Reversible Multicomponent Self-Assembly Mediated By Bismuth Ions

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Electronic Supplementary Information



1. Mass Spectral Data

Figure S-1. Full ESI-MS spectra (MeCN) of $1 + Bi(OTf)_3$ indicating formation of the M₂L₂, M₂L₃, and M₂L₄ complexes.





Figure S-3. ESI-MS spectra (MeCN) of 2₃Bi₃·9OTf and undefined aggregates.

2. NMR Spectra of Synthesized Compounds



Figure S-4. ¹H NMR spectrum of diethyl 1,1':3',1''-terphenyl-4,4''-dicarboxylate (CDCl₃, 400 MHz, 298K)



Figure S-5. ¹³C NMR spectrum of diethyl 1,1':3',1''-terphenyl-4,4''-dicarboxylate (CDCl₃, 100 MHz, 298K)



Figure *S*-6. ¹H NMR spectrum of hydrazide **3** (DMSO-*d*₆, 400 MHz, 298K)



Figure *S-10.* ¹H NMR spectrum of hydrazide 4 (DMSO-*d*₆, 400 MHz, 298K)



Figure S-11. ¹³C NMR spectrum of hydrazide 4 (DMSO-*d*₆, 100 MHz, 298K)





Figure *S-14.* ¹H NMR spectrum of self-assembled complex 1₂Bi₂·6(OTf) (CD₃CN, 400 MHz, 298K)



170 168 166 164 162 160 158 156 154 152 150 148 146 144 142 140 138 136 134 132 130 128 126 124 122 120 **Figure S-15.** ¹³C NMR spectrum of self-assembled complex $1_2Bi_2 \cdot 6(OTf)$ (CD₃CN, 100 MHz, 298K)



Figure *S***-16.** ¹H NMR spectrum of self-assembled complex **2**₃**Bi**₃**·9(OTf)** (CD₃CN, 400 MHz, 298K)



Figure *S***-1***7***.** ¹³C NMR spectrum of self-assembled complex **2**₃**Bi**₃**·9(OTf)** (CD₃CN, 100 MHz, 298K)



Figure S-18. ¹H NMR titration of Bi(OTf)₃ into ligand 1: (a) 0.5 eq; (b) 0.67 eq; (c) 1 eq; (d) 2 eq; (e) 3 eq; (CD₃CN, 400 MHz, 298 K)



Figure *S-19.* ¹H NMR titration of ligand **1** into **1**₂**·Bi**₂: (a) **1**₂**·Bi**₂; (b) 1.0 eq; (c) 1.8 eq; (d) 2.9 eq; (e) 4.2 eq; (f); 6.0 eq; (CD₃CN, 400 MHz, 298 K)



Figure *S-20.* ¹H NMR titration of Bi(OTf)₃ into ligand **1**·Na₂: (a) 0.5 eq; (b) 0.75 eq; (c) 1 eq; (d) 1.5 eq; (e) 3 eq; (f) 5 eq; (CD₃CN, 400 MHz, 298 K)





Figure *S*-22. ¹H NMR spectrum of complex 1·BiBr₃. (DMSO-*d*₆, 400 MHz, 298 K)



Figure *S-23.* ¹H NMR titration of Bi(OTf)₃ into ligand **2**: (a) 0.33 eq; (b) 0.66 eq; (c) 1 eq; (d) 1.5 eq; (e) 2 eq; (f) 3 eq; (CD₃CN, 400 MHz, 298 K).



9.9 9.8 9.7 9.6 9.5 9.4 9.3 9.2 9.1 9.0 8.9 8.8 8.7 8.6 8.5 8.4 8.3 8.2 8.1 8.0 **Figure S-24.** DOSY-NMR of **2**₃•**Bi**₃ (CD₃CN, 600 MHz, 298 K, $\Delta = 17$ ms, $\delta = 7000 \ \mu$ s, Diffusion Coefficient = $4.88 \times 10^{-10} \ \text{m}^2/\text{s}$).

