

**Influence of terahertz waves on the binding of choline to choline
acetyltransferase: insights from molecular dynamics simulations**

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Table S1 GROMACS parameters (including atom types, electric charges and mass) for choline.**We used RESP2 for the calculation of charge.**

No.	Type	Atom	Charge	Mass
1	Oh	O	-0.646070965	15.999405
2	N4	N	0.155798932	14.006703
3	C3	C	-0.420941554	12.010736
4	C3	C	-0.440659971	12.010736
5	C3	C	-0.245637696	12.010736
6	C3	C	0.356035158	12.010736
7	C3	C	-0.198375958	12.010736
8	Ho	H	0.431640718	1.007941
9	Hx	H	0.195700039	1.007941
10	Hx	H	0.195700039	1.007941
11	Hx	H	0.195700039	1.007941
12	Hx	H	0.209203437	1.007941
13	Hx	H	0.209203437	1.007941
14	Hx	H	0.209203437	1.007941
15	Hx	H	0.16150935	1.007941
16	Hx	H	0.16150935	1.007941
17	Hx	H	0.16150935	1.007941
18	H1	H	0.016704068	1.007941
19	H1	H	0.016704068	1.007941
20	Hx	H	0.137782362	1.007941
21	hx	H	0.137782362	1.007941

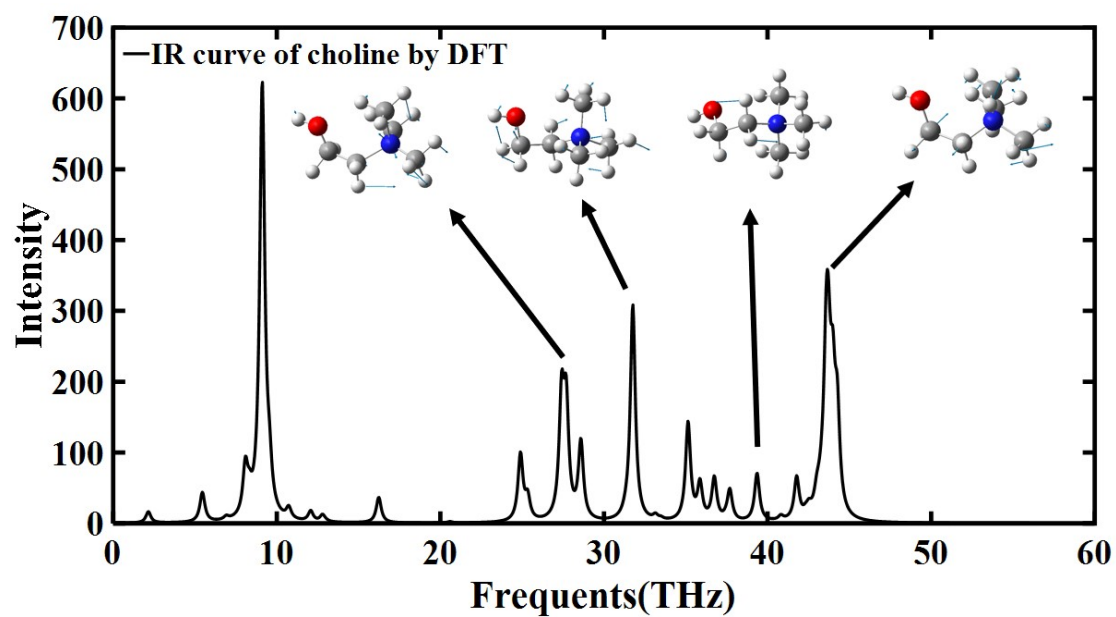


Figure S1 The vibration spectrum of choline calculated based on DFT, using the functional B3LYP, the basis set def2-TZVP, and the auxiliary basis set def2/J and D3BJ dispersion correction. We consider the stronger absorption peaks (45.3 THz).

