

Lodz University of Technology

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A NEW DIBROMETHANE MODEL FOR SIMULATIONS IN LIQUID PHASE

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Dibromomethane (DBM)





Experimental density = 2.477 g/cm³ Experimental dipole moment = 1.43 D

Can they be reproduce ?

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¿What is a isotope effect and why ought I to care ?





Geometry optimisation of DBM

- Density Functional Theory (DFT): **B3LYP & M06-2X**
- Coupled cluster (CC): CCSD
- Møller–Plesset perturbation theory (MP): MP2
- Basis set : 6-311+g(d,p)
- QM package : Gaussian 9 D.

	Electrostatic partial charges			
Atom type	B3LYP	CCSD	M06-2X	MP2
СТ	-0.638	-0.605	-0.664	-0.602
НС	0.315	0.316	0.327	0.315
НС	0.316	0.317	0.327	0.315
Br	0.003	-0.014	0.005	-0.014
μ (D)	1.79	2.00	1.85	1.99

Experimental dipole moment = 1.43 D



	Bond length, Å		Bond angle (°)		
Level of theory	CT - Br	CT - HC	HC - CT - HC	HC - CT - Br	Br - CT - Br
B3LYP	1.95	1.08	112.5	107.5	114.4
CCSD	1.94	1.08	111.5	107.9	114.0
M06-2X	1.93	1.08	112.1	107.8	113.8
MP2	1.93	1.09	111.5	107.9	114.0



Geometry vs general AMBER force field parameters of DBM

	Bond length, Å		Bond angle (°)		
Level of theory	CT - Br	CT - HC	HC - CT - HC	HC - CT - Br	Br - CT - Br
B3LYP	1.95	1.08	112.47	107.53	114.39
CCSD	1.94	1.08	111.5	107.86	113.95
M06-2X	1.93	1.08	112.14	107.75	113.78
MP2	1.93	1.09	111.52	107.86	113.96



Bond Parameters				
BOND	K _b (kcal ∙mol⁻¹∙Ų)	r ₀ (Å)		
Br - CT	159	1.944		
CT - HC	340	1.09		
Angle Parameters				
Angle	K _θ (kcal ∙mol⁻¹∙rad²)	θ _o (deg)		
HC - CT - HC	35	109.5		
HC - CT - Br	43.18	108.111		
Br - CT - Br	66.91	113.001		
Atom Van der Waals parameters				
Atom	ε (kcal ∙mol⁻¹)	R (Å)		
СТ	0.1094	1.908		
НС	0.0157	1.287		
Br	0.42	2.02		



Simulation flow

DBM system is named, based on the level of theory used for the geometry optimisation of the molecule: B3LYP - M06-2X - CCSD - MP2

40 Å box - Periodic 298.15 K Time-step : 0.5 fs Heating time : 0.3 ns Langevin Thermostat Simulation time : 2.2 ns AMBER 14





MD > density & radial distribution function



Simulation flow

40 Å box - Periodic 298.15 K QM : PM6 Time-step : 0.5 fs Heating time : 0.3 ns Langevin Thermostat Simulation time : 2.2 ns





QM/MM MD > Density 9.55 4.55 **B3LYP** 1.40798 1.4 -CCSD 2.4 -M06-2X 1.2 MP2 1.06341 Density (g/cm³) Model 1.0 Density (g/cm³) 2.4422 **B3LYP** RDF (ρ_{C_C}) 9.0 CCSD 2.4576 M06-2X 2.4485 MP2 2.4559 Experimental density = 2.477 g/cm³ ٠ 0.4 1.8 **Restarted Simulations** ÷ 0.2 0.38 1.6 0.0 0.3 0.6 0.9 1.2 0.0 10 12 0 2 6 8 14 4 Time (ns) r (Å)



QM/MM MD > Energy of the system



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Simulation flow

Restart file from QM/MM MD 298.15 K Time-step : 0.2 fs Simulation time : 0.8 ns Nosé-Hoover chain thermostat





Path Integral Molecular Dynamics (PIMD)



SklogWiki

Path integral formalism represents an isomorphism between a quantum system and an equivalent classical model system.

Hamiltonian for the one-dimensional system

$$H = \frac{p^2}{2m} + v(x) = T + V \qquad [T,V] = / 0$$



Path Integral Molecular Dynamics (PIMD)



Canonical partition function

$$Z(\beta) = \lim_{\mathbf{P}\to\infty} \left(\frac{m\mathbf{P}}{2\pi\beta\hbar^2}\right)^{\mathbf{P}/2} \int_{x_{\mathbf{P}+1}=x_1} dx_1 \cdots dx_{\mathbf{P}} \ e^{-\beta U_{eff}},$$

Effective potential

$$U_{eff} = \sum_{i=1}^{P} \left[\frac{mP}{2\beta^2\hbar^2} \left(x_{i+1} - x_i \right)^2 + \left(\frac{1}{P} U\left(x_i \right) \right] \right],$$

Harmonic springs





PIMD > Conserved Energy

Performed simulations with 8, 16, 24, & 32 "beads"





PIMD > RDF comparisons





Equilibrium Isotope Effects (EIE)





EIE> (Bromide)



⁸¹₃₅Br



EIE> (Carbon)





Experimental value : 0.999



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Thanks for your attention ③



means

Equilibrium Isotope Effect

by allacronyms.com

