

Electronic Supplementary Information

for

Combined Structural and Theoretical Investigation on Differently Substituted Bispidine Ligands: Predicting the Properties of their Corresponding Coordination Polymers.

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Synthesis of the Bispidine Ligands L1-L7

Procedures for obtaining Ligand **L1**, Ligand **L4** and Piperidone **A** were previously reported by us (ref. 9)

Ligand L2: Piperidone **A** (1 g, 2.6 mmol) was suspended in methanol. A second solution consisting of paraformaldehyde (470 mg, 15.7 mmol) and isopropylamine (0.7 mL, 7.8 mmol) in methanol was then added to the piperidone. The reaction was stirred and refluxed overnight. The solution was left to cool, and while the solvent slowly evaporated, crystals were formed. After recrystallization from methanol, 900 mg of product were obtained, affording a 75 % yield. ^1H NMR (400 MHz, Chloroform-*d*) δ 8.73 (d, J = 5.2 Hz, 2H), 8.57 (d, J = 5.1 Hz, 2H), 8.16 (d, J = 4.9 Hz, 2H), 7.08 (d, J = 5.9 Hz, 2H), 4.56 (s, 2H), 3.77 (s, 6H), 3.10 (d, J = 13.0 Hz, 2H), 2.84 (d, J = 12.9 Hz, 2H), 2.28 (s, 1H), 1.89 (s, 3H), 1.17 (d, J = 6.6 Hz, 6H); ^{13}C NMR (101 MHz, CDCl_3) δ 203.14, 167.95 (2C), 149.89 (2C), 149.64 (2C), 148.17 (2C), 124.54 (2C), 124.15 (2C), 71.59 (2C), 62.80 (2C), 54.72, 54.05 (2C), 52.74 (2C), 43.56, 18.30 (2C). MS-ESI *calcd* for $\text{C}_{25}\text{H}_{30}\text{N}_4\text{O}_5$ 466.22; found: $[M+H]^+$: 467.3.

Ligand L3: Piperidone **A** (1 g, 2.6 mmol) was dissolved in methanol, and a second solution consisting of paraformaldehyde (470 mg, 15.7 mmol) and cyclohexylamine (0.9 mL, 7.8 mmol) in methanol was then added. The reaction was stirred and refluxed overnight. A white solid precipitated, which was then filtrated and washed with cold methanol. The remaining solution was recrystallized from methanol and left to evaporate to afford more product, giving a total of 800 mg (61 % yield). ^1H -NMR (400 MHz, Chloroform-*d*) δ 8.74 (d, J = 5.1 Hz, 2H), 8.57 (d, J = 5.1 Hz, 2H), 8.17 (d, J = 5.1 Hz, 2H), 7.08 (d, J = 5.1 Hz, 2H), 4.56 (s, 2H), 3.77 (s, 6H), 3.13 (d, J = 13.0 Hz, 2H), 2.92 (d, J = 12.2 Hz, 2H), 2.39 (d, J = 10.1 Hz, 1H), 2.05 – 1.98 (m, 4H), 1.88 (s, 3H), 1.69 (d, J = 12.6 Hz, 1H), 1.39 – 1.22 (m, 5H). ^{13}C -NMR (101 MHz, CDCl_3) δ 203.17, 167.98 (2C), 149.92 (2C), 149.73 (2C), 148.08 (2C), 124.56 (2C), 124.11 (2C), 71.59, 63.82 (2C), 62.94 (2C), 54.45 (2C), 52.70 (2C), 43.53, 28.77 (2C), 26.17 (2C), 26.06. MS-ESI *calcd* for $\text{C}_{28}\text{H}_{34}\text{N}_4\text{O}_5$ 506.25; found: $[M+H]^+$: 507.4

Ligand L5: Piperidone **A** (500 mg, 1.3 mmol) was dissolved in methanol. A second solution consisting of paraformaldehyde (235 mg, 7.8 mmol) and 4-methoxybenzylamine (0.5 mL, 3.9 mmol) in methanol was then added to the piperidone. The reaction was stirred and refluxed for 6 hours. A white solid precipitated, which was then filtrated and washed with cold methanol, while the remaining solution was left to evaporate to afford more product. Yield 64% (450 mg). ^1H NMR (400 MHz, Chloroform-*d*) δ 8.60 (d, J = 5.4 Hz, 2H), 8.47 (d, J = 5.4 Hz, 2H), 8.08 (d, J = 5.4 Hz, 2H), 7.37 – 7.29 (m, 4H), 7.05 (d, J = 8.6 Hz, 2H), 4.64 (s, 2H), 3.95 (s, 3H), 3.77 (s, 6H), 3.44 (s, 2H), 3.12 (d, J = 13.4 Hz, 2H), 2.80 (d, J = 12.5 Hz, 2H), 1.83 (s, 3H). ^{13}C NMR (101 MHz, CDCl_3) δ 202.86, 167.62 (2C), 159.72, 149.73 (2C), 147.51 (2C), 147.94 (2C), 131.74 (2C), 128.49, 124.22 (4C), 114.23 (2C), 71.76 (2C), 62.65 (2C), 62.08, 57.83 (2C), 55.60, 52.79 (2C), 43.45. MS-ESI *calcd* for $\text{C}_{30}\text{H}_{32}\text{N}_4\text{O}_6$ 544.23; found: $[M+Na]^+$: 567.4

Ligand L6: Piperidone **A** (500 mg, 1.3 mmol) was suspended in methanol. A second solution consisting of paraformaldehyde (235 mg, 7.8 mmol) and 4-(trifluoromethyl)benzylamine (0.56 mL, 3.9 mmol) in methanol was then added to first solution. The reaction was stirred and refluxed for 5 hours. A white solid precipitated, which was then filtrated and washed with cold methanol, while the remaining solution was left to evaporate to afford more product. 350 mg (46 % yield). ^1H NMR (400 MHz, Chloroform-*d*) δ 8.55 (d, 2H), 8.46 (s, 2H), 7.85 (s, 2H), 7.79 (d, J = 7.8 Hz, 2H), 7.58 (d, J = 7.8 Hz, 2H), 7.10 (d, J = 4.7 Hz, 2H), 4.52 (s, 2H), 3.76 (s, 6H), 3.58 (s, 2H), 3.17 (d, J = 11.2 Hz, 2H), 2.80 (d, J = 12.3 Hz, 2H), 1.83 (s, 3H). ^{13}C NMR (101 MHz, CDCl_3) δ 202.36, 167.41 (2C), 149.97 (2C), 149.45 (2C), 147.69 (2C),

140.20, 130.92 (3C), 125.87 (2C), 125.83, 124.26 (2C), 123.82 (2C), 71.71 (2C), 62.58 (2C), 62.28, 57.86 (2C), 52.86 (2C), 43.46. MS-ESI *calcd* for C₃₀H₂₉F₃N₄O₅ 582.21; found: [M+Na]⁺: 605.3

Ligand L7: Piperidone **A** (500 mg, 1.3 mmol) was suspended in methanol. A second solution consisting of paraformaldehyde (235 mg, 7.8 mmol) and 4-(trifluoromethoxy)benzylamine (0.6 mL, 3.9 mmol) in methanol was then added to the suspension. The reaction was stirred and refluxed for 4 hours. A white solid precipitated, which was then filtrated and washed with cold methanol, while the remaining solution was left to evaporate to afford more product. 350 mg of **L7** were obtained (45 % yield). ¹H NMR (400 MHz, Chloroform-*d*) δ 8.54 (d, 2H), 8.46 (d, 2H), 7.91 (d, 2H), 7.46 (d, *J* = 8.1 Hz, 2H), 7.36 (d, *J* = 8.0 Hz, 2H), 7.13 (d, *J* = 4.7 Hz, 2H), 4.53 (s, 2H), 3.74 (s, 6H), 3.50 (s, 2H), 3.14 (d, *J* = 12.5 Hz, 2H), 2.77 (d, *J* = 12.4 Hz, 2H), 1.82 (s, 3H). ¹³C NMR (101 MHz, CDCl₃) δ 202.21, 167.39 (2C), 149.33 (4C), 148.63 (3C), 134.86 (2C), 132.00 (2C), 124.59 (2C), 124.20 (2C), 121.35 (2C), 71.71 (2C), 62.54 (2C), 62.06, 57.83 (2C), 52.96 (2C), 43.56. MS-ESI *calcd* for C₃₀H₂₉F₃N₄O₆ 598.20; found: [M+H]⁺: 599.20

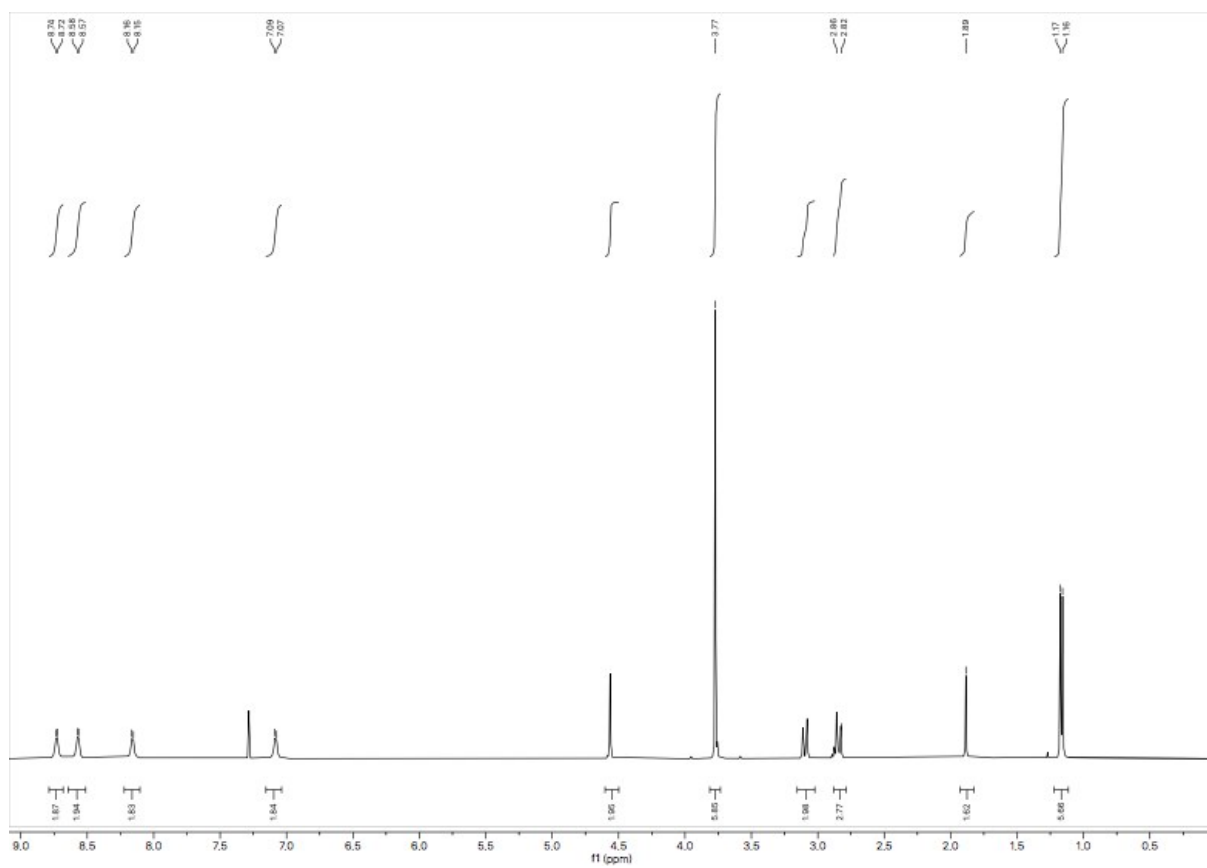


Figure S1. ^1H -NMR spectrum of **L2** in CDCl_3 .

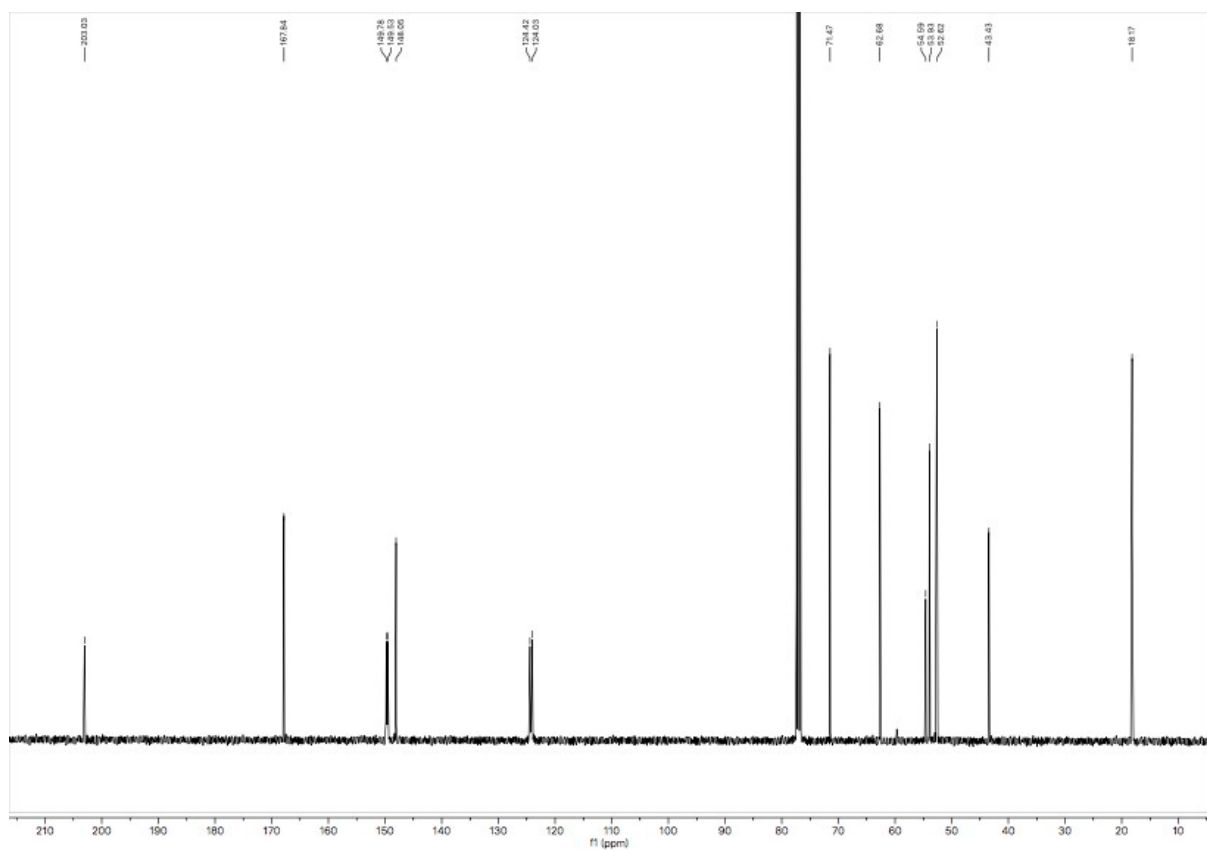


Figure S2. ^{13}C -NMR spectrum of **L2** in CDCl_3 .