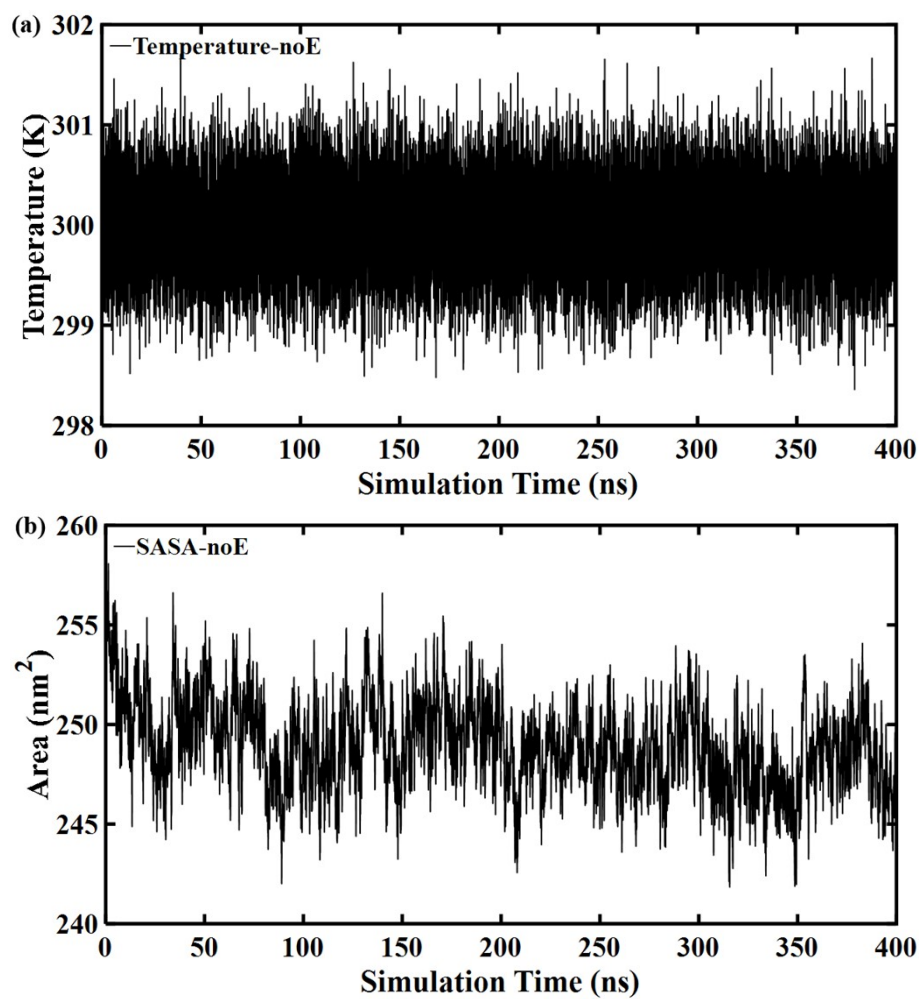


Figure S2 The change curves of system temperature (a) and SASA (b) with simulation time during the 400 ns MD simulation process. Each curve was plotted from the average of 3 sets. The average temperature of the system is 300.0442 K.

