MJ Rosseinsky 'Flexible sorption and transformation behavior in a microporous metal-organic framework' Supplementary Information

Manuscript Number JA0262737

Supplementary Figure Captions

Figure S1 The disordered methanol guests in a single large pore as determined by single crystal X-ray diffraction a) viewed along [100] and b) along [001]. c) and d) show the positions of methanol guests determined by Monte Carlo docking calculations after reducing the symmetry of the (fixed) framework to P1. The C, H and O atoms of the guest molecules are shown as green, white and yellow space filling spheres respectively. Framework Ni, C, H, N and O atoms are shown as small cyan, gray, white, blue and red spheres respectively. Only framework atoms which lie within 7 Å of a guest atom are shown.

Figure S2 The phase purity of the sample was confirmed by powder X-ray diffraction. The pattern calculated from the structure determined by single crystal X-ray diffraction (a) shows excellent agreement with the observed data (b).

Figure S3 The variation of mass of **A** as a function of temperature. Guest methanol molecules were lost whilst handling the sample at room temperature before the thermogravimetric analysis began.

Figure S4 *In-situ* variable temperature X-ray powder diffraction from A at room temperature and 175 °C. Both patterns can be fully indexed using the structure determined by single crystal X-ray diffraction.

Figure S5 The variation in the lattice parameters and cell volume of **A** as a function of temperature. These parameters were determined by refinement against powder X-ray diffraction data collected *in-situ* from **A** contained in a glass capillary.

Figure S7 X-ray powder diffraction data collected from i) a sample of pristine A.2CH₃OH and ii) A.1.2toluene. Both patterns can be fully indexed using a unit cell of similar dimensions to those observed in the single crystal diffraction experiments. These give unit cells parameters of i) a = 11.292(4) Å, b = 20.598(9) Å, c = 34.462(16) Å, V = 8015.4(97) Å³ and ii) a = 11.285(5) Å, b = 20.632(11) Å, c = 34.447(18) Å, V = 8020.7(58) Å³.

Figure S8 The variation of mass of **A** in response to exposure to a) 1,3,5 triethylbenzene (TB) vapour, b) 2ethyl butan-1-ol (EB) vapour and c) benzyl alcohol (BA) vapour. The mass change to the plateau value in a) corresponds to an uptake of 0.13TB per $Ni_2bip_3(NO_3)_4$ formula unit whilst the maximum uptake in b) gives 0.08 EB molecules per formula unit and c) gives 0.06 BA molecules per formula unit. Dashed black lines indicate the switching of the He flow between dry and saturated with toluene vapour.

Figure S9 Gas chromatographs obtained for a) a standard mixture of toluene (1.85 min) and 2ethyl butan-1-ol (2.38 min) in benzyl alcohol, b) a mixture of ethyl butan-1-ol (2.38 min) and benzyl alcohol (5.58 min) before addition of toluene loaded sample **A** and c) the same mixture of ethyl butan-1-ol in benzyl alcohol 1 hour after addition of toluene-loaded sample **A**.

Figure S9 The rate of reaction for the transformation **B** to **A**. The phase fractions were estimated by following the intensities (relative to the main peak at $2\theta = 9.2^{\circ}$) of Bragg reflections from each phase in angular regions of the powder diffraction pattern where no other Bragg peaks are observed. These peaks examined were at $2\theta = 11.8^{\circ}$ for methanol phase **A** and $2\theta = 18.9^{\circ}$ for the ethanol phase, **B**. The phase fraction of the two phases as a function of methanol exposure is shown. The peak intensities of **B** and **A** are indicated by white squares and triangles respectively. The phase fractions of **A** and **B** thus determined for phase pure MeOH templated material **A** are shown as a red square and triangle, demonstrating the precision of the phase fraction estimation.

