

Supplementary material

Halogen Bonding (HaB) in E-I...X-M systems: influence of the halogen donor in the HaB nature.

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1. GEOMETRICAL PARAMETERS

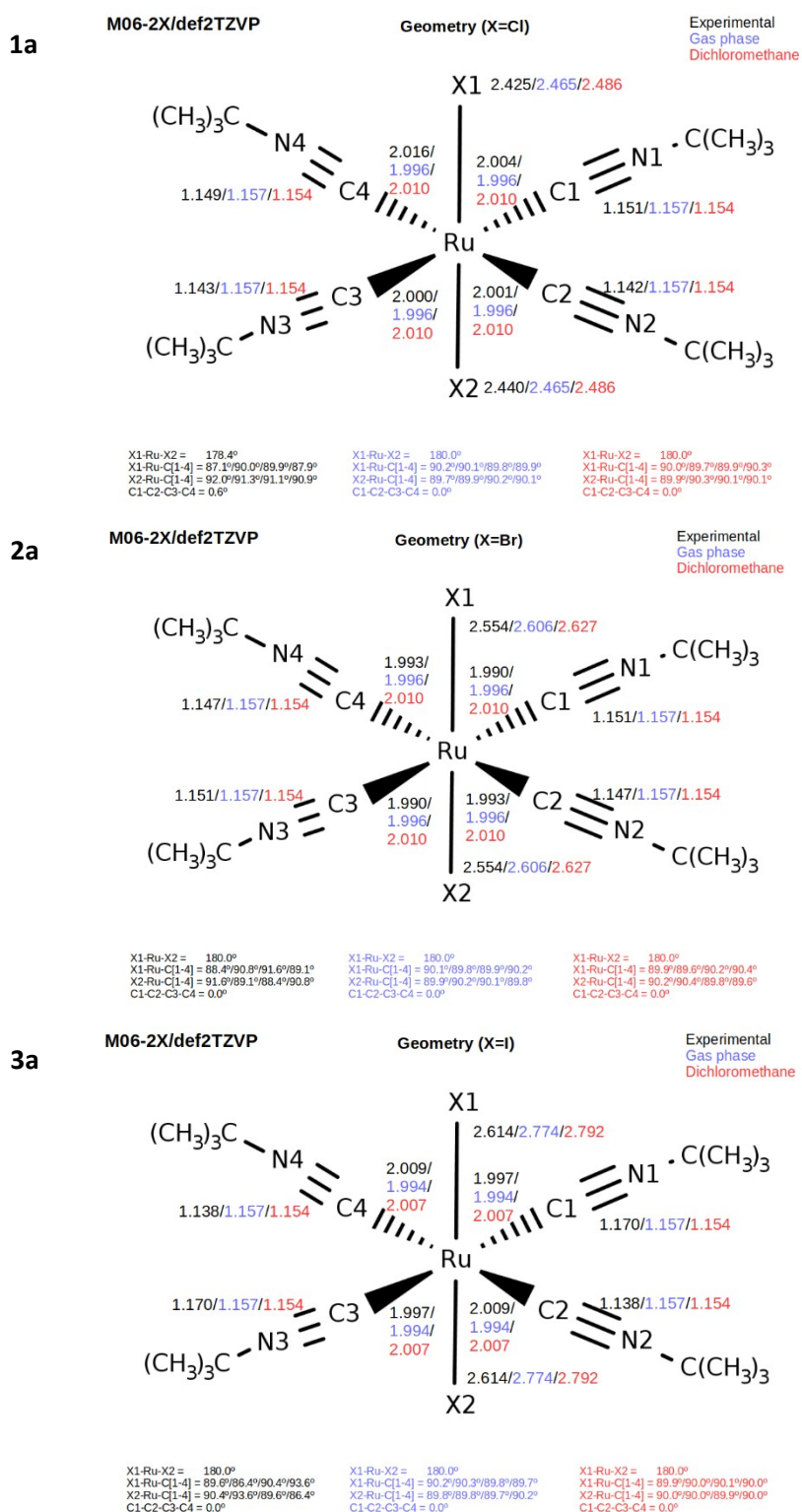


Figure S.1: Selected geometrical parameters for compounds **1a**, **2a** and **3a**. Experimental data from crystallographic information, optimized DFT in gas phase and optimized DFT in CH₂Cl₂ are given in black, blue and red, respectively. Bond lengths are shown in Angstrom and angles in degrees.