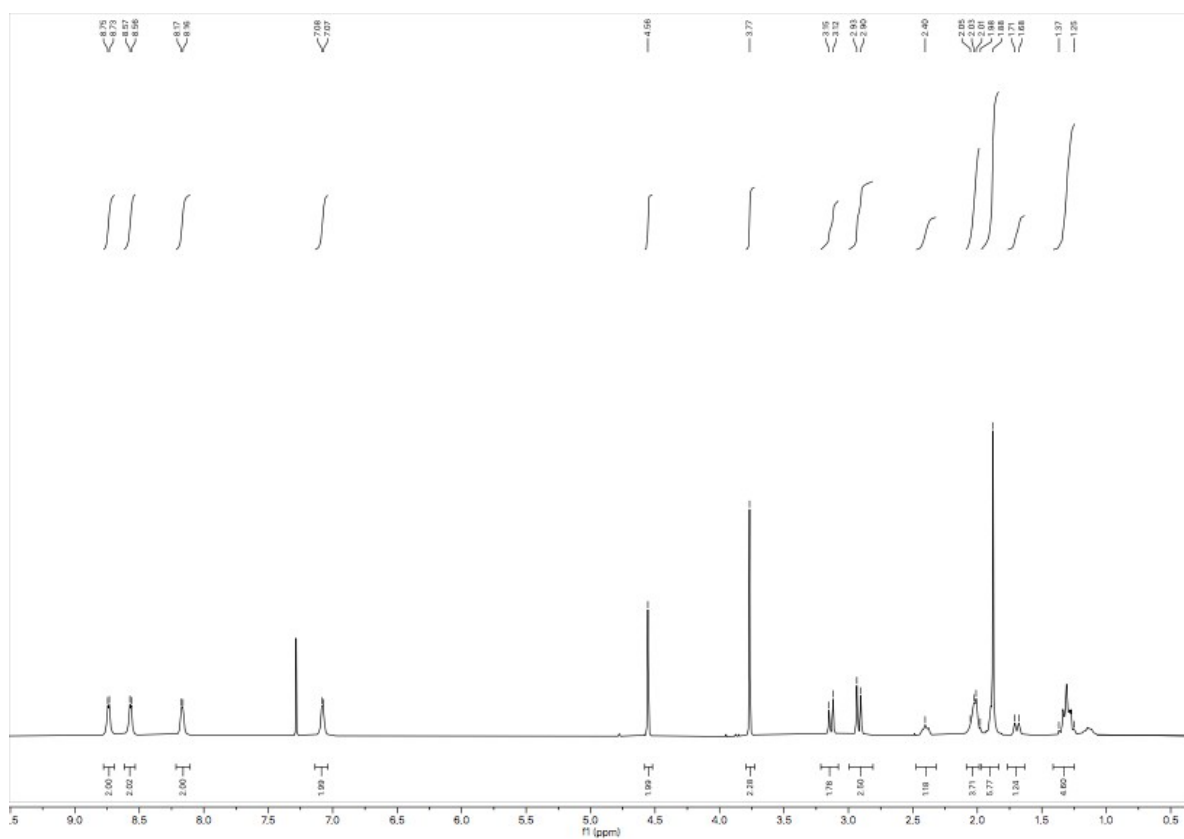


Figure S3. ^1H -NMR spectrum of **L3** in CDCl_3 .

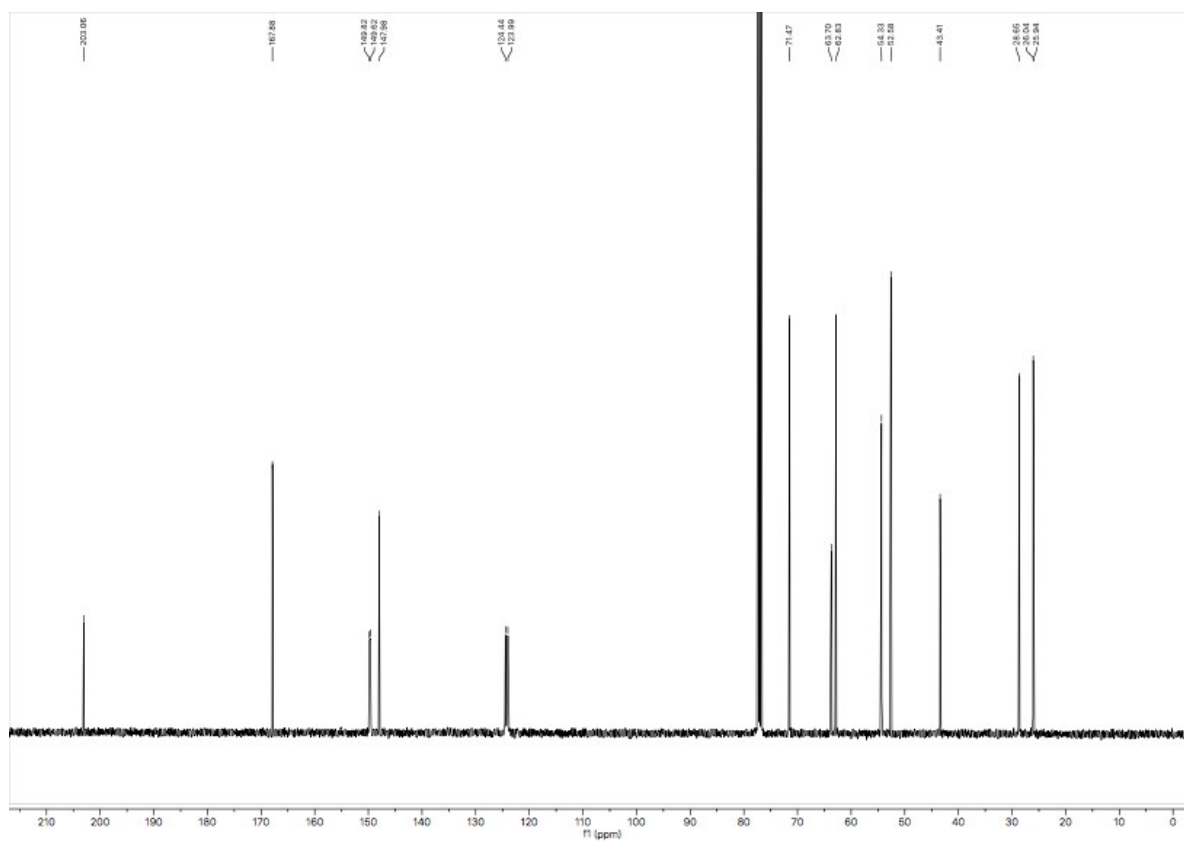


Figure S4. ^{13}C -NMR spectrum of **L3** in CDCl_3 .

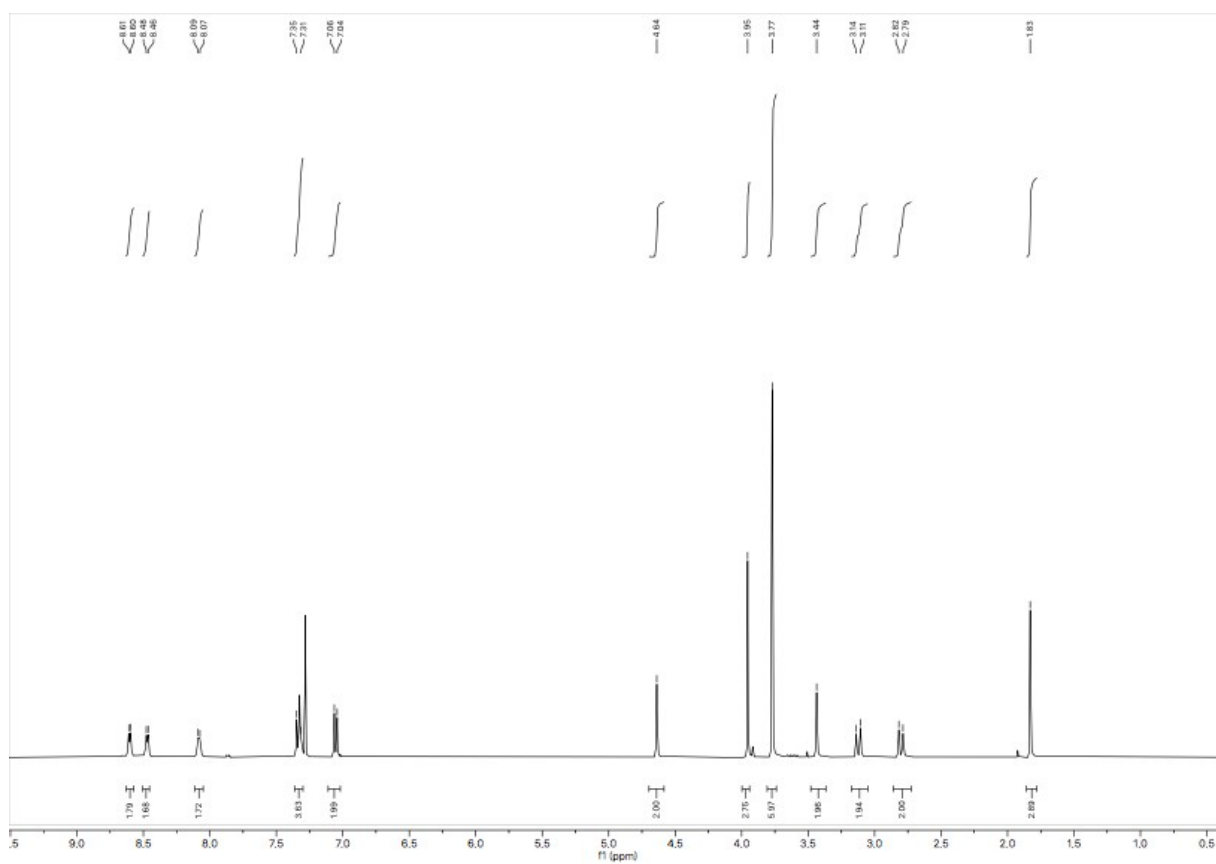


Figure S5. $^1\text{H-NMR}$ spectrum of **L5** in CDCl_3 .

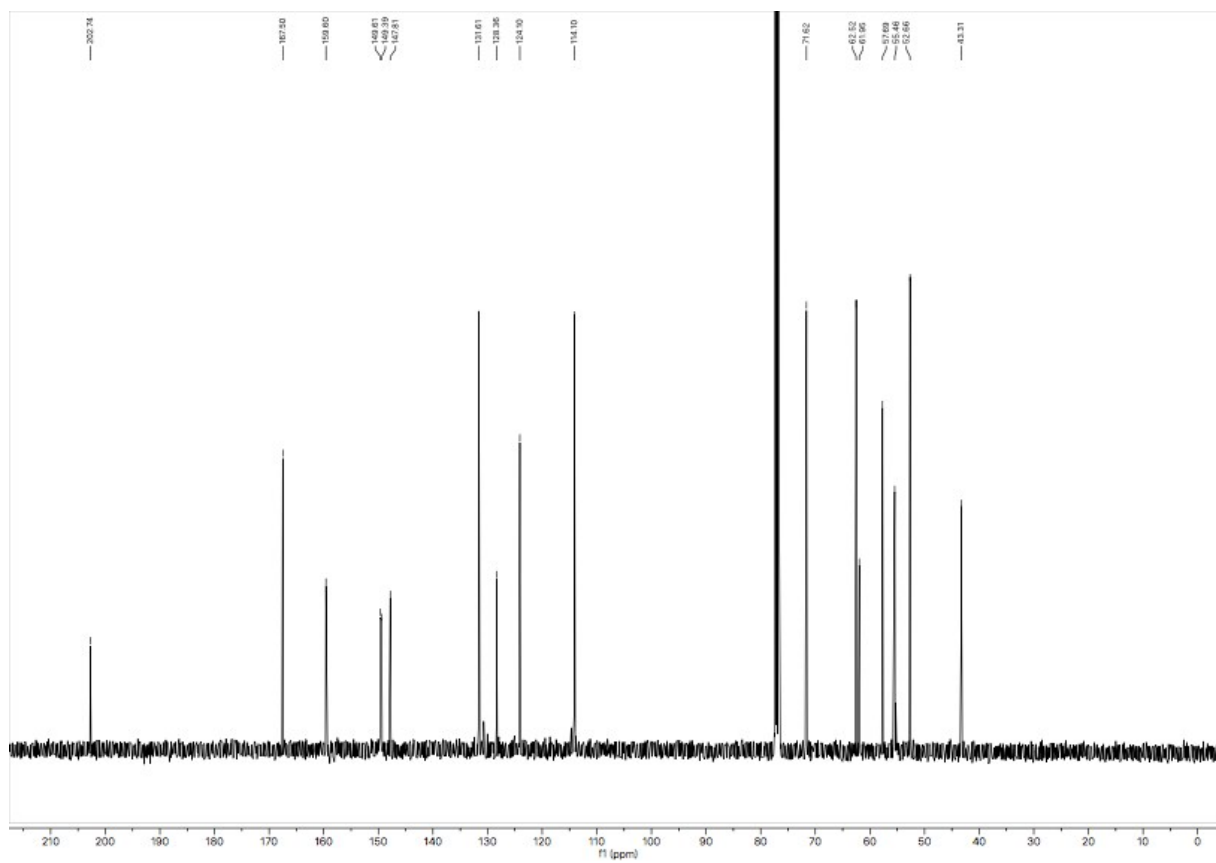


Figure S6. $^{13}\text{C-NMR}$ spectrum of **L5** in CDCl_3 .

