Supplementary Information for:

Anisotropy of Dodecahedral Water Cages for Guest Gas Occupancy in Semiclathrate Hydrates

Daisuke Yuhara^{a,c}, Kenji Yasuoka^a, Satoshi Takeya^b and Sanehiro Muromachi^{c*}

^a Department of Mechanical Engineering, Keio University, Yokohama 223-8522, Japan.

^b National Metrology Institute of Japan (NMIJ), National Institute of Advanced Industrial Science and Technology (AIST), Tsukuba Central 5, 1-1-1 Higashi, Tsukuba, 305-8565, Japan

^c Research Institute of Energy Frontier, National Institute of Advanced Industrial Science and Technology (AIST), 16-1 Onogawa, Tsukuba, 305-8569, Japan.

* Author to whom correspondence should be addressed. (S. M.)

E-mail: s-muromachi@aist.go.jp

Tell: +81-29-861-4287

Fax: +81-29-861-8706

1. Experimental details

The materials used in this study were TBAB (Sigma-Aldrich, 99 in mole fraction), Xe gas (Tokyo Rare Gases, >0.99999 in mole fraction), Kr gas (Tokyo Rare Gases, >0.99999 in mole fraction) and Ar gas (Taiyo Nippon Sanso, >0.99999 in mole fraction). Water was sterilized by ultraviolet ramp and filtrated by activated carbon.

The single crystals were formed in a high pressure cell equipped with glass windows. The formation conditions of the single crystals are summarized in Table S1. An aqueous solution of TBAB was gravimetrically prepared with the aid of electronic balance (A&D, GX-6100). The aqueous solution was injected into the high pressure cell. The cell was immersed in a bath filled with a propylene glycol aqueous solution. The bath temperature was controlled by a cooling water circulator (EYELA, CTP-3000). A gas pressure was supplied into the cell from a gas cylinder up to a prescribed pressure. The bath temperature was cooled down to a temperature which gives subcooling for hydrate crystal growth. The crystal growth was observed under an optical microscope (Edmund Optics, VZM-450) and a CCD camera (Sentech, STC-MC152USB). After sufficient amount of the crystal formed, the crystals and the residual solution was separated and the cell was cooled down to ~250 K. The cell pressure was released to atmospheric pressure. Under subsequent processes, the crystals were kept at below 250 K.

The pressure and temperature of the system were measured by a pressure sensor (KEYENCE, GP-M100) and a platinum resistance thermometer (Eutech Instruments, EcoScan Temp 6), respectively. Measurement uncertainties for pressure, temperature and TBAB composition in aqueous solution are 0.3 K, 0.1 MPa and 0.006 in mass fraction, respectively.

Gas	Xe	Kr	Ar
TBAB composition	0.204	0.200	0.200
(mass fraction)			
Temperature /K	285.2	286.2	286.2
Pressure /MPa	0.4	1.0	4.2
Subcooling temperature	~3	~3	~6
/K			

Table S1. Formation conditions for single crystals

The single crystal X-ray diffraction measurements were performed by a diffractometer (Bruker, AXS CCD). The sample temperature was maintained by cold nitrogen flow at 123 K. The structure was solved and refined by SHELXTL program^{S1}. All atoms except for hydrogen and rare gas molecules were refined with anisotropic thermal parameters. Hydrogen atoms in the TBA cation were automatically placed by the program. Hydrogen of atoms in water molecules were manually placed using a difference Fourier map. The measurement and refinement results are summarized in Table S2 in Supplementary Information. CCDC 1935565-1935567 report CIF data for the presently found crystal structures. The whole cage arrangements in the presently determined structures are provided in Fig. S1.

Table S2. Cry	stal data and	structure refinement	results for the	TBAB + 0	(Xe, Kr	or Ar)
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hydrate.