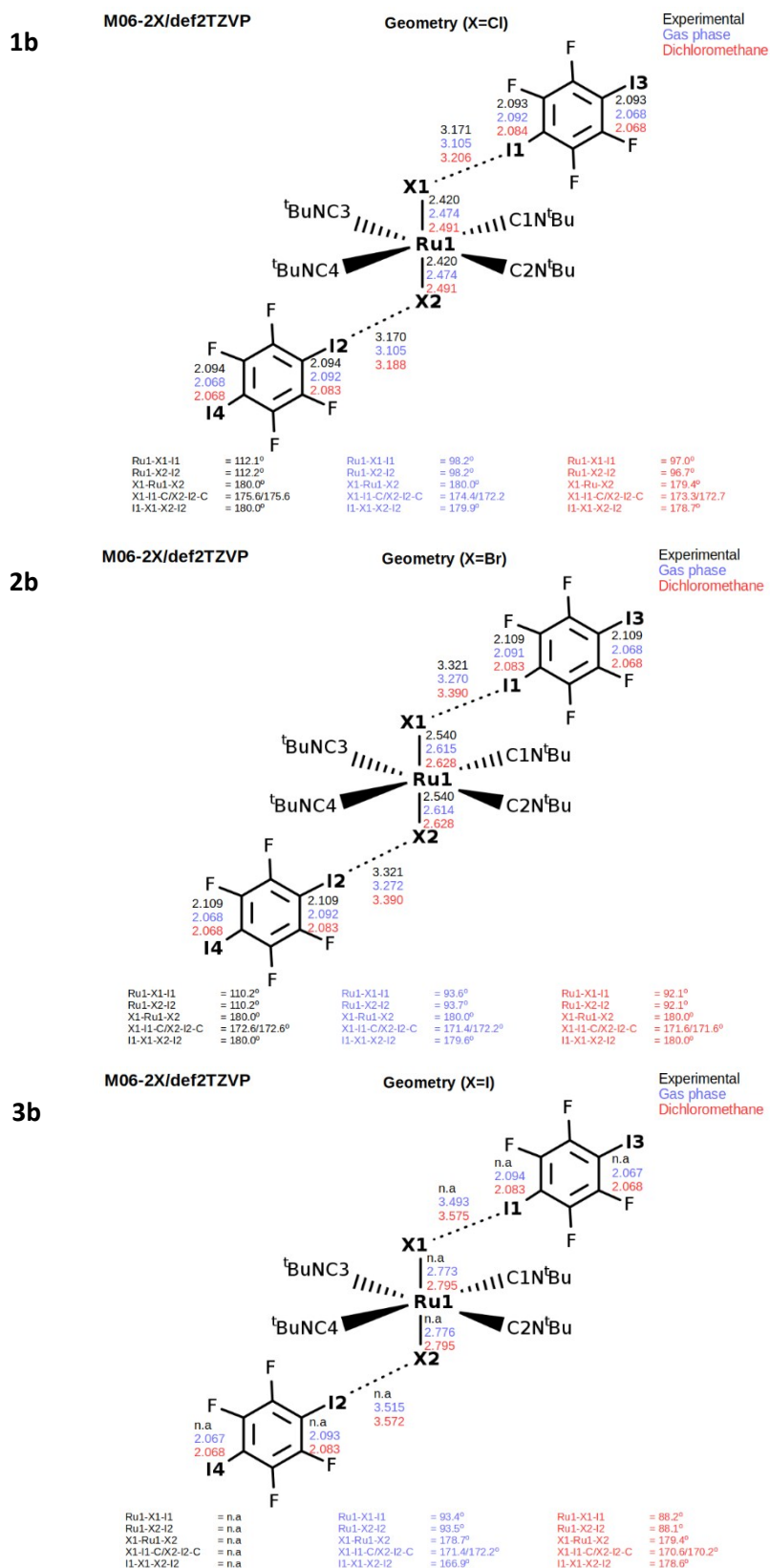


Figure S.2: Selected geometrical parameters for compounds **1b**, **2b** and **3b**. Experimental data from crystallographic information, optimized DFT in gas phase and optimized DFT in CH₂Cl₂ are given in