3. X-Ray Structure Determination



Figure S-25. a) Structure of the complex $1_2 \cdot Bi_2 \cdot OTf_6$ as determined by X-ray diffraction analysis (counterions and solvent removed for clarity; b) Structure of the unit cell of complex $1_2 \cdot Bi_2 \cdot OTf_6$, indicating disordered solvent molecules and triflate counterions.

A colorless fragment of a prism (0.35 x 0.17 x 0.07 mm³) was used for the single crystal X-ray diffraction study of $1_2 \cdot Bi_2 \cdot (OTf)_6$ (CCDC submission #892045). The crystal was coated with paratone oil and mounted on to a cryo-loop glass fiber. X-ray intensity data were collected at 100(2) K on a Bruker APEX2¹ platform-CCD X-ray diffractometer system (fine focus Moradiation, $\lambda = 0.71073$ Å, 50KV/35mA power). The CCD detector was placed at a distance of 5.0000 cm from the crystal.

A total of 4800 frames were collected for a sphere of reflections (with scan width of 0.3° in ω or ϕ , starting ω and 2 θ angles of -30° , and ϕ angles of 0° , 90° , 120° , 180° , 240° , and 270° for every 600 frames, and 1200 frames with ϕ -scan from $0-360^{\circ}$, 20 sec/frame exposure time). The frames were integrated using the Bruker SAINT software package² and using a narrow-frame integration algorithm. Based on a triclinic crystal system, the integrated frames yielded a total of 68323 reflections at a maximum 2 θ angle of 54.96° (0.77 Å resolution), of which 13040 were independent reflections ($R_{int} = 0.0256$, $R_{sig} = 0.0194$, redundancy = 5.2, completeness = 99.8%) and 12130 (93.0%) reflections were greater than $2\sigma(I)$. The unit cell parameters were, a = 10.5697(3) Å, b = 13.7043(4) Å, c = 20.0249(6) Å, $\alpha = 98.057(1)$ $\beta = 92.112(1)^{\circ}$, $\gamma = 96.452(1)$ V = 2849.71(14) Å³, Z = 2, calculated density $D_c = 1.622$ g/cm³. Absorption corrections were applied (absorption coefficient $\mu = 3.433$ mm⁻¹; max/min transmission = 0.8001/0.3770) to the raw intensity data using the SADABS program.³

The Bruker SHELXTL software package⁴ was used for phase determination and structure refinement. The distribution of intensities and no systematic absent reflections indicated two possible space groups, P-1 and P1. The space group P-1 (#2) was later determined to be correct. Direct methods of phase determination followed by two Fourier cycles of refinement led to an electron density map from which most of the non-hydrogen atoms were identified in the asymmetry unit of the unit cell. With subsequent isotropic refinement, all of the non-hydrogen atoms were identified. There were one ligand of $C_{32}H_{24}N_6O_2$, one Bi-cation, three disordered SO₃CF₃ anions (site occupancy ratios are 80%/20%, 81%/19%, 75%/25%), one disordered CHCl₃ (site occupancy ratio is 58%/42%), one disordered CH₃CN (site occupancy ratio is 73%/27%), one partially occupied CH₃CN (80% occupied), and two partially occupied H₂O (66% and 39% occupied) present in the asymmetry unit of the unit cell. The symmetry unit of the unit cell. The symmetry unit of the unit cell to a symmetry unit of the unit symmetry unit of the unit symmetry unit of the unit cell to a non-hydrogen atoms were identified.

molecule near the inversion centered was modeled without its hydrogen atoms. One of the two H-atoms of the 66% occupied water didn't have an H-atom acceptor within the rigid model distance as the H-acceptor. All the alerts level B, C and G warning are either because of disordered and partially occupied solvents (water, acetonitrile and chloroform) or the disordered SO₃CF₃ anions. All possible hydrogen bonding distances and angles are given in Table 7. The DFIX, SADI, SIMU, DELU, and EADP, restraints were to stabilize the final refinement of the atomic positions. Although the distribution of intensities ($E^2-1 = 0.705$) indicated a possible racemic twin P1 chiral space group, the refinement using the racemic twin P1 space group was highly unstable for most of the solvent molecules giving rise to non-definite positive thermal parameters. The final structure model was refined using the P-1 space group.

