bradykinin	H <sup>+</sup>	1061	10.2	9.94
<sup>b</sup> TGPNLHGLFGR (cytC)	H <sup>+</sup>	1169	11.8	11.5

<sup>a</sup>Molecules examined in this study. <sup>b</sup>Molecules used as calibrant. <sup>c</sup>All ions are singly charged. <sup>d</sup>Mass dependent corrected drift time.

**Table S2.** Optimized partial charge distribution of protonated phosphate from the DFT calculation of protonated dimethyl phosphate. The partial charges with atom types for CHARMM force field are tabulated.



	Mulliken Charge <sup>a</sup>	Force Field Charge	Force Field type
Pa	1.16	1.50	PL
Oa	-0.51	-0.49	OSL
Ob	-0.54	-0.52	OHL
Oc	-0.57	-0.56	O2L
Ha	0.35	0.36	HOL

<sup>a</sup>Computed from density functional theory (DFT) calculation using Jaguar 6.0 of Schroedinger company with B3LYP functional and 6-31G\*\* basis set.

**Table S3.**

Name	<sup>a</sup> Mass	Applied Voltage (V)	<i>t<sub>d</sub></i> (ms)	<sup>b</sup> <i>K<sub>0</sub></i> (cm <sup>2</sup> V <sup>-1</sup> s <sup>-1</sup> )
8:0-8:0 PC	510	7	6.46	0.447
		7.5	5.504	0.453
		8	4.99	0.448
		8.5	4.16	0.463
14:0-16:0 PC	706	7	10.8	0.344
		7.5	9.28	0.347
		8	8.06	0.350
		8.5	7.04	0.353
18:0-18:0 PC	790	7	12.3	0.323
		7.5	10.6	0.324
		8	9.41	0.324
		8.5	8.16	0.328

<sup>a</sup>All ions are singly charged. <sup>b</sup>Evaluated using equations from Shavartsburg and Smith.<sup>29</sup>