black, blue and red, respectively. Bond lengths are shown in Angstrom and angles in degrees (n.a stands for not available)

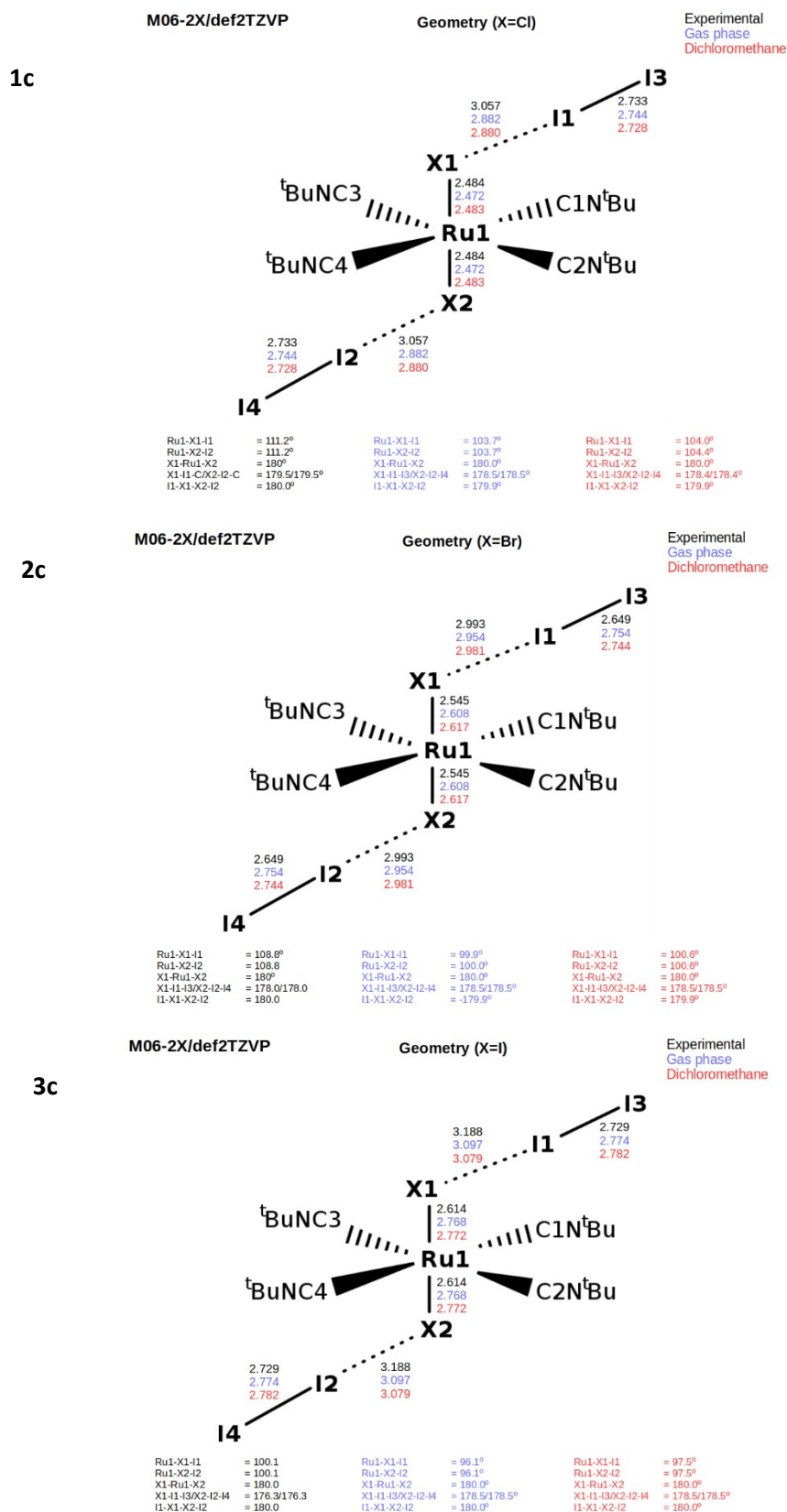
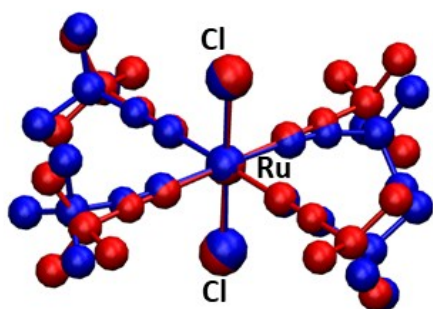
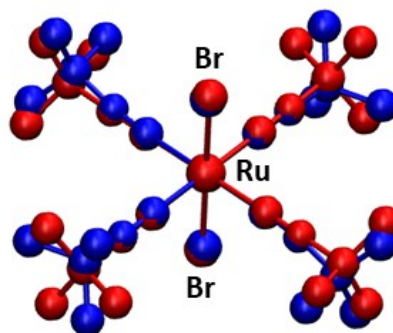