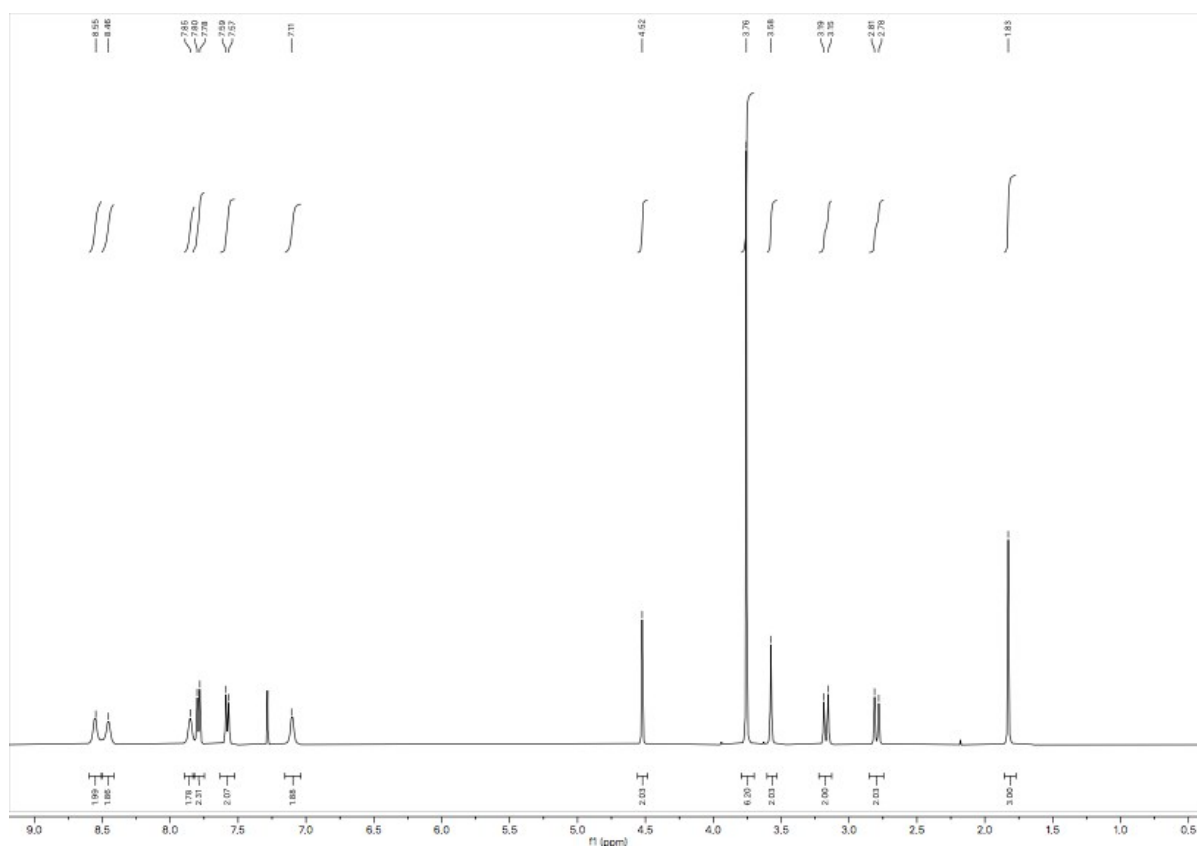


Figure S7. ^1H -NMR spectrum of **L6** in CDCl_3 .

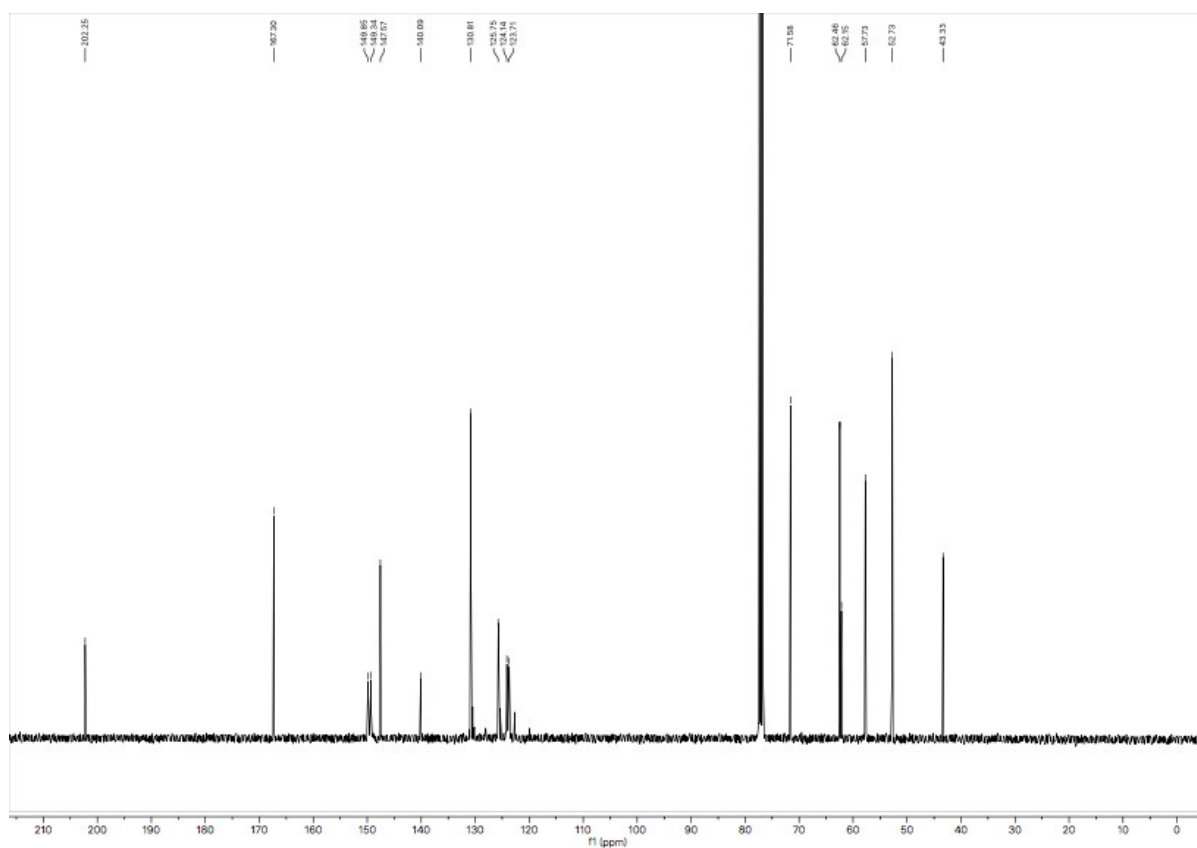


Figure S8. ^{13}C -NMR spectrum of **L6** in CDCl_3 .

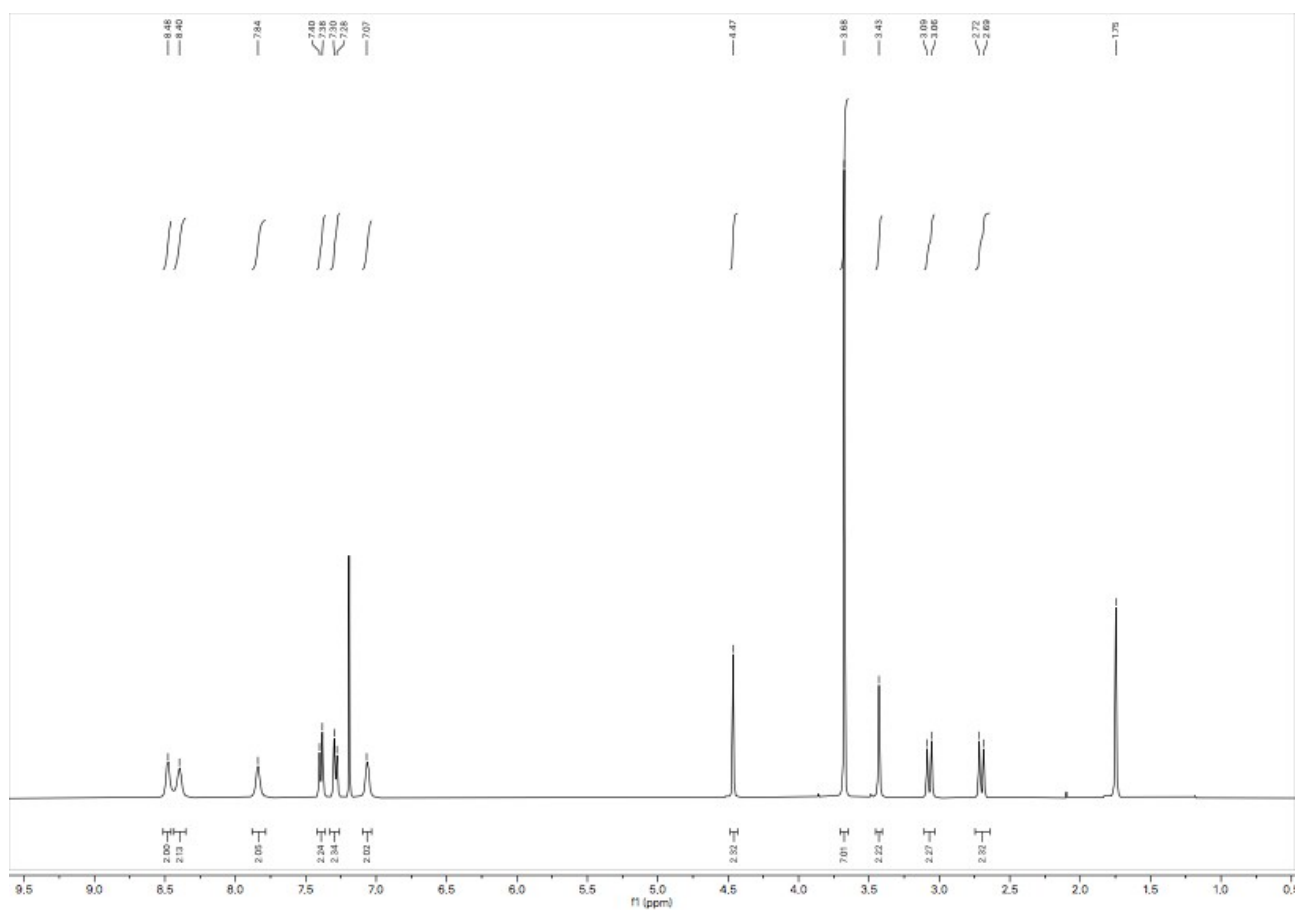


Figure S9. ^1H -NMR spectrum of **L7** in CDCl_3 .

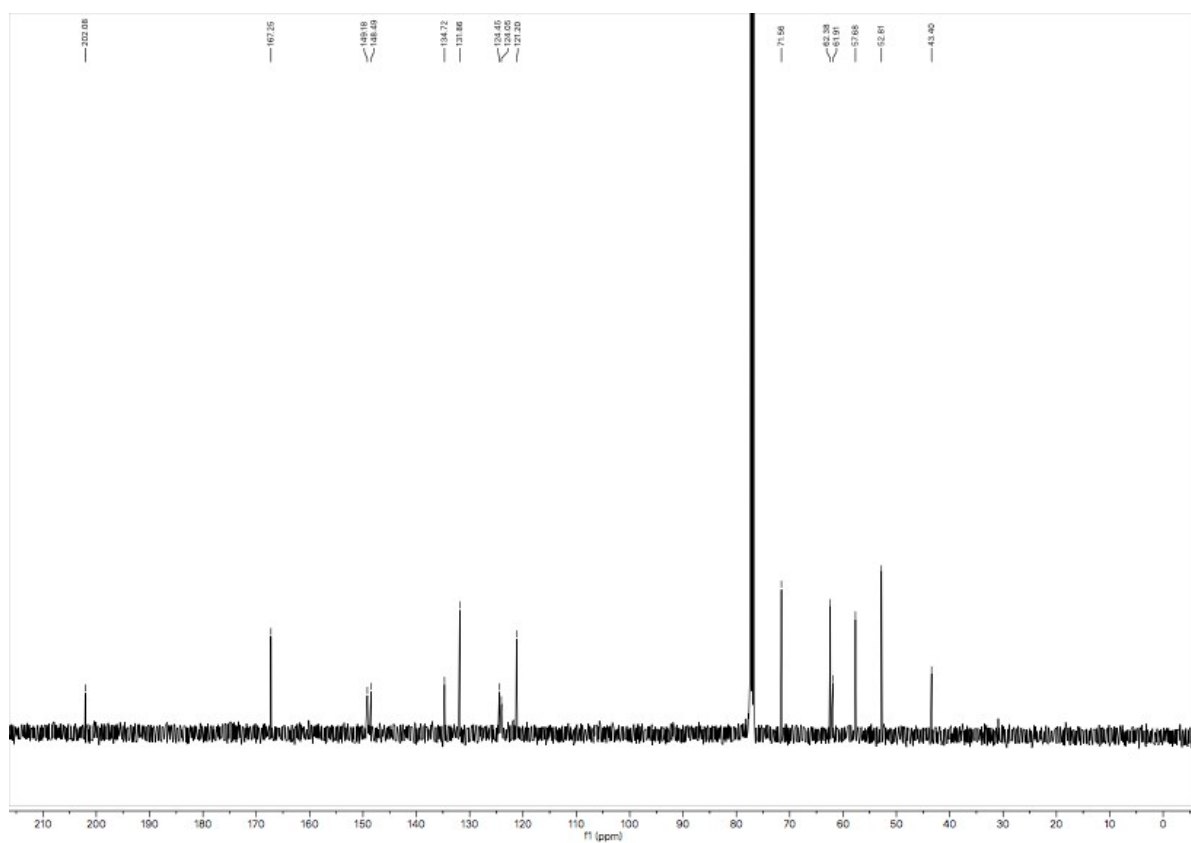


Figure S10. ^{13}C -NMR spectrum of **L7** in CDCl_3 .

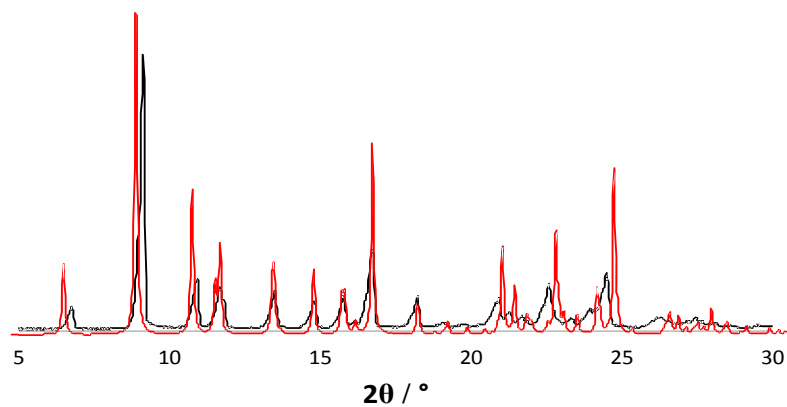


Figure S11. X-ray powder diffraction pattern for **L1** (black line) compared to simulated form SC data (red line).

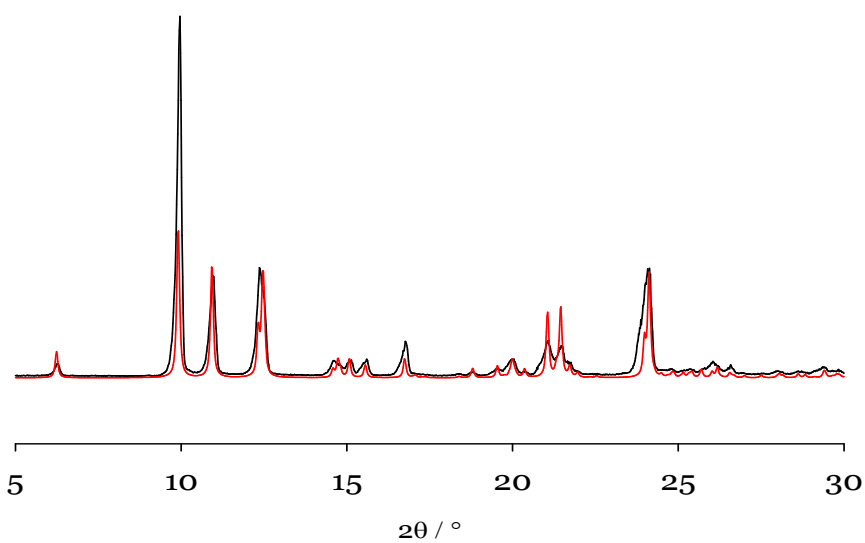


Figure S12. X-ray powder diffraction pattern for **L2** (black line) compared to simulated form SC data (red line).