Crystallographic Information follows the supplementary Figures



Figure S1



Figure S2



Figure S3



Figure S4



Figure S5



START 11				a)		
			1 85	2.38		
STOP						
RUN #	28		SE	P/14/01	12:09:48	
AREA% RT		AREA	TYPE	AR/HT	AREA%	
1.85 2.38		7119 23831	PB PB	0.035 0.091	23.002 76.998	
TOTAL A MUL FAC	REA= TOR= 1	30 . 0000E	950 +00			



Figure S6



Figure S7



Figure S8



Figure S9

Crystallographic Data

data edc4

'x+1/2, y+1/2, z' '-x+1/2, y+3/4, z+1/4' 'x+3/4, -y+1/2, z+1/4' '-x+3/4, -y+5/4, z+1/2'

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cell length b
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cell length c
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cell angle beta
                                  90.00
cell angle gamma
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diffrn reflns theta max
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reflns number total
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reflns number gt
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reflns threshold expression
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computing cell refinement
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computing data reduction
                                 'INTEGRATE (STOE, 1997c)'
computing structure solution
                                 'SHELXS-97 (Sheldrick, 1990)'
computing structure refinement
                                 'SHELXL-97 (Sheldrick, 1997)'
computing molecular graphics
                                 ?
computing publication material
                                 'SHELXL-97 (Sheldrick, 1997)'
refine special details
Refinement of F^2 against ALL reflections. The weighted R-factor wR
and
 goodness of fit S are based on F^2^, conventional R-factors R are
based
on F, with F set to zero for negative F^2^2. The threshold expression
of
 F^2 > 2sigma(F^2^2) is used only for calculating R-factors(gt) etc.
and is
not relevant to the choice of reflections for refinement. R-factors
based
on F^2 are statistically about twice as large as those based on F,
and R-
factors based on ALL data will be even larger.
This material contains a framework composed of Ni atoms linked by
bipyridyl
molecules which form ladders directed along the c-direction of the
unit
cell. The bypyridyl molecules link Ni atoms atoms along this
direction are
disordered. They rock around the axis of the molecule and this has
been
modelled by splitting of these atoms over two sites. The temperature
factors of the split atoms were refined isotropically. The occupancy
of
the two sites refined to 0.557(6)/0.443(6). The bypyridyl molecules
forming the cross struts of the ladder were succesfully modelled
without
the introduction of split atomic positions.
Careful inspection of the cavities within the framework has allowed us
```

Careful inspection of the cavities within the framework has allowed us to locate methanol molecules. The methanol is disordered about a 2-fold axis and has 2 1/2-occupied orientations. In trial refinements the

```
C-O bond length was shorter (1.35A) than the literature value of
1.43A.
It was therefore restained to the literature value with no appreciable
effect on the R-factors for the fit.
Elemental microanalysis and thermogravimetric experiments are
consistent
with the stoichiometry determined from the single crystal diffraction
experiment.
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refine ls matrix type
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atom sites solution hydrogens
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_atom_site_refinement flags
_atom_site_disorder_assembly
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C1B C 0.6235(10) 0.3425(5) 0.0689(3) 0.0292(18) Uiso 0.557(6) d P . .
H1B H 0.5810 0.3204 0.0880 0.035 Uiso 0.557(6) calc PR . .
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H2B H 0.5845 0.4329 -0.0044 0.037 Uiso 0.557(6) calc PR . .
C3 C 0.8085(4) 0.3761(4) 0.04135(15) 0.0335(12) Uani 1 d . . .
C4A C 0.7419(10) 0.3779(7) 0.0748(3) 0.0297(19) Uiso 0.443(6) d P . .
H4A H 0.7785 0.3787 0.0990 0.036 Uiso 0.443(6) calc PR . .
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C4B C 0.7433(8) 0.3417(6) 0.0705(3) 0.0297(19) Uiso 0.557(6) d P . .
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angles
 and torsion angles; correlations between esds in cell parameters are
only
used when they are defined by crystal symmetry. An approximate
(isotropic)
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O2 N4 O1 116.2(8) . . ?
O3 N4 O1 118.2(7) . . ?
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C8 C7 C7 121.3(4) 12 554 18 565 ?
C8 C7 C7 121.3(4) . 18_565 ?
C7 C8 C9 119.6(8) . . ?
N3 C9 C8 123.5(7) . . ?
C10 C10 O4 146(6) 19 755 . ?
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refine diff density rms
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 'x-1/4, y-1/4, -z'
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 'x+1/2, -y-1/4, -z+1/4'
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 'x+1/4, y-3/4, -z'
 '-x+1/2, -y+1/2, -z'
 'x+1/2, -y+1/4, -z-1/4'
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 'x+1/4, y-1/4, -z-1/2'
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_cell_length_b
                                  20.408(18)
_cell_length_c
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exptl crystal density meas
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_exptl_crystal F 000
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 ?
;
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diffrn radiation source
                                  'fine-focus sealed tube'
diffrn radiation monochromator
                                  graphite
diffrn measurement device type
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diffrn measurement method
                                  ?
diffrn detector area resol mean
                                  ?
 diffrn standards_number
                                  ?
 diffrn standards interval count
                                  ?
 diffrn standards interval time
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 diffrn standards decay %
                                  ?
diffrn_reflns_number
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diffrn reflns av R equivalents
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diffrn reflns av sigmaI/netI
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12
                                  -21
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computing publication material ?