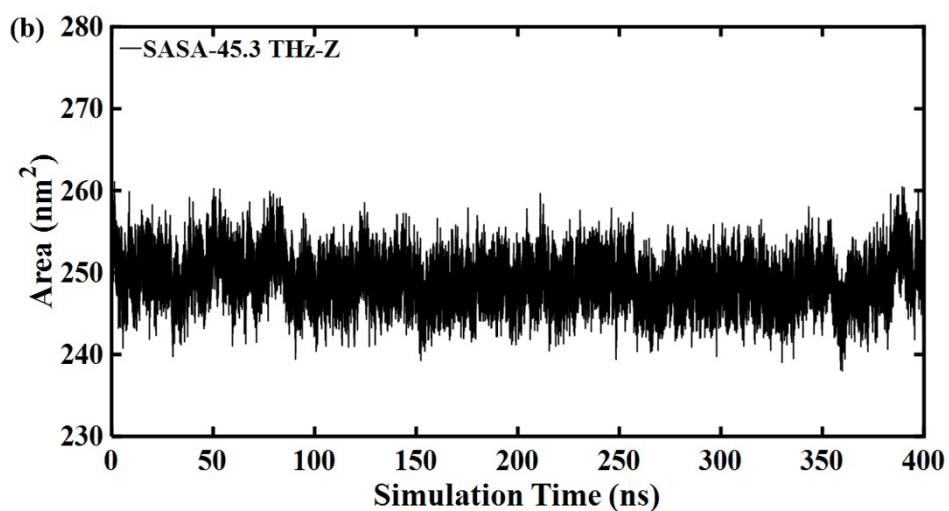
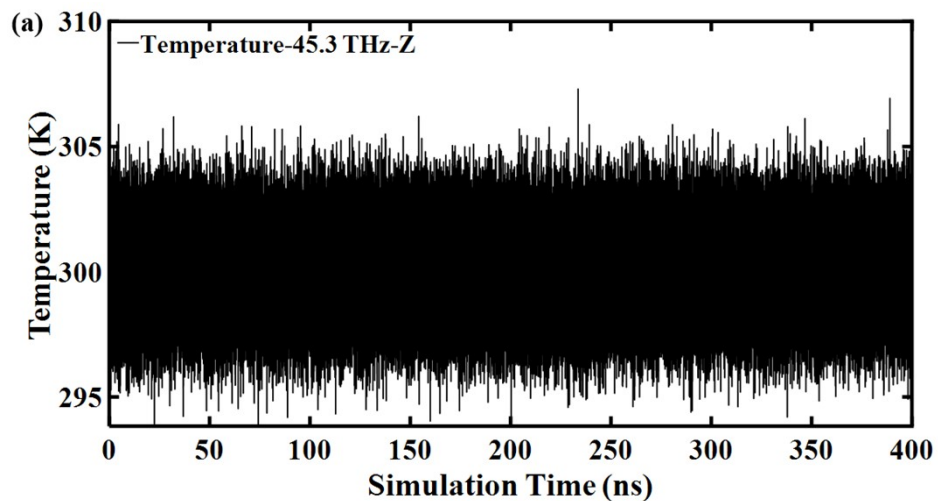
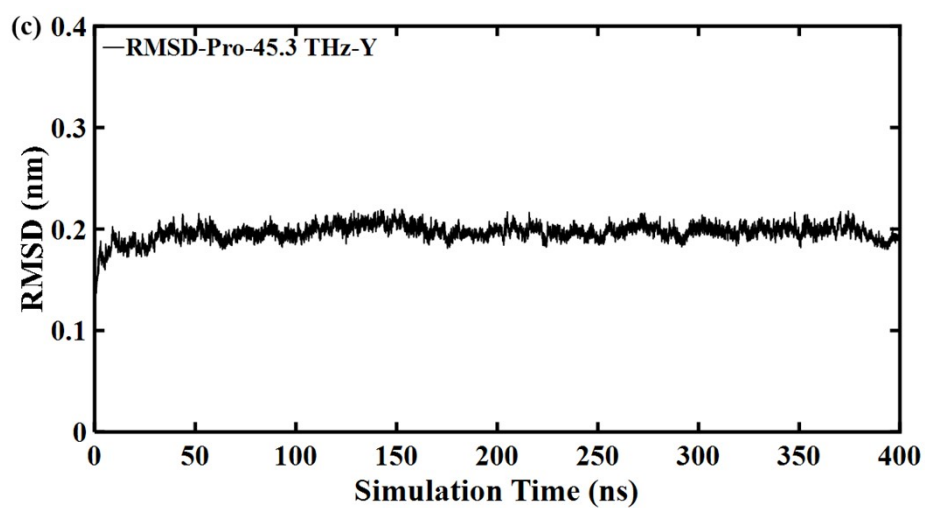