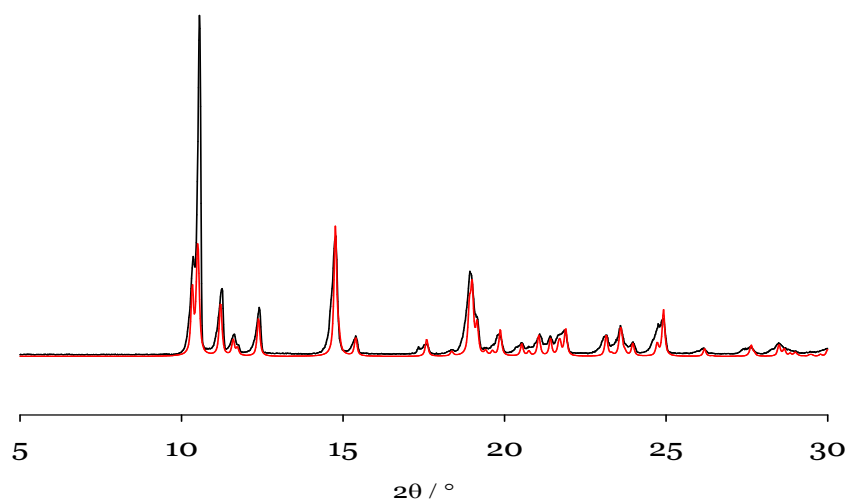


Figure S13. X-ray powder diffraction pattern for **L3** (black line) compared to simulated form SC data (red line).

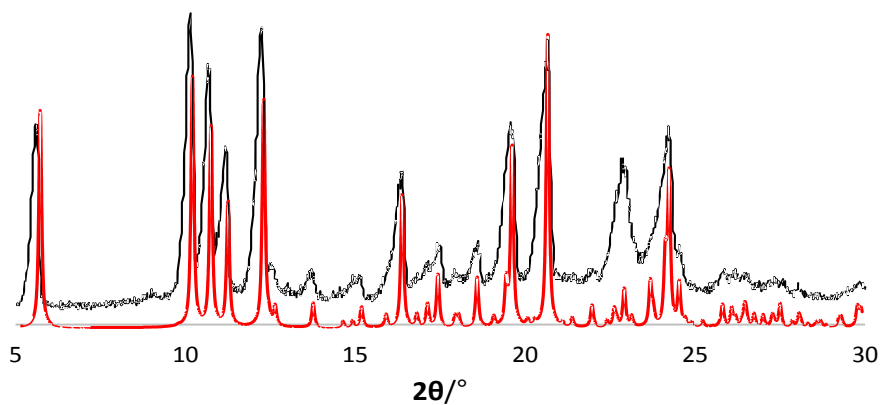


Figure S14. X-ray powder diffraction pattern for **L4** (black line) compared to simulated form SC data (red line).

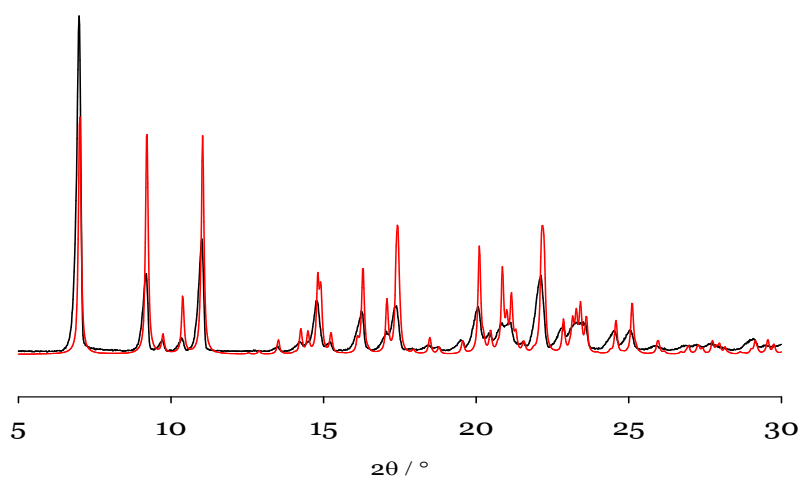


Figure S15. X-ray powder diffraction pattern for **L5** (black line) compared to simulated form SC data (red line).

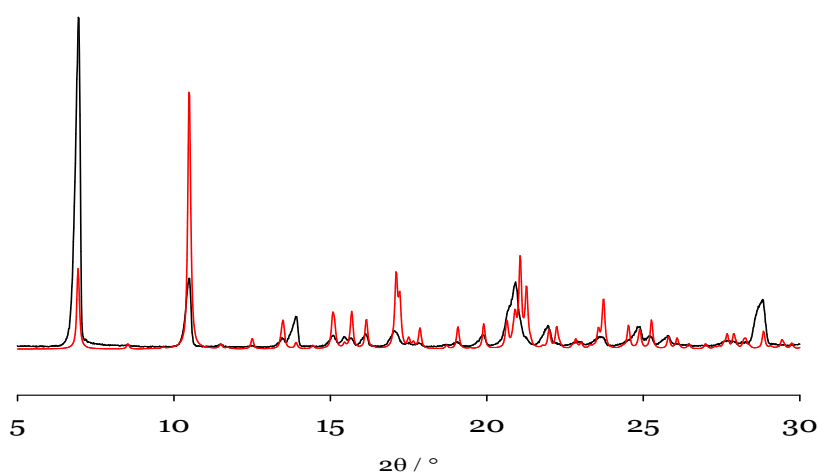


Figure S16 X-ray powder diffraction pattern for **L6** (black line) compared to simulated form SC data (red line).

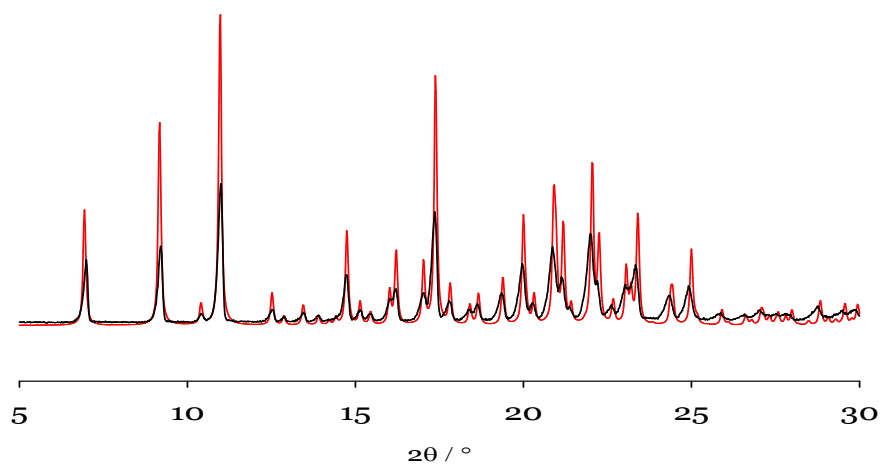


Figure S17. X-ray powder diffraction pattern for **L7** (black line) compared to simulated form SC data (red line).

DFT-CALCULATIONS

Solid-state DFT calculations were performed assuming the GGA PBE functional¹. A numerical double zeta numerical basis set plus polarisation functions on all atoms (i.e. DNP set, roughly comparable with the usual 6-31G** gaussian contracted basis) centered on atoms has been used. Explicit van der Waals corrections² were also included to include important subtle inter and intra-particle interactions.³ The DMol³ package⁴ was employed for all the solid-state calculations.

In the case of solid-state calculations, fixed experimental X-ray determined unit cells were used while atomic coordinates of all atoms were free to relax maintaining space group symmetry constraints. Lattice energies have been estimated as the difference (normalised by the number of the molecules) between the unit cell (immersed into crystalline architectures) energy and the sum of the energy of the free molecules. Lattice energies were roughly decomposed into van der Waals and dipole components of the interaction by the usage of explicit van der Waals corrections. Geometrical parameters optimised at the PBE/DNP level are listed below in pdb format.

Dipole moments, polarizabilities, volumes and surfaces have been evaluated for isolated molecules assuming the geometrical parameters of solid-state calculations. The corresponding B3LYP/6-31G** calculations have been performed by Gaussian09 suite of programs.⁶

Table S1. Summary of the lattice energy, E_{dimer} values, their break down into van der Waals, E_{vdW} and electrostatic E_{electr} terms(kcal/mol), ($E^* = E_{\text{dimer}} / 2$) and Dipole μ (D).

	E_{dimer}	E^*	E_{vdW}	E_{Electr}	μ	
L1	-125.45	-62.725	-81.31	-44.14	0	
L2	-125.51	-62.755	-83.49	-42.01	0	
L3	-149.42		-93.57	-55.84	6.0765	Dimer 1
	-156.34		-96.30	-60.04	4.0319	Dimer 2
	-150.61		-93.71	-56.90	5.9315	Dimer 3
L4	-166.75		-106.25	-60.49	1.6614	Dimer 1
	-152.76		-106.25	-46.51	3.9757	Dimer 2
	-161.12	-80.56	-105.18	-55.94	0	Dimer 3
L5	-161.31		-102.73	-58.58	4.4619	Dimer 1
	-150.23		-96.86	-53.36	1.9313	Dimer 2
	-156.50		-98.04	-58.47	3.3153	Dimer 3
L6	-136.77	-68.385	-91.50	-45.27	0	
L7	-166.05		-109.22	-56.84	13.4777	Dimer 1
	-160.01		-103.50	-56.50	10.2553	Dimer 2
	-146.05		-98.86	-47.19	5.4034	Dimer 3
	-155.80		-103.03	-52.77	5.5904	Dimer 4

X-ray characterization.

Prism-like colorless single crystals of ligands **L2**, **L3**, **L6** and **L7** and of the **L6** 2:1 complex suitable for SC-XRD are obtained by slow evaporation of a methanol solution at room temperature. A single crystal is glued in a glass fiber and mounted for X-ray diffraction data analysis. The SC-XRD data were recorded at room temperature for **L2** and **L3**, while for **L6** and **L7** at 120 K and 150 K, respectively. The data of the **L6**-complex were also collected at 120K.

Intensity data were collected on a Bruker Apex II CCD diffractometer, using graphite-monochromatized Mo-K α radiation ($\lambda = 0.71073 \text{ \AA}$). Intensity data were corrected for Lorentz-polarization effects and for absorption (SADABS ⁷). The structures were solved by direct methods (SIR-97 ⁸) and completed by iterative cycles of full-matrix least squares refinement on F_o^2 and ΔF synthesis using the SHELXL-18 ⁹ program (WinGX suite ¹⁰).

The hydrogen atoms bonded to carbon were included at geometrically calculated positions and refined using a riding model. Uiso(H) were defined as 1.2Ueq of the parent carbon atoms for phenyl and methylene residues and 1.5Ueq of the parent carbon atoms for the methyl group. The hydrogen atoms related to the H₂O molecule in the **L6** dimeric complex were not located. These data can be obtained free of charge via www.ccdc.cam.ac.uk/conts/retrieving.html (or from the Cambridge Crystallographic Data Centre, 12, Union Road, Cambridge CB21EZ, UK; fax: ++44 1223 336 033; or deposit@ccdc.cam.ac.uk). CCDC-1921625 (**L2**), CCDC-1921624 (**L3**), CCDC-1921632 (**L6**), CCDC-1921627 (**L7**) and CCDC-1983773 (**L6**, 2:1 Mn-complex) numbers contain the supplementary crystallographic data for this paper. Crystallographic data were summarized in Tables S2-S7.

L5: A block-like colorless single crystal of **L5** was mounted in a nylon loop for single crystal X-ray analysis. Single-crystal XRD data were collected on a Bruker X8 Prospector APEX-II/CCD diffractometer equipped with a microfocusing mirror (Cu-K α radiation, $\lambda = 1.54178 \text{ \AA}$) at room temperature. The structure was determined using direct methods (SHELXTL 97) and refined (based on F2 using all independent data) by full-matrix least-squares methods (SHELX 2014). All non-hydrogen atoms were located from different Fourier maps and refined with anisotropic displacement parameters. Hydrogen atoms were added in riding positions. CCDC-1986612

1. J. P. Perdew, K. Burke and M. E. Ernzerhof, *Phys. Rev. Lett.*, 1996, 77, 3865–3868; (b) J. P. Perdew, K. Burke and M. E. Ernzerhof, *Phys. Rev. Lett.*, 1997, 78, 1396–1396.
2. S. Grimme, *J. Chem. Phys.*, 2006, 124, 34108;
3. a) A. Baggioli, S. V. Meille, G. Raos, R. Po, M. Brinkmann and A. Famulari, *Int. J. Quantum Chem.*, 2013, 113, 2154; b) A. Baggioli and A. Famulari, *Phys. Chem. Chem. Phys.*, 2014, 16, 3983.
4. B. Delley, *J. Chem. Phys.*, 2000, 113, 7756.
5. Gaussian 09, Revision A.02, M. J. Frisch, G. W. Trucks, H. B. Schlegel, G. E. Scuseria, M. A. Robb, J. R. Cheeseman, G. Scalmani, V. Barone, G. A. Petersson, H. Nakatsuji, X. Li, M. Caricato, A. Marenich, J. Bloino, B. G. Janesko, R. Gomperts, B. Mennucci, H. P. Hratchian, J. V. Ortiz, A. F. Izmaylov, J. L. Sonnenberg, D. Williams-Young, F. Ding, F. Lipparini, F. Egidi, J. Goings, B. Peng, A. Petrone, T. Henderson, D. Ranasinghe, V. G. Zakrzewski, J. Gao, N. Rega, G. Zheng, W. Liang, M. Hada, M. Ehara, K. Toyota, R. Fukuda, J. Hasegawa, M. Ishida, T. Nakajima, Y. Honda, O. Kitao, H. Nakai, T. Vreven, K. Throssell, J. A. Montgomery, Jr., J. E. Peralta, F. Ogliaro, M. Bearpark, J. J. Heyd, E. Brothers, K. N. Kudin, V. N. Staroverov, T. Keith, R. Kobayashi, J. Normand, K. Raghavachari, A. Rendell, J. C. Burant, S. S. Iyengar, J. Tomasi, M. Cossi, J. M. Millam, M. Klene, C. Adamo, R. Cammi, J. W. Ochterski, R. L. Martin, K. Morokuma, O. Farkas, J. B. Foresman, and D. J. Fox, Gaussian, Inc., Wallingford CT, 2016.
6. L. J. Farrugia, *J. Appl. Cryst.*, 1999, 32, 837.
7. G. M. Sheldrick, SADABS Area-Detector Absorption Correction Program, Bruker AXS Inc., Madison, WI, USA, 2000.
8. Altomare; M. C. Burla, M. Camalli, G. L. Cascarano, C. Giacovazzo, A. Guagliardi, A. G. G. Moliterni, G. Polidori, R. Spagna, *J. Appl. Cryst.*, 1999, 32, 115.
9. Sheldrick, G. M. *Acta Cryst. C* 2015, 71, 3-8.
10. L. J. Farrugia, *J. Appl. Cryst.*, 2012, 45, 849.