	TBAB + Xe hydrate	TBAB + Kr hydrate	TBAB + Ar hydrate
empirical formula	C ₁₆ H ₁₁₂ NBrO38Xe _{1.17}	$C_{16}H_{112}NBrO_{38}Kr_{1.05}$	C16H112NBrO38Ar1.23
formula weight, g·mol ⁻¹	1203.92	1090.77	1055.91
temperature, K	123 (2)	123 (2)	123 (2)
wavelength, Å	0.71070	0.71070	0.71070
crystal system, space group	Orthorhombic, Pmma	Orthorhombic, Pmma	Orthorhombic, Pmma
unit cell dimensions, Å	a = 21.088(5) b = 12.630(3) c = 12.063(3)	a = 21.064(3) b = 12.6451(19) c = 12.0298(18)	a = 21.041(3) b = 12.6523(15) c = 12.0228(14)
volume, Å ³	3212.9(12)	3204.2(8)	3200.7(7)
Z, calculated density, $g \cdot cm^{-3}$	2, 1.160	2, 1.131	2, 1.096
absorption coefficient mu	1.324	1.405	0.784
 F(000)	1270	1180	1152
crystal size, mm	$0.15\ \times 0.30 \times 0.30$	$0.15~\times 0.20 \times 0.20$	$0.10\ \times 0.10 \times 0.15$
θ range for data collection	2.516, 28.275	2.337, 28.279	2.337, 28.281
	−27 <h< 24<="" td=""><td>-28 <h< 26<="" td=""><td>−23 <h< 27<="" td=""></h<></td></h<></td></h<>	-28 <h< 26<="" td=""><td>−23 <h< 27<="" td=""></h<></td></h<>	−23 <h< 27<="" td=""></h<>
index ranges	-13 <k< 16<="" td=""><td>-16 <k< 11<="" td=""><td>-16 <k< 16<="" td=""></k<></td></k<></td></k<>	-16 <k< 11<="" td=""><td>-16 <k< 16<="" td=""></k<></td></k<>	-16 <k< 16<="" td=""></k<>
reflections	'/ <l< 16<br="">4059/ 3869</l<>	-16 <1< 13 4113/ 3800	-12 <1< 15 4266/ 3859
completeness to 2θ	0.949	0.964	0.978
refinement method	F^2 against all reflections	F^2 against all reflections	F^2 against all reflections
data/restraints/parameters	4059/61/387	4113/ 105/ 428	4166/78/386
goodness-of-fit on F^2	1.012	1.098	1.112
final R indices $[I > 2\Sigma(I)]$ R ₁ , wR ₂	0.0310, 0.0825	0.0417, 0.1251	0.0402, 0.1264
R indices (all data) R_1 , w R_2	0.0325, 0.0846	0.0452, 0.1272	0.0427, 0.1278



Fig. S1. Whole cage arrangements in the presently determined structure. (a) TBAB + Xe hydrate (b) TBAB + Kr hydrate (c) TBAB + Ar hydrate. Ball: Red, oxygen of water molecule; Light blue, Xe; Orange, Kr; Blue, Ar; Cyan, N; Black, C; Brown, Br.

2. Supplementary Information for D cage shapes

Fig. S2 shows the three D cages found in each of the present three structures. This figure shows the distortion of the D_{d1} cages with two indented water molecules. In the D_{d1} cage Xe and Kr stay mostly in one position, i.e., the centre of the cage. Contrary to this, the Ar has three positions (two of them are in a symmetry-related position) in the D_{d1} cage. Compared to relatively large Xe and Kr molecules, the smallest Ar molecule was able to distribute in the cage. However, the possible positions align along the *a* axis, which means that the molecular orientation in the D_{d1} cage is still restricted even with a smaller molecular size such as Ar.



Fig. S2. Guest distributions in the D cages.. (a) TBAB + Xe hydrate (b) TBAB + Kr hydrate
(c) TBAB + Ar hydrate. Ball: Red, oxygen of water molecule; Light blue, Xe; Orange, Kr;
Blue, Ar. Bar: Hydrogen bond between water molecules.

Table S3 shows distances between cage center and cage water molecules in the D cages.

Cage	Xe	Kr	Ar		
Longest distances					
Dr (blue)	4.0735	4.0172	4.0227		
D _r (green)	4.0796	4.0203	4.0094		
D _{d1}	4.0838	4.0274	4.0079		
Shortest distances					
Dr (blue)	3.7251	3.7285	2.9856		
D _r (green)	3.7088	3.7090	2.9990		
D _{d1}	3.7028	3.7047	3.0121		
Average distances					
Dr (blue)	3.8742	3.8625	3.8642		
D _r (green)	3.8707	3.8664	3.8613		
D _{d1}	3.8180	3.8153	3.8151		

Table S3. Distances between cage center and cage water molecules in the D cages. D_r with"blue" and "green" denote the two different D_r cages in Fig. 4 in the context. Units are Å.

References in Supplementary Information

S1 G. M. Sheldrick, Acta Crystallogr., 1990, A46, 467.