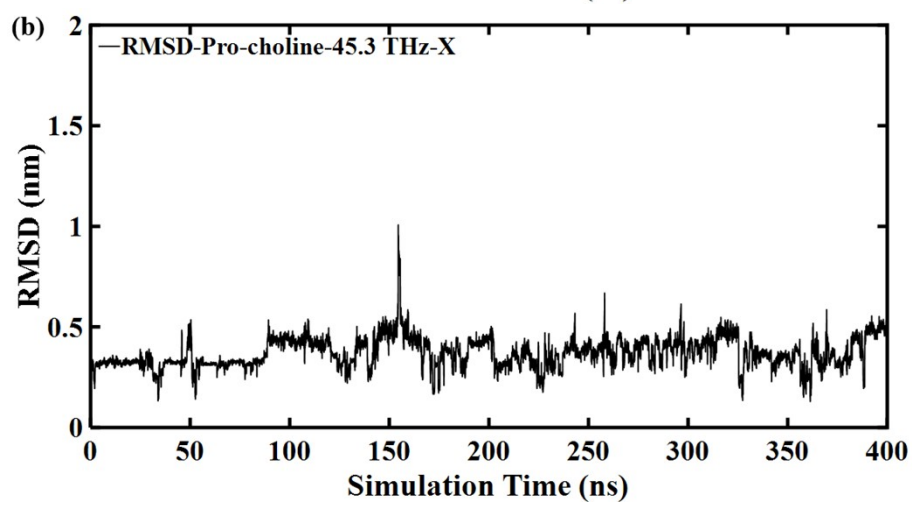
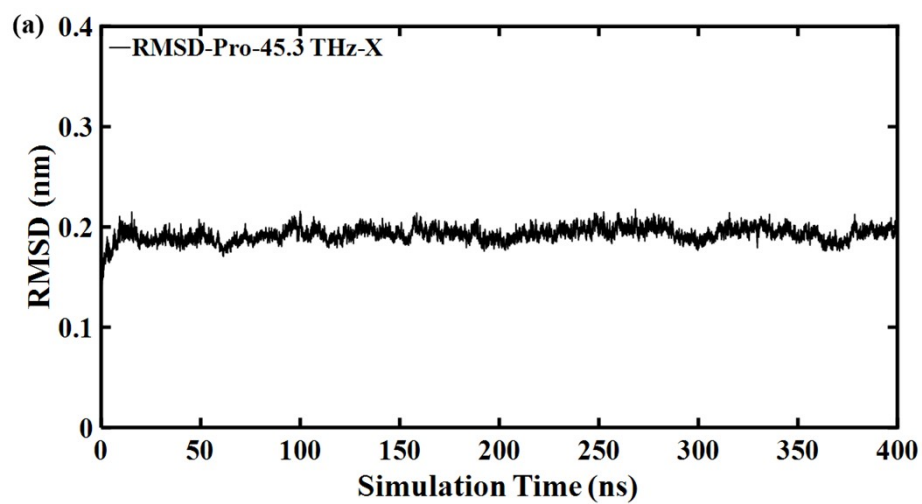