Table S2: Crystallographic data of ligand **L2**.

Parameters	L2
Empirical formula	C25 H30 N4 O5
Formula weight	466.53
Temperature	294(2) K
Wavelength	0.710738 Å
Crystal system	Monoclinic
Space group	P 2 ₁ /c
Unit cell dimensions	$a = 14.548(7)$ Å $b = 11.382(2)$ Å $\beta = 103.41(3)$ ° $c = 14.751(3)$ Å
Volume	2375.8(9) Å ³
Z	4
Density (calculated)	1.304 mg/m ³
Absorption coefficient	0.082 mm ⁻¹
F (000)	992
Crystal size	N/A
θ range for data collection	1.439 to 31.529°
Index ranges	-21 ≤ h ≤ 21, -16 ≤ k ≤ 16, -21 ≤ l ≤ 21
Reflections collected	24216
Independent reflections	7403 [R(int) = 0.0203]
Completeness to $\theta = 25.242^\circ$	99.9%
Absorption correction	N/A
Refinement method	Full-matrix least-squares on F ²
Data / Restraints / Parameters	7403 / 0 / 427
Goodness-of-fit on F ²	1.036
Final R indices [I > 2σ(I)]	R1 = 0.0591, wR2 = 0.1473
R indices (all data)	R1 = 0.0770, wR2 = 0.1638

Largest diff. peak and hole 0.396 and -0.306 e.Å⁻³

Table S3: Crystallographic data of ligand **L3**.

Parameters	L3
Empirical formula	C28 H34 N4 O5
Formula weight	506.59
Temperature	294(2) K
Wavelength	0.071073 Å
Crystal system	Monoclinic
Space group	P 2 ₁
Unit cell dimensions	$a = 9.2923(19)$ Å $b = 16.814(3)$ Å $\beta = 114.86(3)$ ° $c = 9.4272(12)$ Å
Volume	1336.4(6) Å ³
Z	2
Density (calculated)	1.259 mg/m ³
Absorption coefficient	0.087 mm ⁻¹
F (000)	534
Crystal size	N/A
θ range for data collection	2.381 to 31.674°
Index ranges	-13 ≤ h ≤ 13, -24 ≤ k ≤ 24, -13 ≤ l ≤ 13
Reflections collected	14015
Independent reflections	7970 [R(int) = 0.0164]
Completeness to $\theta = 25.242^\circ$	100.0%
Absorption correction	N/A
Refinement method	Full-matrix least-squares on F ²
Data / Restraints / Parameters	7970 / 0 / 394
Goodness-of-fit on F ²	1.051
Final R indices [I > 2σ(I)]	R1 = 0.0485, wR2 = 0.1192
R indices (all data)	R1 = 0.0559, wR2 = 0.1274

Largest diff. peak and hole

0.269 and -0.244 e.Å⁻³**Table S4:** Crystallographic data of ligand **L5**.

Empirical formula	C ₃₀ H ₃₂ N ₄ O ₆	
Formula weight	544.59	
Temperature	296(2) K	
Wavelength	1.54178 Å	
Crystal system	Orthorhombic	
Space group	P b c a	
Unit cell dimensions	a = 13.089(11) Å	α = 90°.
	b = 17.019(14) Å	β = 90°.
	c = 25.19(2) Å	γ = 90°.
Volume	5611(8) Å ³	
Z	8	
Density (calculated)	1.289 Mg/m ³	
Absorption coefficient	0.746 mm ⁻¹	
F(000)	2304	
Crystal size	0.100 x 0.100 x 0.050 mm ³	
Theta range for data collection	11.426 to 51.052°.	
Index ranges	-12 ≤ h ≤ 10, -14 ≤ k ≤ 17, -25 ≤ l ≤ 22	
Reflections collected	9061	
Independent reflections	2685 [R(int) = 0.2320]	
Completeness to theta = 51.052°	88.8 %	
Refinement method	Full-matrix least-squares on F ²	
Data / restraints / parameters	2685 / 0 / 365	
Goodness-of-fit on F ²	0.976	
Final R indices [I > 2σ(I)]	R1 = 0.0667, wR2 = 0.1242	
R indices (all data)	R1 = 0.1540, wR2 = 0.1527	
Extinction coefficient	n/a	
Largest diff. peak and hole	0.187 and -0.198 e.Å ⁻³	

Table S5: Crystallographic data of ligand **L6**.

Parameters	L6
Empirical formula	C30 H29 F3 N4 O5
Formula weight	582.57
Temperature	120(2) K
Wavelength	0.71073 Å
Crystal system	Monoclinic
Space group	P 2 ₁ /c
Unit cell dimensions	$a = 12.767(3)$ Å $b = 13.128(3)$ Å $\beta = 98.68(3)$ ° $c = 16.753(3)$ Å
Volume	2779.0(10) Å ³
Z	4
Density (calculated)	1.392 mg/m ³
Absorption coefficient	0.109 mm ⁻¹
F (000)	1216
Crystal size	N/A
θ range for data collection	1.612 to 31.644°
Index ranges	-18 ≤ h ≤ 17, -19 ≤ k ≤ 19, -23 ≤ l ≤ 24
Reflections collected	31388
Independent reflections	8757 [R(int) = 0.0185]
Completeness to $\theta = 25.242^\circ$	100.0%
Absorption correction	N/A
Refinement method	Full-matrix least-squares on F ²
Data / Restraints / Parameters	8757/ 0 / 379
Goodness-of-fit on F ²	1.058
Final R indices [$I > 2\sigma(I)$]	R1 = 0.0517, wR2 = 0.1202
R indices (all data)	R1 = 0.0667, wR2 = 0.1299

Largest diff. peak and hole

0.56 and -0.57 e.Å⁻³**Table S6:** Crystallographic data of ligand **L7**.

Parameters	L7
Empirical formula	C30 H29 F3 N4 O6
Formula weight	598.20
Temperature	150(2) K
Wavelength	0.71073 Å
Crystal system	Orthorhombic
Space group	P b c a
	$a = 13.1269(3)$ Å
	$b = 16.7438(3)$ Å
Unit cell dimensions	$c = 25.5484(5)$ Å
Volume	5615.4(2) Å ³
Z	8
Density (calculated)	1.42 mg/m ³
Absorption coefficient	0.113 mm ⁻¹
F(000)	2496
Crystal size	N/A
θ range for data collection	1.594 to 21.228°
Index ranges	-13 ≤ h ≤ 13, -17 ≤ k ≤ 16, -25 ≤ l ≤ 25
Reflections collected	22575
Independent reflections	3083 [R(int) = 0.0431]
Completeness to θ = 21.228°	100.0%
Absorption correction	N/A
Refinement method	Full-matrix least-squares on F ²
Data / Restraints / Parameters	2122 / 0 / 388
Goodness-of-fit on F ²	1.015
Final R indices [I > 2σ(I)]	R1 = 0.0425, wR2 = 0.0984
R indices (all data)	R1 = 0.0734 wR2 = 0.1079

Largest diff. peak and hole

0.49 and -0.41 e.Å⁻³**Table S7:** Crystallographic data of L6 dimeric complex.

Parameters	6·TCM^{SC} H₂O MeOH
Empirical formula	C ₃₂ H ₃₈ Cl ₄ F ₃ Mn _{0.5} N ₄ O ₈
Formula weight	830.92
Temperature	120(2) K
Wavelength	0.71073 Å
Crystal system	Monoclinic
Space group	P 2 ₁ /n
Unit cell dimensions	$a = 8.3380(17)$ Å $b = 27.317(6)$ Å $\beta = 94.12(3)$ ° $c = 16.519(3)$ Å
Volume	3752.8(13) Å ³
Z	4
Density (calculated)	1.471 mg/m ³
Absorption coefficient	0.544 mm ⁻¹
F (000)	1710
Crystal size	0.040 x 0.300 x 0.030 mm ³
Θ range for data collection	1.443 to 26.371°
Index ranges	-10 ≤ h ≤ 10, -34 ≤ k ≤ 34, -20 ≤ l ≤ 20
Reflections collected	28376
Independent reflections	7686 [R(int) = 0.0258]
Completeness to θ = 26.371°	100.0%
Refinement method	Full-matrix least-squares on F ²
Data / Restraints / Parameters	7686 / 0 / 477
Goodness-of-fit on F ²	1.065
Final R indices [I > 2σ(I)]	R1 = 0.1022, wR2 = 0.2700
R indices (all data)	R1 = 0.1237, wR2 = 0.2892
Largest diff. peak and hole	2.22 and -2.33 e.Å ⁻³

Structure L1 (pdb file)

REMARK L1 PDB file

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ORIGX3 0.000000 0.000000 1.000000 0.000000
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SCALE2 0.000000 0.101994 -0.006339 0.000000
SCALE3 0.000000 0.000000 0.075786 0.000000
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ATOM 3 O1 MOL 2 2.252 2.363 13.479 1.00 0.06 O1-
ATOM 4 O3 MOL 2 0.360 1.078 11.482 1.00 0.05 O1-
ATOM 5 O4 MOL 2 0.735 -1.636 10.226 1.00 0.05 O
ATOM 6 C10 MOL 2 3.100 -0.230 9.743 1.00 0.03 C
ATOM 7 H8 MOL 2 3.048 -0.843 10.506 1.00 0.04 H
ATOM 8 N3 MOL 2 4.155 0.757 10.035 1.00 0.03 N
ATOM 9 N4 MOL 2 4.308 -2.595 6.324 1.00 0.06 N1-
ATOM 10 N5 MOL 2 2.433 2.631 8.625 1.00 0.04 N
ATOM 11 C1 MOL 2 -0.193 -2.737 10.057 1.00 0.06 C
ATOM 12 H3 MOL 2 -1.093 -2.411 10.135 1.00 0.09 H
ATOM 13 H1 MOL 2 -0.033 -3.398 10.734 1.00 0.09 H
ATOM 14 H27 MOL 2 -0.069 -3.130 9.190 1.00 0.09 H
ATOM 15 C2 MOL 2 0.653 -0.655 9.331 1.00 0.04 C
ATOM 16 C3 MOL 2 1.695 0.434 9.572 1.00 0.03 C
ATOM 17 C4 MOL 2 3.839 1.643 11.168 1.00 0.03 C
ATOM 18 H22 MOL 2 3.869 1.103 11.985 1.00 0.04 H
ATOM 19 C5 MOL 2 4.915 2.709 11.281 1.00 0.04 C
ATOM 20 C6 MOL 2 5.388 3.397 10.178 1.00 0.05 C
ATOM 21 H23 MOL 2 5.040 3.225 9.333 1.00 0.05 H
ATOM 22 C7 MOL 2 6.382 4.344 10.346 1.00 0.05 C
ATOM 23 H24 MOL 2 6.689 4.795 9.593 1.00 0.06 H
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ATOM 25 C9 MOL 2 3.487 -1.048 8.521 1.00 0.04 C
ATOM 26 C10 MOL 2 3.497 -2.428 8.572 1.00 0.05 C
ATOM 27 H7 MOL 2 3.225 -2.867 9.345 1.00 0.06 H
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ATOM 29 H6 MOL 2 3.920 -4.081 7.537 1.00 0.07 H
ATOM 30 C12 MOL 2 4.272 -1.263 6.281 1.00 0.05 C
ATOM 31 H5 MOL 2 4.521 -0.846 5.488 1.00 0.06 H
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ATOM 33 H4 MOL 2 3.904 0.461 7.248 1.00 0.05 H
ATOM 34 C14 MOL 2 5.393 0.035 10.359 1.00 0.05 C
ATOM 35 H9 MOL 2 6.095 0.667 10.535 1.00 0.07 H
ATOM 36 H10 MOL 2 5.643 -0.522 9.618 1.00 0.07 H
ATOM 37 H11 MOL 2 5.252 -0.511 11.137 1.00 0.07 H
ATOM 38 C15 MOL 2 2.417 2.293 11.082 1.00 0.03 C
ATOM 39 C16 MOL 2 2.153 2.941 12.440 1.00 0.04 C
ATOM 40 C17 MOL 2 1.548 4.846 13.632 1.00 0.07 C
ATOM 41 H12 MOL 2 0.798 4.408 14.042 1.00 0.10 H
ATOM 42 H14 MOL 2 1.342 5.773 13.495 1.00 0.10 H
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ATOM 56 H26 MOL 2 5.210 2.561 13.280 1.00 0.06 H
ATOM 57 C23 MOL 2 6.468 3.968 12.573 1.00 0.06 C
ATOM 58 H25 MOL 2 6.835 4.156 13.406 1.00 0.07 H
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CONECT 2 16
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Structure L2 (pdb file)

REMARK L2 PDB file

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ORIGX3 0.000000 0.000000 1.000000 0.000000
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SCALE2 0.000000 0.087858 0.000000 0.000000
SCALE3 0.000000 0.000000 0.069692 0.000000
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ATOM 2 C2 MOL 2 5.755 1.006 15.859 1.00 0.03 C
ATOM 3 C3 MOL 2 6.750 1.599 16.881 1.00 0.03 C
ATOM 4 C4 MOL 2 7.786 -0.526 17.212 1.00 0.04 C
ATOM 5 C5 MOL 2 6.841 -1.205 16.190 1.00 0.03 C
ATOM 6 C6 MOL 2 7.302 -1.198 14.690 1.00 0.03 C
ATOM 7 C7 MOL 2 6.225 1.006 14.365 1.00 0.03 C
ATOM 8 C8 MOL 2 6.624 -2.648 16.659 1.00 0.04 C
ATOM 9 C9 MOL 2 4.410 1.736 15.887 1.00 0.04 C
ATOM 10 C10 MOL 2 5.720 -4.750 16.129 1.00 0.07 C
ATOM 11 C11 MOL 2 3.142 3.473 16.813 1.00 0.08 C
ATOM 12 C12 MOL 2 8.899 1.486 17.968 1.00 0.05 C
ATOM 13 C13 MOL 2 10.217 0.766 18.092 1.00 0.09 C
ATOM 14 C14 MOL 2 9.161 2.956 17.681 1.00 0.07 C
ATOM 15 C18 MOL 2 7.614 0.054 12.681 1.00 0.04 C
ATOM 16 C19 MOL 2 6.511 2.430 13.920 1.00 0.03 C
ATOM 17 C20 MOL 2 5.578 3.162 13.206 1.00 0.04 C
ATOM 18 C21 MOL 2 5.893 4.461 12.836 1.00 0.06 C
ATOM 19 C22 MOL 2 7.914 4.355 13.822 1.00 0.05 C
ATOM 20 C23 MOL 2 7.719 3.046 14.218 1.00 0.04 C
ATOM 21 C24 MOL 2 8.632 -1.915 14.535 1.00 0.03 C
ATOM 22 C25 MOL 2 8.705 -3.206 14.041 1.00 0.04 C
ATOM 23 C26 MOL 2 9.948 -3.807 13.910 1.00 0.05 C
ATOM 24 C27 MOL 2 11.015 -1.982 14.708 1.00 0.05 C
ATOM 25 C28 MOL 2 9.829 -1.290 14.862 1.00 0.04 C
ATOM 26 N1 MOL 2 8.029 0.884 16.917 1.00 0.03 N
ATOM 27 N2 MOL 2 7.412 0.164 14.136 1.00 0.03 N
ATOM 28 N3 MOL 2 7.028 5.076 13.140 1.00 0.06 N
ATOM 29 N4 MOL 2 11.099 -3.229 14.241 1.00 0.05 N
ATOM 30 O1 MOL 2 4.515 -0.868 16.754 1.00 0.05 O
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ATOM 33 O4 MOL 2 7.027 -3.082 17.689 1.00 0.08 O
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ATOM 35 H6 MOL 2 6.624 -1.698 14.197 1.00 0.03 H
ATOM 36 H7 MOL 2 5.451 0.690 13.854 1.00 0.03 H
ATOM 37 H20 MOL 2 4.725 2.777 12.954 1.00 0.05 H
ATOM 38 H21 MOL 2 5.266 4.974 12.308 1.00 0.08 H
ATOM 39 H22 MOL 2 8.771 4.792 14.082 1.00 0.06 H
ATOM 40 H23 MOL 2 8.395 2.577 14.700 1.00 0.04 H
ATOM 41 H25 MOL 2 7.895 -3.654 13.761 1.00 0.05 H
ATOM 42 H26 MOL 2 10.009 -4.667 13.504 1.00 0.07 H
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ATOM 63 2H13 MOL 2 10.173 -0.171 18.410 1.00 0.13 H
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Structure L3 (pdb file)