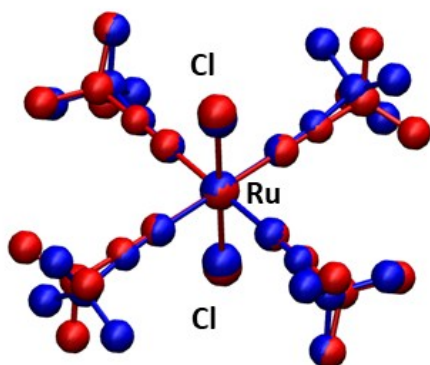
Figure S.3: Selected geometrical parameters for compounds **1c**, **2c** and **3c**. Experimental data from crystallographic information, optimized DFT in gas phase and optimized DFT in CH₂Cl₂ are given in black, blue and red, respectively. Bond lengths are shown in Angstrom and angles in degrees (n.a stands for not available)



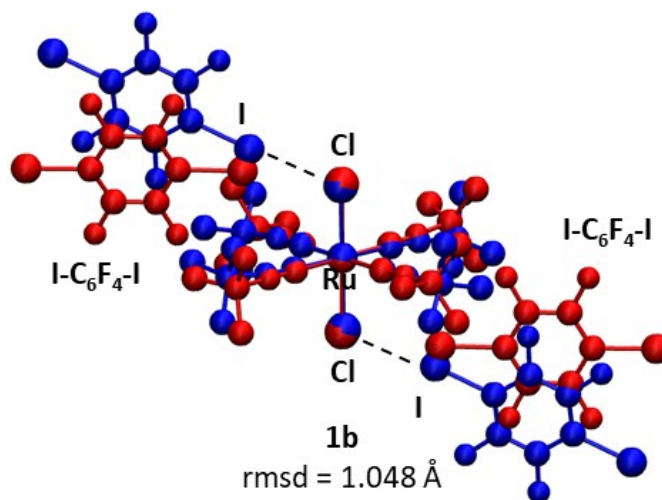
1a
rmsd = 0.674 Å



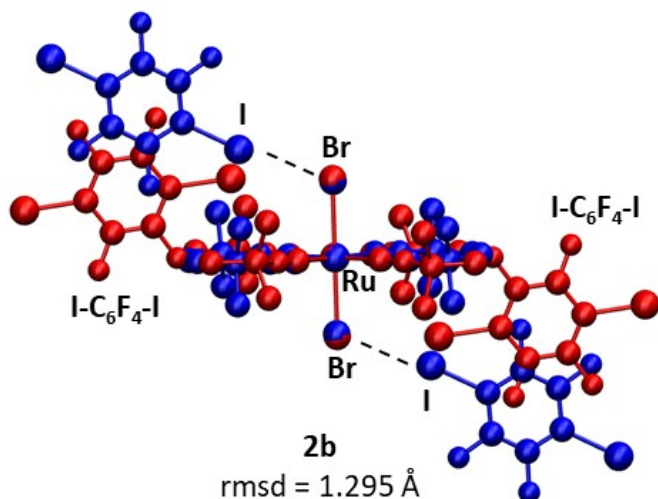
2a
rmsd = 0.683 Å



3a
rmsd = 0.759 Å



1b
rmsd = 1.048 Å



2b
rmsd = 1.295 Å

Figure S.4: Superimposition of optimized structures (red) and X-ray structures (blue) Root mean square deviation (rmsd)

Table S.1: Root mean square error (RMSE), mean square error (MAE) and Maximum in bond and bend angles differences between the optimized DFT and the experimental structures. The hydrogen atoms have not been considered in the error calculation.

	Distances (Å)			Bend angles (°)		
	RMSE	MAE	Maximum	RMSE	MAE	Maximum
1a	0.039	0.025	0.144 ¹⁾	3.6	2.6	11.0 ²⁾
2a	0.033	0.023	0.074	2.4	1.8	7.3 ²⁾
3a	0.052	0.032	0.162 ³⁾	3.4	2.4	11.0 ²⁾
1b	0.022	0.016	0.071	2.8	1.5	15.3 ⁴⁾
2b	0.037	0.029	0.088	3.3	1.7	18.1 ⁴⁾
3b	n.d	n.d	n.d	n.d	n.d	n.d
1c						
2c						
3c						

¹⁾ The maximum difference corresponds to an unreliable C-C bond in a ^tBu group of the X-Ray structure (Label 21 and 13).

²⁾ The C-N-C bend angles in the experimental structure are around 168°-172° instead of the expected 180°.

³⁾ The maximum difference corresponds to the Ru-I bond (Label 1 and 2).

⁴⁾ The Ru-X-I bend angles in the experimental structure are around 112° versus 97° in the DFT optimized. This might be due to the crystallographic packing.