Atomic coordinates, isotropic and anisotropic displacement parameters of all the non-hydrogen atoms were refined by means of a full matrix least-squares procedure on F^2 . The H-atoms were included in the refinement in calculated positions riding on the atoms to which they were attached, except the two NH-group hydrogen atoms were refined unrestrained. The refinement converged at R1 = 0.0293, wR2 = 0.0774, with intensity, I>2 σ (I). The largest peak/hole in the final difference map was 1.675/-0.680 e/Å³. The high electron density peak/hole ratio (2.46) near the Bi-atom was probably due to absorption correction error.

| [C ₃₂ H ₂₄ N ₆ O ₂] ₂ [Bi] ₂ [SO ₃ C 1391.94 100(2) K | 2F ₃] ₆ |
|-------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1391.94 100(2) K | |
| 100(2) K | |
| | |
| 0.71073 Å | |
| Triclinic | |
| P-1 (#2) | |
| a = 10.5697(3) Å | $\alpha = 98.057(1)^{\circ}$. |
| <i>b</i> = 13.7043(4) Å | $\beta = 92.112(1)^{\circ}.$ |
| c = 20.0249(6) Å | $\gamma = 96.452(1)^{\circ}$. |
| 2849.71(14) Å ³ | |
| 2 | |
| 1.622 Mg/m ³ | |
| 3.433 mm ⁻¹ | |
| 1366 | |
| $0.35 \ge 0.17 \ge 0.07 \text{ mm}^3$ | |
| 1.51 to 27.48°. | |
| -13<=h<=13, -17<=k<=17, -25<=l<=25 | |
| 68323 | |
| 13040 [$R_{int} = 0.0256$] | |
| 99.8 % | |
| Semi-empirical from equivalents | |
| 0.8001 and 0.3770 | |
| Full-matrix least-squares on F2 | |
| 13040 / 849 / 981 | |
| 1.077 | |
| R1 = 0.0293, wR2 = 0.0774 | |
| R1 = 0.0328, wR2 = 0.0795 | |
| 1.675 and -0.680 <i>e</i> .Å ⁻³ | |
| | 100(2) K 0.71073 Å Triclinic P-1 (#2) a = 10.5697(3) Å b = 13.7043(4) Å c = 20.0249(6) Å 2849.71(14) Å ³ 2 1.622 Mg/m ³ 3.433 mm ⁻¹ 1366 0.35 x 0.17 x 0.07 mm ³ 1.51 to 27.48°. -13<= h <=13, -17<= k <=17 68323 13040 [R _{int} = 0.0256] 99.8 % Semi-empirical from equil 0.8001 and 0.3770 Full-matrix least-squares 13040 / 849 / 981 1.077 R1 = 0.0293, wR2 = 0.075 R1 = 0.0328, wR2 = 0.075 1.675 and -0.680 e.Å ⁻³ |

Table *S*-1. Crystal data and structure refinement for 1₂•Bi₂•(OTf)₆.



Figure S-26. a) Structure of the complex $1_2 \cdot Bi_2 \cdot OTf_6$ as determined by molecular modeling (SPARTAN, AM1 forcefield).

References

- 1) APEX 2, version 2012.2-0, Bruker (2012), Bruker AXS Inc., Madison, Wisconsin, USA.
- 2) SAINT, version V8.18C, Bruker (2011), Bruker AXS Inc., Madison, Wisconsin, USA.
- 3) SADABS, version 2008/1, Bruker (2008), Bruker AXS Inc., Madison, Wisconsin, USA.
- 4) SHELXTL, version 2008/4, Bruker (2008), Bruker AXS Inc., Madison, Wisconsin, USA.