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ORIGX2 0.000000 1.000000 0.000000 0.000000
ORIGX3 0.000000 0.000000 1.000000 0.000000
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SCALE2 0.000000 0.059474 0.000000 0.000000
SCALE3 0.000000 0.000000 0.116909 0.000000
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ATOM 2 O3 MOL 2 -1.430 14.067 -2.875 1.00 0.05 O
ATOM 3 N1 MOL 2 -0.326 15.692 1.528 1.00 0.03 N
ATOM 4 O4 MOL 2 2.911 13.059 1.488 1.00 0.05 O1-
ATOM 5 C2 MOL 2 -0.901 14.727 -0.672 1.00 0.03 C
ATOM 6 O1 MOL 2 1.150 13.778 -1.492 1.00 0.05 O1-
ATOM 7 C4 MOL 2 0.808 14.783 1.668 1.00 0.03 C
ATOM 8 H8A MOL 2 0.919 14.556 2.605 1.00 0.04 H
ATOM 9 H8B MOL 2 1.615 15.233 1.374 1.00 0.04 H
ATOM 10 C1 MOL 2 0.381 13.917 -0.583 1.00 0.03 C
ATOM 11 C5 MOL 2 0.624 13.479 0.847 1.00 0.03 C
ATOM 12 C19 MOL 2 -3.349 14.725 -0.093 1.00 0.03 C
ATOM 13 C12 MOL 2 -0.194 16.935 2.335 1.00 0.04 C
ATOM 14 C6 MOL 2 -0.567 12.560 1.281 1.00 0.03 C
ATOM 15 H13 MOL 2 -0.581 11.781 0.688 1.00 0.03 H
ATOM 16 C24 MOL 2 -0.367 12.066 2.700 1.00 0.03 C
ATOM 17 C7 MOL 2 -2.098 13.866 -0.150 1.00 0.03 C
ATOM 18 5H01 MOL 2 -2.256 13.148 -0.797 1.00 0.04 H
ATOM 19 N3 MOL 2 -5.625 16.368 -0.072 1.00 0.06 N1-
ATOM 20 C28 MOL 2 -0.792 12.784 3.809 1.00 0.04 C
ATOM 21 O2 MOL 2 -1.164 16.236 -2.521 1.00 0.08 O1-
ATOM 22 C25 MOL 2 0.251 10.849 2.941 1.00 0.05 C
ATOM 23 9H01 MOL 2 0.534 10.317 2.233 1.00 0.06 H
ATOM 24 C3 MOL 2 -0.586 16.009 0.141 1.00 0.03 C
ATOM 25 AH02 MOL 2 0.190 16.450 -0.240 1.00 0.04 H
ATOM 26 BH02 MOL 2 -1.336 16.620 0.085 1.00 0.04 H
ATOM 27 C17 MOL 2 -0.423 16.663 3.809 1.00 0.05 C
ATOM 28 C27 MOL 2 -0.578 12.274 5.071 1.00 0.06 C
ATOM 29 2H02 MOL 2 -0.882 12.766 5.800 1.00 0.07 H
ATOM 30 N4 MOL 2 0.042 11.112 5.310 1.00 0.07 N1-
ATOM 31 C9 MOL 2 -1.167 15.125 -2.121 1.00 0.04 C
ATOM 32 C23 MOL 2 -4.248 14.724 -1.147 1.00 0.05 C
ATOM 33 5H02 MOL 2 -4.108 14.179 -1.888 1.00 0.06 H
ATOM 34 C20 MOL 2 -3.629 15.548 0.985 1.00 0.04 C
ATOM 35 C10 MOL 2 3.062 10.762 0.168 1.00 0.05 C
ATOM 36 CH02 MOL 2 3.542 10.875 -0.860 1.00 0.06 H
ATOM 37 C18 MOL 2 -2.933 12.262 1.391 1.00 0.05 C
ATOM 38 DH02 MOL 2 -2.884 11.572 0.725 1.00 0.06 H
ATOM 39 EH02 MOL 2 -3.786 12.699 1.336 1.00 0.06 H
ATOM 40 FH02 MOL 2 -2.829 11.872 2.262 1.00 0.06 H
ATOM 41 C22 MOL 2 -5.361 15.555 -1.078 1.00 0.06 C
ATOM 42 C14 MOL 2 1.099 19.020 2.942 1.00 0.07 C
ATOM 43 C16 MOL 2 -0.419 17.972 4.616 1.00 0.06 C
ATOM 44 C21 MOL 2 -4.758 16.355 0.942 1.00 0.06 C
ATOM 45 C26 MOL 2 0.440 10.436 4.247 1.00 0.07 C
ATOM 46 4H03 MOL 2 0.878 9.628 4.387 1.00 0.08 H
ATOM 47 C15 MOL 2 0.856 18.741 4.411 1.00 0.07 C
ATOM 48 C13 MOL 2 1.099 17.719 2.127 1.00 0.05 C
ATOM 49 C11 MOL 2 -1.652 14.300 -4.276 1.00 0.09 C
ATOM 50 AH03 MOL 2 -2.332 14.970 -4.385 1.00 0.11 H
ATOM 51 BH03 MOL 2 -1.935 13.485 -4.696 1.00 0.11 H
ATOM 52 CH03 MOL 2 -0.837 14.604 -4.683 1.00 0.11 H
ATOM 53 O5 MOL 2 1.854 11.554 0.225 1.00 0.04 O
ATOM 54 C8 MOL 2 1.934 12.691 0.911 1.00 0.03 C
ATOM 55 H1 MOL 2 -1.226 13.603 3.670 1.00 0.04 H
ATOM 56 H10 MOL 2 -3.053 15.568 1.736 1.00 0.04 H
ATOM 57 H11 MOL 2 -4.982 16.949 1.728 1.00 0.06 H
ATOM 58 H12 MOL 2 -5.979 15.536 -1.856 1.00 0.07 H
ATOM 59 AH12 MOL 2 -0.950 17.520 2.070 1.00 0.05 H
ATOM 60 AH17 MOL 2 0.353 16.091 4.191 1.00 0.07 H
ATOM 61 AH16 MOL 2 -1.050 18.529 4.251 1.00 0.05 H
ATOM 62 BH17 MOL 2 -1.351 16.192 3.918 1.00 0.07 H
ATOM 63 BH13 MOL 2 1.216 17.873 1.146 1.00 0.08 H
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ATOM	64	BH14	MOL	2	1.927	19.538	2.720	1.00	0.08	H
ATOM	65	AH13	MOL	2	1.847	17.133	2.472	1.00	0.09	H
ATOM	66	AH14	MOL	2	0.234	19.555	2.643	1.00	0.07	H
ATOM	67	BH16	MOL	2	-0.566	17.772	5.594	1.00	0.08	H
ATOM	68	AH15	MOL	2	1.698	18.159	4.739	1.00	0.09	H
ATOM	69	BH15	MOL	2	0.818	19.588	4.953	1.00	0.09	H
ATOM	70	H	MOL	2	12.100	9.666	0.350	1.00	0.00	H
ATOM	71	H	MOL	2	13.082	11.122	0.968	1.00	0.00	H
TER	72									
CONNECT	2	18	15	38						
CONNECT	3	32	50							
CONNECT	4	25	8	14						
CONNECT	5	55								
CONNECT	6	11	32	25	18					
CONNECT	7	11								
CONNECT	8	4	12	9	10					
CONNECT	9	8								
CONNECT	10	8								
CONNECT	11	6	7	12						
CONNECT	12	8	11	55	15					
CONNECT	13	35	33	18						
CONNECT	14	4	28	49	60					
CONNECT	15	2	12	17	16					
CONNECT	16	15								
CONNECT	17	15	23	21						
CONNECT	18	2	6	13	19					
CONNECT	19	18								
CONNECT	20	42	45							
CONNECT	21	17	29	56						
CONNECT	22	32								
CONNECT	23	17	46	24						
CONNECT	24	23								
CONNECT	25	4	6	26	27					
CONNECT	26	25								
CONNECT	27	25								
CONNECT	28	14	44	61	63					
CONNECT	29	21	31	30						
CONNECT	30	29								
CONNECT	31	29	46							
CONNECT	32	3	6	22						
CONNECT	33	13	42	34						
CONNECT	34	33								
CONNECT	35	13	45	57						
CONNECT	36	54	37							
CONNECT	37	36								
CONNECT	38	2	39	40	41					
CONNECT	39	38								
CONNECT	40	38								
CONNECT	41	38								
CONNECT	42	20	33	59						
CONNECT	43	48	49	65	67					
CONNECT	44	28	48	62	68					
CONNECT	45	20	35	58						
CONNECT	46	23	31	47						
CONNECT	47	46								
CONNECT	48	43	44	69	70					
CONNECT	49	14	43	64	66					
CONNECT	50	3	51	52	53					
CONNECT	51	50								
CONNECT	52	50								
CONNECT	53	50								
CONNECT	54	36	55							
CONNECT	55	5	12	54						
CONNECT	56	21								
CONNECT	57	35								
CONNECT	58	45								
CONNECT	59	42								
CONNECT	60	14								
CONNECT	61	28								
CONNECT	62	44								
CONNECT	63	28								
CONNECT	64	49								

CONECT 65 43
CONECT 66 49
CONECT 67 43
CONECT 68 44
CONECT 69 48
CONECT 70 48
END

Structure L4 (pdb file)

REMARK L4 PDB file
CRYST1 16.527 11.175 14.691 90.00 106.39 90.00 P21/C
ORIGX1 1.000000 0.000000 0.000000 0.000000
ORIGX2 0.000000 1.000000 0.000000 0.000000
ORIGX3 0.000000 0.000000 1.000000 0.000000
SCALE1 0.060506 0.000000 0.017796 0.000000
SCALE2 0.000000 0.089486 0.000000 0.000000
SCALE3 0.000000 0.000000 0.070952 0.000000
ATOM 1 O1 MOL 2 3.476 6.466 11.702 1.00 0.00 O
ATOM 2 O2 MOL 2 3.691 2.893 11.614 1.00 0.00 O
ATOM 3 O3 MOL 2 4.521 4.138 13.256 1.00 0.00 O
ATOM 4 O4 MOL 2 0.991 8.629 10.707 1.00 0.00 O
ATOM 5 O5 MOL 2 1.999 8.929 12.661 1.00 0.00 O
ATOM 6 N3 MOL 2 0.007 4.662 11.487 1.00 0.00 N
ATOM 7 C20 MOL 2 0.641 6.734 13.697 1.00 0.00 C
ATOM 8 H2 MOL 2 1.260 7.274 14.231 1.00 0.00 H
ATOM 9 N4 MOL 2 0.609 5.380 14.279 1.00 0.00 N
ATOM 10 C1 MOL 2 -2.268 2.381 11.684 1.00 0.00 C
ATOM 11 H29 MOL 2 -2.705 3.078 12.118 1.00 0.00 H
ATOM 12 C2 MOL 2 -1.279 2.661 10.749 1.00 0.00 C
ATOM 13 C3 MOL 2 -0.875 4.082 10.456 1.00 0.00 C
ATOM 14 H26 MOL 2 -0.421 4.109 9.601 1.00 0.00 H
ATOM 15 H27 MOL 2 -1.674 4.628 10.383 1.00 0.00 H
ATOM 16 C4 MOL 2 0.218 6.074 11.177 1.00 0.00 C
ATOM 17 H24 MOL 2 -0.639 6.528 11.157 1.00 0.00 H
ATOM 18 H25 MOL 2 0.617 6.152 10.297 1.00 0.00 H
ATOM 19 C5 MOL 2 1.136 6.762 12.217 1.00 0.00 C
ATOM 20 C6 MOL 2 -0.741 7.352 13.827 1.00 0.00 C
ATOM 21 C7 MOL 2 -1.886 6.639 13.515 1.00 0.00 C
ATOM 22 H20 MOL 2 -1.827 5.760 13.217 1.00 0.00 H
ATOM 23 C8 MOL 2 -3.116 7.250 13.653 1.00 0.00 C
ATOM 24 H19 MOL 2 -3.874 6.760 13.429 1.00 0.00 H
ATOM 25 N1 MOL 2 -3.287 8.499 14.086 1.00 0.00 N
ATOM 26 C10 MOL 2 1.785 4.539 14.035 1.00 0.00 C
ATOM 27 H13 MOL 2 2.518 4.878 14.590 1.00 0.00 H
ATOM 28 C11 MOL 2 1.483 3.118 14.476 1.00 0.00 C
ATOM 29 C12 MOL 2 2.408 2.376 15.184 1.00 0.00 C
ATOM 30 H7 MOL 2 3.245 2.731 15.382 1.00 0.00 H
ATOM 31 C13 MOL 2 2.077 1.106 15.594 1.00 0.00 C
ATOM 32 H6 MOL 2 2.702 0.639 16.098 1.00 0.00 H
ATOM 33 N2 MOL 2 0.938 0.503 15.324 1.00 0.00 N
ATOM 34 C15 MOL 2 0.062 1.215 14.635 1.00 0.00 C
ATOM 35 H4 MOL 2 -0.753 0.815 14.427 1.00 0.00 H
ATOM 36 C16 MOL 2 0.272 2.514 14.205 1.00 0.00 C
ATOM 37 H3 MOL 2 -0.390 2.973 13.740 1.00 0.00 H
ATOM 38 C17 MOL 2 2.262 4.556 12.544 1.00 0.00 C
ATOM 39 C18 MOL 2 2.450 6.005 12.133 1.00 0.00 C
ATOM 40 C19 MOL 2 3.618 3.854 12.520 1.00 0.00 C
ATOM 41 C20 MOL 2 4.965 2.201 11.561 1.00 0.00 C
ATOM 42 H8 MOL 2 5.647 2.812 11.272 1.00 0.00 H
ATOM 43 H10 MOL 2 4.906 1.469 10.943 1.00 0.00 H
ATOM 44 H9 MOL 2 5.183 1.866 12.434 1.00 0.00 H
ATOM 45 C21 MOL 2 1.284 3.947 11.510 1.00 0.00 C
ATOM 46 H11 MOL 2 1.687 3.982 10.628 1.00 0.00 H
ATOM 47 H12 MOL 2 1.125 3.015 11.729 1.00 0.00 H
ATOM 48 C22 MOL 2 0.456 5.514 15.740 1.00 0.00 C
ATOM 49 H15 MOL 2 0.360 4.643 16.133 1.00 0.00 H
ATOM 50 H16 MOL 2 -0.325 6.040 15.933 1.00 0.00 H
ATOM 51 H14 MOL 2 1.231 5.947 16.105 1.00 0.00 H
ATOM 52 C23 MOL 2 -2.184 9.159 14.403 1.00 0.00 C
ATOM 53 H18 MOL 2 -2.275 10.027 14.725 1.00 0.00 H
ATOM 54 C24 MOL 2 -0.906 8.639 14.289 1.00 0.00 C
ATOM 55 H17 MOL 2 -0.166 9.154 14.518 1.00 0.00 H
ATOM 56 C25 MOL 2 1.354 8.197 11.760 1.00 0.00 C
ATOM 57 C26 MOL 2 2.256 10.299 12.301 1.00 0.00 C
ATOM 58 H23 MOL 2 2.818 10.326 11.523 1.00 0.00 H
ATOM 59 H21 MOL 2 2.696 10.745 13.030 1.00 0.00 H
ATOM 60 H22 MOL 2 1.426 10.741 12.111 1.00 0.00 H
ATOM 61 C27 MOL 2 -0.671 1.599 10.103 1.00 0.00 C
ATOM 62 H28 MOL 2 -0.022 1.770 9.460 1.00 0.00 H
ATOM 63 C28 MOL 2 -1.011 0.280 10.396 1.00 0.00 C

