Supporting material Structural Prediction, Analysis and Decomposition Mechanism of Solid M(NH₂BH₃)_n (M=Mg, Ca and Al)

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S1: MC packing algorithm

Polymorph's Monte Carlo packing algorithm follows a simulated annealing procedure intended to search for the lowest minima of the energy function E of molecular crystals. The simulated annealing method works around minima value of E by treating the search for the global minimum of E as a thermodynamic problem. At some non-zero temperature, T, the crystal changes its structure randomly, and its energy fluctuates accordingly. To prevent the simulation from becoming trapped in a local minimum, cooling begins at a relatively high temperature; every crystal structure (within the constraints of the space group and asymmetric unit contents) can then theoretically be reached, and ergodicity therefore ensured ^[1].

The simulation consists of two phases, heating and cooling. First, each trial crystal is heated. During heating, one starts from a set minimum temperature (300 K in our case). Each new trial temperature T_{new} is obtained using Eq. 1, where T_{old} is the temperature used in a previous step and T_h is a heating factor (1 in our case). Heating continues until either a pre-set maximum temperature is reached (3×10⁵ K in our case) or a specified number of consecutive trial moves have been accepted.

$$T_{new} = T_{old} \times (1.0 + T_h) \tag{1}$$

The cooling phase simulates the annealing of a heated structure. At high temperatures the algorithm is able to globally sample the phase space of possible packing arrangements. At low temperatures the algorithm samples areas of energetically favourable packing arrangements more locally. If a trial is accepted during cooling, the temperature to be used in the next trial step, T_{new} , is obtained using Eq. 2, where T_{old} is the temperature used in a previous step and T_c is a user-definable cooling factor (0.0005 in our case).

$$T_{new} = T_{old} \times (1.0 + T_c) \tag{2}$$

The simulation ends when T is so low that the crystal is frozen (300 K in our case). Then one can optimize at 300 K all the found structures during the annealing procedure and determine the structure of the lowest energy.

The determination of space group is based on the principle pointed by Belsky^[2] and determined syngony and cell parameters from XRD experiments ^[3,4].



Figure S1. a) The computationally predicted XRD for MgAB, CaAB and AlAB, (b) experimental powder XRD for MgAB ref. [3], (c) experimental single crystal XRD for CaAB ref. [4].

A: Table S1~S3 Structural information for MABs (M=Ca, Mg, Al) obtained in this study (The values in the brackets are the experimental results)

MgAB				
Syngony		monoclinic		
space group		C2		
a	8.417	α	90.00	
b	6.038	β	126.08	
с	7.293	γ	90.00	
Fractional coordinates in Å (x y z)				
B1	0.772	0.289	0.169	
N2	0.975	0.284	0.208	
H3	0.760	0.450	0.269	
H4	0.137	0.799	0.962	
H5	0.247	0.622	0.244	
H6	0.083	0.251	0.377	
H7	0.010	0.439	0.181	
Mg8	0.000	0.063	0.000	

Table S1 Structural information for MgAB obtained after geometry optimization with CASTEP

Table S2 Structural information for CaAB obtained after geometry optimization with CASTEP

CaAB					
Syngony		monoclinic			
space group		C2			
a	9.256(9.100)	α	90.00		
b	4.415(4.371)	β	92.92(93.19)		
с	6.613(6.441)	γ	90.00		
Fractional coordinates in Å (x y z)					
H1	0.922	0.914	0.713		
H2	0.137	0.341	0.250		
H3	0.857	0.051	-0.017		
H4	0.643	0.123	0.601		
H5	0.343	0.786	0.299		
N6	0.674	0.012	0.733		
B7	0.834	0.078	0.796		
Ca8	0.000	0.604	0.000		

Table S3 Structural information for AlAB obtained after geometry optimization with CASTEP

AlAB					
Syngony		orthorhombic			
space group		PBCA			
a		17.151			
b		7.562			
с		12.387			
Fractional co	oordinates in Å (x y z)				
All	0.329	0.802	0.040		
N2	0.341	0.548	0.024		
H3	0.400	0.525	0.045		
H4	0.340	0.528	-0.059		
N5	0.336	0.880	-0.110		
H6	0.392	0.928	-0.123		
H7	0.301	0.988	-0.125		
N8	0.423	0.896	0.098		
H9	0.419	0.909	0.181		
H10	0.434	1.023	0.068		
H11	0.226	0.478	0.111		
H12	0.280	0.274	0.031		
H13	0.320	0.363	0.169		
H14	0.362	0.611	-0.190		
H15	0.249	0.677	-0.172		
H16	0.312	0.790	-0.288		
H17	0.490	0.630	0.113		
H18	0.498	0.754	-0.031		
H19	0.557	0.843	0.099		
B20	0.497	0.774	0.068		
B21	0.291	0.411	0.087		
B22	0.314	0.730	-0.194		

	This work	Ref 4	Ref 4	Ref 5	Ref 5	Ref 6
	Calc	Exp	Calc	Calc	Calc	Calc
		ESI	Table 1/ESI	Table 2/	Table 2/	Table2
				CASTEP	VASP	
CaAB						
Ca-N	2.480	2.452	2.466	2.446	2.435	2.476
N-B	1.547	1.547	1.546	1.538	1.541	1.546
N-H	1.031/1.031	1.022/1.022	1.025/1.025	1.027/1.031	1.020/1.022	1.022/1.022
B-H	1.231/1.243/	1.243/1.245/	1.230/1.243/	1.226/1.240/	1.228/1.247/	1.229/1.242/
	1.249	1.251	1.250	1.252	1.260	1.249
MgAB						
Mg-N	2.123	-	-	-	-	2.111
N-B	1.556	-	-	-	-	1.556
N-H	1.033/1.034	-	-	-	-	1.023/1.024/
						1.025
B-H	1.218/1.245/	-	-	-	-	1.237/1.245/
	1.256					1.254/

Table S4. Comparison of CaAB and MgAB structural parameters determined in this work with the ones determined in other experimental and computational studies.

[1] Accelery, Polymorph Predictor http://accelrys.com/products/datasheets/polymorph-predictor.pdf. 2011

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