n.d: not determined

$$RMSE = \sqrt{\frac{\sum_{i=1}^N (x_{i,exp} - x_{i,DFT})^2}{N}}$$

RMSE stands for root mean square error defined as

$$MSE = \frac{\sum_{i=1}^N (x_{i,exp} - x_{i,DFT})^2}{N}$$

for mean square error

2. CRYSTAL PACKING

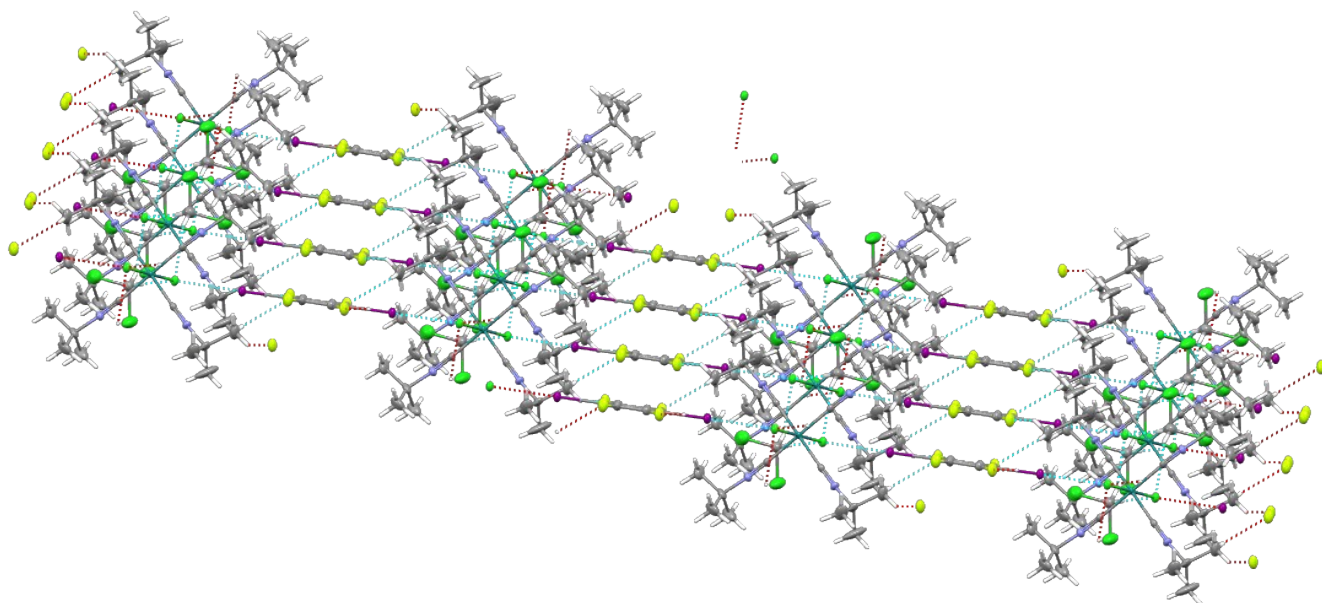


Figure S.5: Packing in the solid state for **1b**.

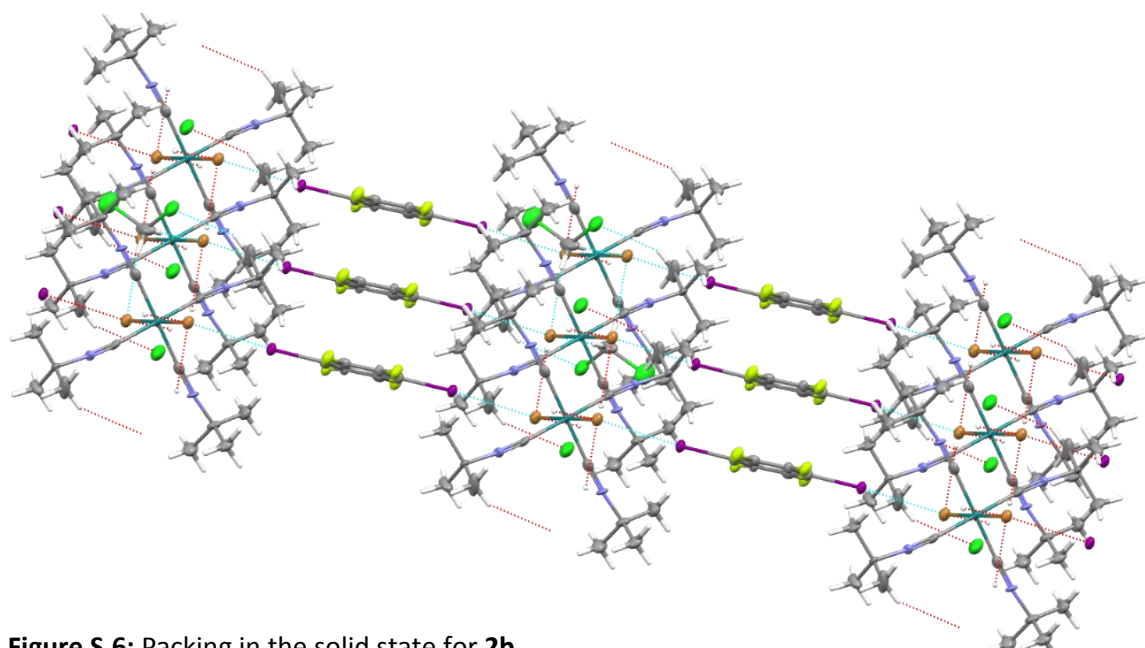


Figure S.6: Packing in the solid state for **2b**.