refine special details ; Refinement of F² against ALL reflections. The weighted R-factor wR and goodness of fit S are based on F^2 , conventional R-factors R are based on F, with F set to zero for negative F^2^{-1} . The threshold expression of F^2 > 2sigma(F^2) is used only for calculating R-factors(gt) etc. and is not relevant to the choice of reflections for refinement. R-factors based on F^2 are statistically about twice as large as those based on F, and Rfactors based on ALL data will be even larger. This material contains a framework composed of Ni atoms linked by bipyridyl molecules which form ladders directed along the c-direction of the unit The bypyridyl molecules link Ni atoms atoms along this cell. direction are disordered. They rock around the axis of the molecule and this has been modelled by splitting of these atoms over two sites. The temperature factors of the split atoms were refined isotropically. The occupancy of the two sites refined to 0.557(6)/0.443(6). The bypyridyl molecules forming the cross struts of the ladder were succesfully modelled without the introduction of split atomic positions. Data were collected from а crystal which had been desolvated ex-situ. ; refine ls structure factor coef Fsqd full _refine_ls_weighting_scheme 'calc w=1/[\s^2^(Fo^2^)+(0.1000P)^2^+0.0000P] where $P = (Fo^2 + 2Fc^2) / 3'$ _atom_sites_solution primary direct _atom_sites_solution_secondary difmap _atom_sites_solution_hydrogens geom _refine_ls_hydrogen treatment mixed _refine_ls_extinction_method none _refine_ls_extinction coef ? _refine_ls_number reflns 1317 _refine_ls_number_parameters 120 _refine_ls_number_restraints 0 _refine_ls_R_factor all 0.1558 _refine_ls_R_factor_gt 0.0561 _refine_ls_wR_factor_ref 0.1703 _refine_ls_wR_factor_gt 0.1411 _refine_ls_goodness_of_fit_ref 0.722 _refine_ls_restrained S all 0.722 _refine_ls_shift/su_max 0.000 refine ls shift/su mean 0.000