ATOM	64	AH28	MOL	2	-0.591	-0.424	9.956	1.00	0.00	H
ATOM	65	C10	MOL	2	-1.967	0.035	11.334	1.00	0.00	C
ATOM	66	OH10	MOL	2	-2.191	-0.843	11.547	1.00	0.00	H
ATOM	67	C10	MOL	2	-2.603	1.072	11.969	1.00	0.00	C
ATOM	68	1H10	MOL	2	-3.266	0.892	12.597	1.00	0.00	H
TER	69									
CONNECT	1	68								
CONNECT	2	40								
CONNECT	3	41	42							
CONNECT	4	41								
CONNECT	5	57								
CONNECT	6	57	58							
CONNECT	7	14	17	46						
CONNECT	8	9	10	20	21					
CONNECT	9	8								
CONNECT	10	8	27	49						
CONNECT	11	12	13	68						
CONNECT	12	11								
CONNECT	13	11	14	62						
CONNECT	14	7	13	15	16					
CONNECT	15	14								
CONNECT	16	14								
CONNECT	17	7	18	19	20					
CONNECT	18	17								
CONNECT	19	17								
CONNECT	20	17	8	40	57					
CONNECT	21	8	22	55						
CONNECT	22	21	23	24						
CONNECT	23	22								
CONNECT	24	22	25	26						
CONNECT	25	24								
CONNECT	26	24	53							
CONNECT	27	10	28	29	39					
CONNECT	28	27								
CONNECT	29	27	30	37						
CONNECT	30	29	31	32						
CONNECT	31	30								
CONNECT	32	30	33	34						
CONNECT	33	32								
CONNECT	34	32	35							
CONNECT	35	34	36	37						
CONNECT	36	35								
CONNECT	37	29	35	38						
CONNECT	38	37								
CONNECT	39	27	40	41	46					
CONNECT	40	20	39	2						
CONNECT	41	39	4	3						
CONNECT	42	3	43	44	45					
CONNECT	43	42								
CONNECT	44	42								
CONNECT	45	42								
CONNECT	46	7	39	47	48					
CONNECT	47	46								
CONNECT	48	46								
CONNECT	49	10	50	51	52					
CONNECT	50	49								
CONNECT	51	49								
CONNECT	52	49								
CONNECT	53	26	54	55						
CONNECT	54	53								
CONNECT	55	21	53	56						
CONNECT	56	55								
CONNECT	57	6	20	5						
CONNECT	58	6	59	60	61					
CONNECT	59	58								
CONNECT	60	58								
CONNECT	61	58								
CONNECT	62	13	63	64						
CONNECT	63	62								
CONNECT	64	62	65	66						
CONNECT	65	64								
CONNECT	66	64	67	68						

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CONNECT 67 66  
CONNECT 68 66 11 1  
END
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Structure L5 (pdb file)

```
REMARK L5 PDB file
CRYST1 13.089 17.019 25.190 90.00 90.00 90.00 PBCA
ORIGX1 1.000000 0.000000 0.000000 0.000000
ORIGX2 0.000000 1.000000 0.000000 0.000000
ORIGX3 0.000000 0.000000 1.000000 0.000000
SCALE1 0.076400 0.000000 0.000000 0.000000
SCALE2 0.000000 0.058758 0.000000 0.000000
SCALE3 0.000000 0.000000 0.039698 0.000000
ATOM 1 O1 MOL 2 10.109 0.955 5.497 1.00 0.00 O
ATOM 2 N10 MOL 2 13.501 4.992 5.403 1.00 0.00 N
ATOM 3 C40 MOL 2 8.093 7.752 12.441 1.00 0.00 C
ATOM 4 H40 MOL 2 7.690 8.332 13.047 1.00 0.00 H
ATOM 5 N2 MOL 2 7.317 6.915 11.756 1.00 0.00 N
ATOM 6 O5 MOL 2 14.675 6.082 12.595 1.00 0.00 O
ATOM 7 O6 MOL 2 12.173 7.715 13.900 1.00 0.00 O
ATOM 8 O7 MOL 2 12.276 5.594 14.534 1.00 0.00 O
ATOM 9 O8 MOL 2 15.936 4.148 9.900 1.00 0.00 O
ATOM 10 O9 MOL 2 16.034 6.362 10.054 1.00 0.00 O
ATOM 11 N1 MOL 2 11.847 4.008 10.798 1.00 0.00 N
ATOM 12 C10 MOL 2 13.279 6.438 9.478 1.00 0.00 C
ATOM 13 3H10 MOL 2 13.800 7.266 9.549 1.00 0.00 H
ATOM 14 N3 MOL 2 11.891 6.744 9.817 1.00 0.00 N
ATOM 15 C1 MOL 2 7.936 6.083 10.910 1.00 0.00 C
ATOM 16 H1 MOL 2 7.420 5.475 10.431 1.00 0.00 H
ATOM 17 C2 MOL 2 9.297 6.083 10.718 1.00 0.00 C
ATOM 18 H15 MOL 2 9.682 5.488 10.113 1.00 0.00 H
ATOM 19 C3 MOL 2 10.092 6.961 11.420 1.00 0.00 C
ATOM 20 C4 MOL 2 11.584 6.998 11.245 1.00 0.00 C
ATOM 21 H17 MOL 2 11.896 7.899 11.470 1.00 0.00 H
ATOM 22 C5 MOL 2 12.275 5.977 12.223 1.00 0.00 C
ATOM 23 C6 MOL 2 11.753 4.551 12.154 1.00 0.00 C
ATOM 24 H21 MOL 2 12.265 3.993 12.759 1.00 0.00 H
ATOM 25 H22 MOL 2 10.827 4.535 12.442 1.00 0.00 H
ATOM 26 C7 MOL 2 11.259 2.662 10.751 1.00 0.00 C
ATOM 27 H4 MOL 2 10.439 2.658 11.268 1.00 0.00 H
ATOM 28 H11 MOL 2 11.873 2.036 11.165 1.00 0.00 H
ATOM 29 C8 MOL 2 10.963 2.206 9.381 1.00 0.00 C
ATOM 30 C9 MOL 2 9.840 2.665 8.726 1.00 0.00 C
ATOM 31 H10 MOL 2 9.287 3.259 9.179 1.00 0.00 H
ATOM 32 C10 MOL 2 9.483 2.301 7.439 1.00 0.00 C
ATOM 33 H9 MOL 2 8.713 2.639 7.041 1.00 0.00 H
ATOM 34 C11 MOL 2 10.297 1.431 6.769 1.00 0.00 C
ATOM 35 C12 MOL 2 8.910 1.372 4.847 1.00 0.00 C
ATOM 36 H5 MOL 2 8.151 1.026 5.321 1.00 0.00 H
ATOM 37 H2 MOL 2 8.903 1.038 3.945 1.00 0.00 H
ATOM 38 H6 MOL 2 8.870 2.330 4.833 1.00 0.00 H
ATOM 39 C13 MOL 2 12.497 4.699 6.214 1.00 0.00 C
ATOM 40 H30 MOL 2 11.825 4.149 5.879 1.00 0.00 H
ATOM 41 C14 MOL 2 12.366 5.136 7.505 1.00 0.00 C
ATOM 42 H3 MOL 2 11.632 4.888 8.018 1.00 0.00 H
ATOM 43 C15 MOL 2 13.346 5.957 8.030 1.00 0.00 C
ATOM 44 C16 MOL 2 13.927 5.369 10.415 1.00 0.00 C
ATOM 45 C17 MOL 2 13.230 3.972 10.385 1.00 0.00 C
ATOM 46 H24 MOL 2 13.280 3.616 9.484 1.00 0.00 H
ATOM 47 H23 MOL 2 13.716 3.367 10.968 1.00 0.00 H
ATOM 48 C18 MOL 2 11.411 0.946 7.371 1.00 0.00 C
ATOM 49 H7 MOL 2 11.966 0.358 6.911 1.00 0.00 H
ATOM 50 C19 MOL 2 11.733 1.326 8.680 1.00 0.00 C
ATOM 51 H8 MOL 2 12.491 0.967 9.082 1.00 0.00 H
ATOM 52 C20 MOL 2 11.424 7.900 9.032 1.00 0.00 C
ATOM 53 H14 MOL 2 11.956 8.669 9.246 1.00 0.00 H
ATOM 54 H12 MOL 2 10.504 8.078 9.242 1.00 0.00 H
ATOM 55 H13 MOL 2 11.506 7.705 8.095 1.00 0.00 H
ATOM 56 C21 MOL 2 9.448 7.807 12.300 1.00 0.00 C
ATOM 57 H16 MOL 2 9.941 8.416 12.799 1.00 0.00 H
ATOM 58 C22 MOL 2 13.730 5.890 11.837 1.00 0.00 C
ATOM 59 C23 MOL 2 12.229 6.556 13.626 1.00 0.00 C
ATOM 60 C24 MOL 2 12.220 5.992 15.910 1.00 0.00 C
ATOM 61 H19 MOL 2 13.002 6.504 16.127 1.00 0.00 H
ATOM 62 H18 MOL 2 12.183 5.211 16.468 1.00 0.00 H
ATOM 63 H20 MOL 2 11.436 6.527 16.057 1.00 0.00 H
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ATOM	64	C25	MOL	2	15.401	5.204	10.096	1.00	0.00	C
ATOM	65	C26	MOL	2	17.461	6.275	9.799	1.00	0.00	C
ATOM	66	H25	MOL	2	17.850	5.617	10.381	1.00	0.00	H
ATOM	67	H26	MOL	2	17.868	7.129	9.965	1.00	0.00	H
ATOM	68	H27	MOL	2	17.609	6.022	8.885	1.00	0.00	H
ATOM	69	C27	MOL	2	14.394	6.283	7.207	1.00	0.00	C
ATOM	70	H29	MOL	2	15.077	6.834	7.515	1.00	0.00	H
ATOM	71	C28	MOL	2	14.425	5.788	5.912	1.00	0.00	C
ATOM	72	H28	MOL	2	15.141	6.031	5.367	1.00	0.00	H
TER	73									
CONNECT	1	72								
CONNECT	2	35	36							
CONNECT	3	40	72							
CONNECT	4	5	6	57						
CONNECT	5	4								
CONNECT	6	4	16							
CONNECT	7	59								
CONNECT	8	60								
CONNECT	9	60	61							
CONNECT	10	65								
CONNECT	11	65	66							
CONNECT	12	24	27	46						
CONNECT	13	14	15	44	45					
CONNECT	14	13								
CONNECT	15	13	21	53						
CONNECT	16	6	17	18						
CONNECT	17	16								
CONNECT	18	16	19	20						
CONNECT	19	18								
CONNECT	20	18	21	57						
CONNECT	21	20	15	22	23					
CONNECT	22	21								
CONNECT	23	21	24	59	60					
CONNECT	24	12	23	25	26					
CONNECT	25	24								
CONNECT	26	24								
CONNECT	27	12	28	29	30					
CONNECT	28	27								
CONNECT	29	27								
CONNECT	30	27	31	51						
CONNECT	31	30	32	33						
CONNECT	32	31								
CONNECT	33	31	34	35						
CONNECT	34	33								
CONNECT	35	2	33	49						
CONNECT	36	2	37	38	39					
CONNECT	37	36								
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CONNECT	39	36								
CONNECT	40	3	41	42						
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CONNECT	43	42								
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CONNECT	49	35	50	51						
CONNECT	50	49								
CONNECT	51	49	30	52						
CONNECT	52	51								
CONNECT	53	15	54	55	56					
CONNECT	54	53								
CONNECT	55	53								
CONNECT	56	53								
CONNECT	57	20	4	58						
CONNECT	58	57								
CONNECT	59	23	45	7						
CONNECT	60	8	23	9						
CONNECT	61	9	62	63	64					
CONNECT	62	61								

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CONNECT 63 61
CONNECT 64 61
CONNECT 65 10 11 45
CONNECT 66 11 67 68 69
CONNECT 67 66
CONNECT 68 66
CONNECT 69 66
CONNECT 70 44 71 72
CONNECT 71 70
CONNECT 72 3 70 1
END
```


Structure L6 (pdb file)