Figure S3 The change curves of system temperature (a) and SASA (b) with simulation time during the 400 ns MD simulation process under the external THz wave in the Z direction. Each curve was plotted from the average of 3 sets. During the simulation 45.3 THz, the average temperature of the system is 300.0951 K.



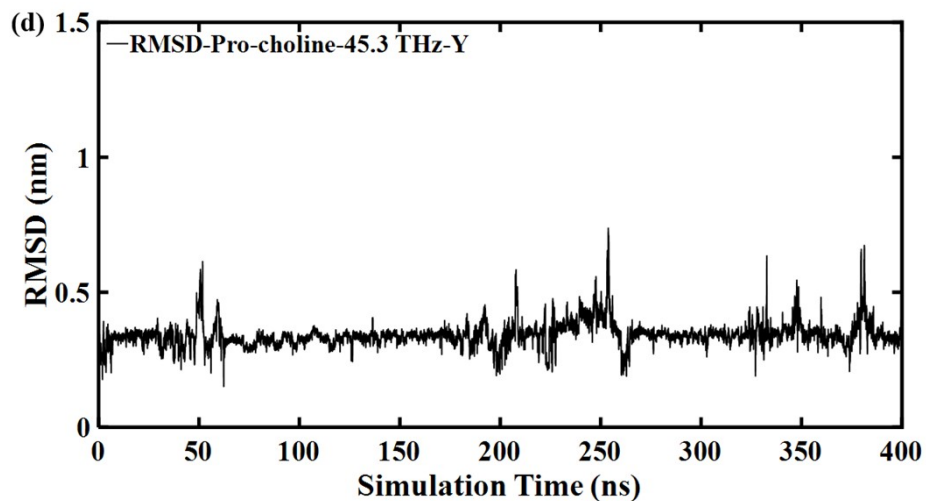


Figure S4 The stability of the whole simulation process during 400 ns simulation under 45.3 THz wave. (a) and (b) are under X direction, (c) and (d) are under Y direction. The (a) and (c) are the RMSD of ChAT skeleton $C\alpha$ relative to initial crystal structure, the (b) and (d) are the RMSD of choline relative to the ChAT skeleton $C\alpha$.

Table S2 Binding free energy of choline-ChAT active site calculated based on the MMPBSA method, data collection started from the 350 ns full equilibrium time point.

Frequency (THz)	Electrostatic energy (kJ/mol)	Polar solvation energy (kJ/mol)	SASA energy (kJ/mol)	van der Waals energy (kJ/mol)	Binding energy (kJ/mol)
noE	-18.774 +/- 0.865	13.740 +/- 3.708	-6.044 +/- 0.062	-21.923 +/- 0.437	-32.830 +/- 3.473
45.3-X	-19.823 +/- 0.957	28.930 +/- 4.318	-6.911 +/- 0.057	-30.603 +/- 0.388	-28.310 +/- 3.922
45.3-Y	-33.743 +/- 0.985	35.068 +/- 12.982	-7.455 +/- 0.052	-34.250 +/- 0.517	-40.847 +/- 13.461
45.3-Z	-20.505 +/- 0.560	-29.604 +/- 32.339	-7.141 +/- 0.053	-32.227 +/- 0.429	-88.895 +/- 32.825

Table S3 Binding free energy of choline-ChAT calculated based on the MMPBSA method, data collection started from the 350 ns full equilibrium time point. The unit of frequency is THz, and the unit of energy is KJ/mol.

	noE	45.3-X	45.3-Y	45.3-Z
Tyr85	0.3241	-0.2173	-0.2180	-0.7784
His324	0.5929	-0.6596	-1.6629	-1.5113
Ser438	0.1445	-0.3355	1.3544	0.3769
Ser538	1.8636	0.8654	1.6434	2.5595
Thr539	-0.5819	0.3464	-1.0104	-1.0598
Tyr552	-0.5258	-2.3865	-1.6016	0.4531
Val555	-0.6734	-2.3738	-1.6720	-3.6663
acetyl-CoA	-0.7197	-0.2473	-1.1440	-0.8778