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 atom site fract y
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 atom site occupancy
 atom site calc flag
 _atom_site refinement flags
 atom site disorder assembly
  atom site disorder group
Ni1 Ni 0.3750 0.3750 0.03782(3) 0.0487(8) Uani 1 d S . .
C1A C 0.6201(15) 0.3729(13) 0.0711(3) 0.025(2) Uiso 0.479(11) d P . .
H1A H 0.5771 0.3706 0.0941 0.030 Uiso 0.479(11) calc PR . .
H1B H 0.5816 0.3152 0.0872 0.030 Uiso 0.521(11) d PR . .
C1B C 0.6240(16) 0.3385(10) 0.0683(3) 0.025(2) Uiso 0.521(11) d P . .
C2A C 0.6281(14) 0.3749(14) 0.0051(4) 0.033(3) Uiso 0.479(11) d P . .
H2A H 0.5891 0.3750 -0.0187 0.040 Uiso 0.479(11) calc PR . .
H2B H 0.5832 0.4356 -0.0038 0.040 Uiso 0.521(11) d PR . .
C2B C 0.6234(17) 0.4094(11) 0.0146(4) 0.033(3) Uiso 0.521(11) d P . .
C3 C 0.8093(6) 0.3746(7) 0.04097(16) 0.030(2) Uani 1 d . . .
C4A C 0.7415(13) 0.3746(13) 0.0743(4) 0.024(2) Uiso 0.479(11) d P . .
H4A H 0.7774 0.3758 0.0987 0.028 Uiso 0.479(11) calc PR . .
H4B H 0.7851 0.3159 0.0883 0.028 Uiso 0.521(11) d PR . .
C4B C 0.7434(14) 0.3392(11) 0.0692(3) 0.024(2) Uiso 0.521(11) d P . .
C5A C 0.7477(14) 0.3754(15) 0.0059(4) 0.029(3) Uiso 0.479(11) d P .
                                                                     .
H5A H 0.7898 0.3763 -0.0174 0.035 Uiso 0.479(11) calc PR . .
H5B H 0.7842 0.4333 -0.0059 0.035 Uiso 0.521(11) d PR . .
C5B C 0.7449(14) 0.4101(11) 0.0128(4) 0.029(3) Uiso 0.521(11) d P . .
O1 O 0.3771(6) 0.2742(4) 0.04178(13) 0.059(2) Uani 1 d . . .
N1 N 0.5609(5) 0.3741(6) 0.03976(15) 0.046(2) Uani 1 d . . .
N3 N 0.3750 0.3750 -0.0225(2) 0.048(4) Uani 1 d S . .
O2 O 0.3571(7) 0.3062(6) 0.09918(19) 0.111(4) Uani 1 d .
N4 N 0.3691(8) 0.2594(7) 0.07641(19) 0.061(3) Uani 1 d . . .
C7 C 0.3750 0.3750 -0.1029(3) 0.054(6) Uani 1 d S . .
O3 O 0.3739(10) 0.2031(9) 0.0861(3) 0.152(7) Uani 1 d .
C8 C 0.3377(9) 0.4278(8) -0.0827(2) 0.064(4) Uani 1 d . . .
H8 H 0.325(9) 0.473(7) -0.094(2) 0.077 Uiso 1 d . . .
C9 C 0.3391(8) 0.4262(7) -0.0424(2) 0.070(5) Uani 1 d . . .
H9 H 0.3135 0.4631 -0.0288 0.084 Uiso 1 calc R . .
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C3 0.018(4) 0.045(8) 0.028(3) 0.008(4) -0.005(3) 0.010(7)
O1 0.034(3) 0.106(8) 0.039(3) -0.002(3) 0.001(3) 0.005(5)
N1 0.016(4) 0.085(8) 0.036(3) 0.009(4) -0.004(3) 0.002(6)
N3 0.020(5) 0.099(13) 0.026(4) 0.000 0.000 0.013(8)
02 \quad 0.082(6) \quad 0.183(13) \quad 0.069(4) \quad -0.075(6) \quad -0.034(4) \quad 0.055(7)
N4 0.035(5) 0.109(12) 0.039(4) 0.015(5) 0.002(4) -0.011(7)
```

```
C7 0.019(7) 0.11(2) 0.029(6) 0.000 0.000 0.000(9)
03 0.098(8) 0.197(19) 0.162(9) 0.099(11) -0.036(7) -0.042(11)
C8 \quad 0.068(8) \quad 0.094(14) \quad 0.031(4) \quad -0.003(5) \quad -0.018(4) \quad 0.019(8)
C9 \ 0.052(7) \ 0.125(15) \ 0.034(4) \ -0.014(5) \ -0.016(4) \ 0.020(7)
geom special details
All esds (except the esd in the dihedral angle between two l.s.
planes)
 are estimated using the full covariance matrix. The cell esds are
taken
 into account individually in the estimation of esds in distances,
angles
 and torsion angles; correlations between esds in cell parameters are
only
used when they are defined by crystal symmetry. An approximate
(isotropic)
treatment of cell esds is used for estimating esds involving l.s.
planes.
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 geom bond atom site label 2
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 geom bond publ flag
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Ni1 O1 2.062(9) . ?
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Ni1 N1 2.095(5) 12 554 ?
Ni1 N1 2.095(5) . ?
C1A N1 1.266(14) . ?
C1A C4A 1.37(2) . ?
C1B C4B 1.34(2) . ?
C1B N1 1.412(18) . ?
C2A C5A 1.35(2) . ?
C2A N1 1.410(15) . ?
C2B N1 1.328(19) . ?
C2B C5B 1.37(2) . ?
C3 C4A 1.377(15) . ?
C3 C5A 1.390(15) . ?
C3 C5B 1.410(19) . ?
C3 C4B 1.418(19) . ?
C3 C3 1.479(13) 12 654 ?
O1 N4 1.231(8) . ?
N3 C9 1.313(12) . ?
N3 C9 1.313(12) 12 554 ?
O2 N4 1.242(15) . ?
N4 O3 1.197(17) . ?
C7 C8 1.349(13) . ?
C7 C8 1.349(13) 12 554 ?
C7 C7 1.518(18) 18 565 ?
C8 C9 1.386(10) . ?
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