REMARK L6 PDB file
CRYST1 12.874 13.172 16.965 90.00 98.68 90.00 P21/C
ORIGX1 1.000000 0.000000 0.000000 0.000000
ORIGX2 0.000000 1.000000 0.000000 0.000000
ORIGX3 0.000000 0.000000 1.000000 0.000000
SCALE1 0.077676 0.000000 0.011858 0.000000
SCALE2 0.000000 0.075919 0.000000 0.000000
SCALE3 0.000000 0.000000 0.059628 0.000000
ATOM 1 C1 UNK C 1 11.302 0.721 5.653 1.00 2.10 C
ATOM 2 C2 UNK C 1 11.679 -0.745 5.789 1.00 2.04 C
ATOM 3 C3 UNK C 1 11.822 -1.288 4.350 1.00 2.24 C
ATOM 4 H3A UNK C 1 12.519 -0.796 3.889 1.00 2.69 H
ATOM 5 H3B UNK C 1 12.087 -2.221 4.384 1.00 2.69 H
ATOM 6 C4 UNK C 1 10.163 0.235 3.525 1.00 2.28 C
ATOM 7 H4A UNK C 1 9.328 0.297 3.036 1.00 2.74 H
ATOM 8 H4B UNK C 1 10.833 0.735 3.034 1.00 2.74 H
ATOM 9 C5 UNK C 1 9.979 0.871 4.924 1.00 2.05 C
ATOM 10 C6 UNK C 1 8.877 0.209 5.812 1.00 2.10 C
ATOM 11 H6 UNK C 1 8.776 0.741 6.628 1.00 2.52 H
ATOM 12 C7 UNK C 1 10.580 -1.444 6.647 1.00 2.15 C
ATOM 13 H7 UNK C 1 10.665 -1.124 7.570 1.00 2.58 H
ATOM 14 C8 UNK C 1 9.700 2.366 4.743 1.00 2.66 C
ATOM 15 C9 UNK C 1 13.022 -0.807 6.533 1.00 2.60 C
ATOM 16 C10 UNK C 1 9.164 4.373 5.866 1.00 4.75 C
ATOM 17 AH10 UNK C 1 10.009 4.813 5.749 1.00 5.71 H
ATOM 18 BH10 UNK C 1 8.769 4.655 6.695 1.00 5.71 H
ATOM 19 CH10 UNK C 1 8.580 4.602 5.140 1.00 5.71 H
ATOM 20 C11 UNK C 1 15.358 -0.755 6.253 1.00 5.40 C
ATOM 21 AH11 UNK C 1 15.540 0.042 6.756 1.00 6.48 H
ATOM 22 BH11 UNK C 1 16.004 -0.842 5.548 1.00 6.48 H
ATOM 23 CH11 UNK C 1 15.411 -1.518 6.832 1.00 6.48 H
ATOM 24 C12 UNK C 1 10.811 -1.708 2.248 1.00 2.84 C
ATOM 25 AH12 UNK C 1 11.294 -2.546 2.322 1.00 3.40 H
ATOM 26 BH12 UNK C 1 11.367 -1.087 1.753 1.00 3.40 H
ATOM 27 C13 UNK C 1 9.538 -1.942 1.484 1.00 2.80 C
ATOM 28 C14 UNK C 1 9.169 -1.136 0.437 1.00 4.28 C
ATOM 29 H14 UNK C 1 9.713 -0.420 0.200 1.00 5.14 H
ATOM 30 C15 UNK C 1 8.003 -1.366 -0.273 1.00 5.34 C
ATOM 31 H15 UNK C 1 7.769 -0.808 -0.979 1.00 6.40 H
ATOM 32 C16 UNK C 1 7.201 -2.412 0.068 1.00 4.69 C
ATOM 33 C17 UNK C 1 7.563 -3.256 1.102 1.00 4.73 C
ATOM 34 H17 UNK C 1 7.023 -3.980 1.324 1.00 5.68 H
ATOM 35 C18 UNK C 1 8.729 -3.021 1.803 1.00 3.90 C
ATOM 36 H18 UNK C 1 8.974 -3.591 2.496 1.00 4.68 H
ATOM 37 C19 UNK C 1 5.957 -2.708 -0.699 1.00 7.28 C
ATOM 38 C20 UNK C 1 8.270 -1.627 7.224 1.00 3.36 C
ATOM 39 AH20 UNK C 1 8.390 -1.107 8.022 1.00 4.03 H
ATOM 40 BH20 UNK C 1 8.436 -2.553 7.418 1.00 4.03 H
ATOM 41 CH20 UNK C 1 7.370 -1.523 6.907 1.00 4.03 H
ATOM 42 C21 UNK C 1 10.772 -2.955 6.653 1.00 2.43 C
ATOM 43 C22 UNK C 1 10.202 -3.750 5.676 1.00 3.22 C
ATOM 44 H22 UNK C 1 9.721 -3.364 4.980 1.00 3.86 H
ATOM 45 C23 UNK C 1 10.354 -5.123 5.742 1.00 3.90 C
ATOM 46 H23 UNK C 1 9.955 -5.639 5.080 1.00 4.68 H
ATOM 47 C24 UNK C 1 11.590 -4.979 7.618 1.00 3.61 C
ATOM 48 H24 UNK C 1 12.082 -5.394 8.289 1.00 4.33 H
ATOM 49 C25 UNK C 1 11.487 -3.594 7.653 1.00 3.04 C
ATOM 50 H25 UNK C 1 11.890 -3.106 8.334 1.00 3.65 H
ATOM 51 C26 UNK C 1 7.548 0.210 5.068 1.00 2.57 C
ATOM 52 C27 UNK C 1 6.663 1.268 5.156 1.00 3.91 C
ATOM 53 H27 UNK C 1 6.857 2.002 5.693 1.00 4.69 H
ATOM 54 C28 UNK C 1 5.479 1.218 4.431 1.00 5.34 C
ATOM 55 H28 UNK C 1 4.904 1.947 4.490 1.00 6.41 H
ATOM 56 C29 UNK C 1 5.977 -0.803 3.587 1.00 4.93 C
ATOM 57 H29 UNK C 1 5.752 -1.529 3.051 1.00 5.91 H
ATOM 58 C30 UNK C 1 7.182 -0.846 4.252 1.00 3.68 C
ATOM 59 H30 UNK C 1 7.746 -1.579 4.152 1.00 4.41 H
ATOM 60 N1 UNK C 1 10.571 -1.169 3.602 1.00 2.18 N
ATOM 61 N2 UNK C 1 9.211 -1.166 6.192 1.00 2.28 N
ATOM 62 N3 UNK C 1 11.035 -5.750 6.694 1.00 3.93 N1-
ATOM 63 N4 UNK C 1 5.113 0.203 3.659 1.00 5.50 N1-

ATOM	64	O1	UNK	C	1	11.995	1.635	6.018	1.00	3.61	O1-
ATOM	65	O2	UNK	C	1	13.132	-0.915	7.711	1.00	4.12	O1-
ATOM	66	O3	UNK	C	1	14.038	-0.673	5.686	1.00	3.72	O
ATOM	67	O4	UNK	C	1	9.798	2.943	3.707	1.00	5.25	O1-
ATOM	68	O5	UNK	C	1	9.364	2.945	5.890	1.00	3.55	O
ATOM	69	F1	UNK	C	1	5.528	-1.656	-1.425	1.00	14.53	F
ATOM	70	F2	UNK	C	1	6.117	-3.523	-1.645	1.00	14.38	F
ATOM	71	F3	UNK	C	1	4.970	-3.024	-0.012	1.00	17.08	F
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CONNECT	56	57	58	63							
CONNECT	57	56									
CONNECT	58	51	56	59							
CONNECT	59	58									
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CONNECT	61	10	12	38							
CONNECT	62	45	47								
CONNECT	63	54	56								

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CONECT 64 1
CONECT 65 15
CONECT 66 15 20
CONECT 67 14
CONECT 68 14 16
CONECT 69 37
CONECT 70 37
CONECT 71 37
END
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Structure L7 (pdb file)

REMARK L7 PDB file
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ORIGX2 0.000000 1.000000 0.000000 0.000000
ORIGX3 0.000000 0.000000 1.000000 0.000000
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SCALE2 0.000000 0.059723 0.000000 0.000000
SCALE3 0.000000 0.000000 0.039142 0.000000
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ATOM 2 O2 UNK C 1 -0.935 7.570 24.151 1.00 0.00 O1-
ATOM 3 O3 UNK C 1 -0.752 5.426 23.532 1.00 0.00 O
ATOM 4 O4 UNK C 1 2.953 6.191 28.075 1.00 0.00 O
ATOM 5 O5 UNK C 1 2.812 3.969 28.169 1.00 0.00 O1-
ATOM 6 N1 UNK C 1 -1.265 3.887 27.282 1.00 0.00 N
ATOM 7 N2 UNK C 1 -1.186 6.635 28.246 1.00 0.00 N
ATOM 8 N3 UNK C 1 0.378 4.993 32.725 1.00 0.00 N1-
ATOM 9 N4 UNK C 1 -5.781 6.793 26.354 1.00 0.00 N1-
ATOM 10 F1 UNK C 1 -4.196 0.797 34.459 1.00 0.00 F
ATOM 11 F2 UNK C 1 -4.952 0.266 32.567 1.00 0.00 F
ATOM 12 F3 UNK C 1 -5.001 2.234 33.180 1.00 0.00 F
ATOM 13 C1 UNK C 1 0.676 5.733 26.252 1.00 0.00 C
ATOM 14 C2 UNK C 1 0.826 5.226 27.666 1.00 0.00 C
ATOM 15 C3 UNK C 1 0.204 6.321 28.606 1.00 0.00 C
ATOM 16 H3 UNK C 1 0.737 7.139 28.520 1.00 0.00 H
ATOM 17 C4 UNK C 1 -1.480 6.871 26.820 1.00 0.00 C
ATOM 18 H4 UNK C 1 -1.169 7.772 26.591 1.00 0.00 H
ATOM 19 C5 UNK C 1 -0.776 5.855 25.857 1.00 0.00 C
ATOM 20 C6 UNK C 1 -1.337 4.420 25.924 1.00 0.00 C
ATOM 21 H6A UNK C 1 -2.261 4.421 25.627 1.00 0.00 H
ATOM 22 H6B UNK C 1 -0.831 3.847 25.327 1.00 0.00 H
ATOM 23 C7 UNK C 1 0.127 3.849 27.728 1.00 0.00 C
ATOM 24 H7A UNK C 1 0.617 3.222 27.174 1.00 0.00 H
ATOM 25 H7B UNK C 1 0.156 3.523 28.641 1.00 0.00 H
ATOM 26 C8 UNK C 1 -1.633 7.811 29.007 1.00 0.00 C
ATOM 27 H8A UNK C 1 -1.206 8.598 28.661 1.00 0.00 H
ATOM 28 H8B UNK C 1 -1.400 7.701 29.932 1.00 0.00 H
ATOM 29 H8C UNK C 1 -2.585 7.901 28.926 1.00 0.00 H
ATOM 30 C9 UNK C 1 -2.989 6.837 26.642 1.00 0.00 C
ATOM 31 C10 UNK C 1 -3.627 7.670 25.743 1.00 0.00 C
ATOM 32 H10 UNK C 1 -3.139 8.264 25.220 1.00 0.00 H
ATOM 33 C11 UNK C 1 -5.006 7.606 25.636 1.00 0.00 C
ATOM 34 H11 UNK C 1 -5.420 8.168 25.021 1.00 0.00 H
ATOM 35 C12 UNK C 1 -5.144 5.999 27.216 1.00 0.00 C
ATOM 36 H12 UNK C 1 -5.652 5.418 27.735 1.00 0.00 H
ATOM 37 C13 UNK C 1 -3.782 5.989 27.380 1.00 0.00 C
ATOM 38 H13 UNK C 1 -3.393 5.407 27.993 1.00 0.00 H
ATOM 39 C14 UNK C 1 0.261 5.867 30.045 1.00 0.00 C
ATOM 40 C19 UNK C 1 2.294 5.035 28.005 1.00 0.00 C
ATOM 41 C15 UNK C 1 -0.738 5.080 30.597 1.00 0.00 C
ATOM 42 H15 UNK C 1 -1.472 4.826 30.085 1.00 0.00 H
ATOM 43 C18 UNK C 1 1.309 6.215 30.882 1.00 0.00 C
ATOM 44 H18 UNK C 1 1.998 6.756 30.568 1.00 0.00 H
ATOM 45 C21 UNK C 1 -0.845 6.394 24.441 1.00 0.00 C
ATOM 46 C28 UNK C 1 -1.446 1.286 29.472 1.00 0.00 C
ATOM 47 H28 UNK C 1 -0.690 0.895 29.098 1.00 0.00 H
ATOM 48 C30 UNK C 1 -2.885 1.583 31.332 1.00 0.00 C
ATOM 49 C27 UNK C 1 -2.229 2.136 28.707 1.00 0.00 C
ATOM 50 C31 UNK C 1 -3.708 2.416 30.603 1.00 0.00 C
ATOM 51 H31 UNK C 1 -4.469 2.792 30.984 1.00 0.00 H
ATOM 52 C32 UNK C 1 -3.364 2.673 29.286 1.00 0.00 C
ATOM 53 H32 UNK C 1 -3.913 3.224 28.776 1.00 0.00 H
ATOM 54 C16 UNK C 1 -0.633 4.677 31.914 1.00 0.00 C
ATOM 55 H16 UNK C 1 -1.315 4.147 32.260 1.00 0.00 H
ATOM 56 C25 UNK C 1 -1.856 2.537 27.312 1.00 0.00 C
ATOM 57 AH25 UNK C 1 -1.220 1.899 26.953 1.00 0.00 H
ATOM 58 BH25 UNK C 1 -2.647 2.520 26.750 1.00 0.00 H
ATOM 59 C17 UNK C 1 1.326 5.753 32.190 1.00 0.00 C
ATOM 60 H17 UNK C 1 2.047 5.991 32.726 1.00 0.00 H
ATOM 61 C29 UNK C 1 -1.779 1.013 30.787 1.00 0.00 C
ATOM 62 H29 UNK C 1 -1.249 0.442 31.295 1.00 0.00 H
ATOM 63 C22 UNK C 1 -0.865 5.809 22.145 1.00 0.00 C

ATOM	64	AH22	UNK	C	1	-1.743	6.160	21.980	1.00	0.00		H
ATOM	65	BH22	UNK	C	1	-0.718	5.041	21.588	1.00	0.00		H
ATOM	66	CH22	UNK	C	1	-0.208	6.480	21.944	1.00	0.00		H
ATOM	67	O6	UNK	C	1	-3.078	1.333	32.709	1.00	0.00		O
ATOM	68	C20	UNK	C	1	4.371	6.099	28.338	1.00	0.00		C
ATOM	69	AH20	UNK	C	1	4.515	5.594	29.141	1.00	0.00		H
ATOM	70	BH20	UNK	C	1	4.734	6.981	28.444	1.00	0.00		H
ATOM	71	CH20	UNK	C	1	4.805	5.661	27.602	1.00	0.00		H
ATOM	72	C24	UNK	C	1	-4.273	1.114	33.187	1.00	0.00		C

TER 73

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CONNECT 64 63
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CONNECT 67 48 72
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CONNECT 69 68
CONNECT 70 68
CONNECT 71 68
CONNECT 72 10 11 12 67
END
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