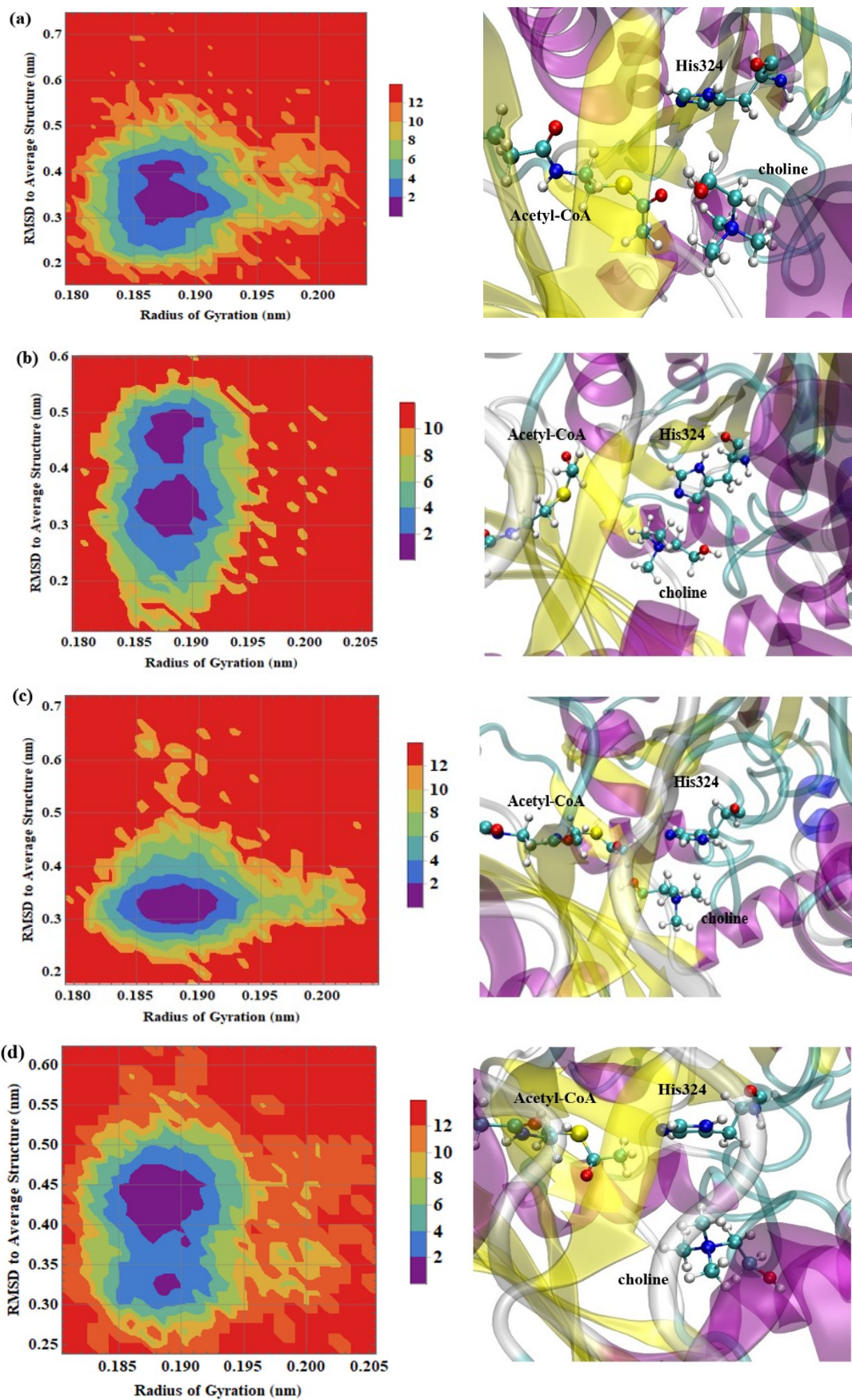


Figure S5 The 2D free energy landscape diagrams as a function of RMSD and Rg as the two coordinates that depict the choline. The free energy is displayed in terms of kJ/mol in the indicated

colour bar where the purple colour represents lowest energy and red the highest energy. The (a) is noE, (b)-(d) are 45.3 THz wave in X-Z direction, The right side of the free energy surface diagram shows representative conformations in the lower free energy region.