

SUPPORTING INFORMATION

## Solvent-driven chirality for luminescent self- assembled structures: experiments and theory

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### Synthesis of the ligand and of the complex:

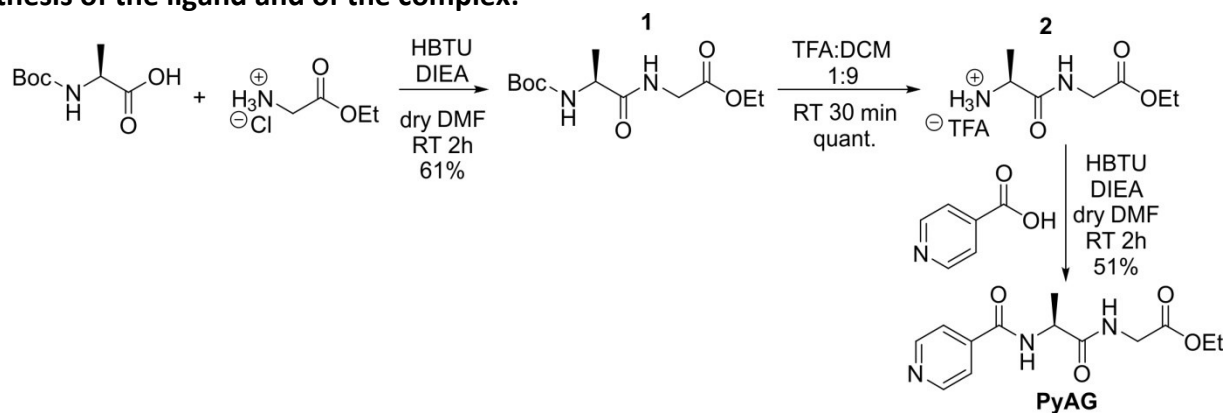


Figure S1: Reaction Scheme for the synthesis of **PyAG**

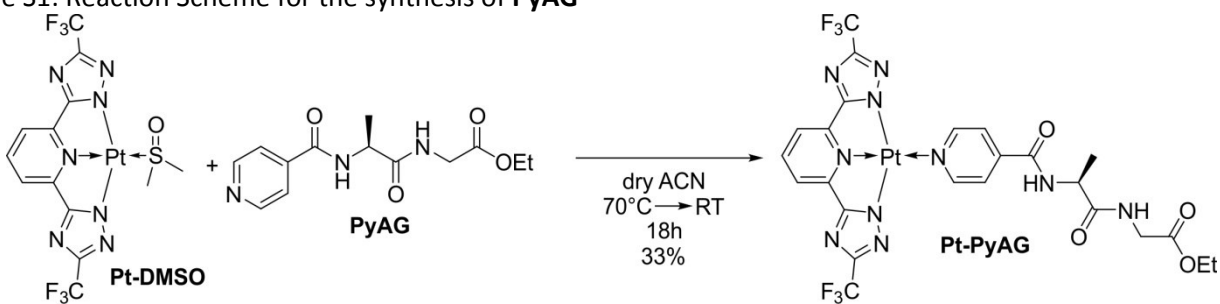


Figure S2: Reaction Scheme for the synthesis of **Pt-PyAG**

### Characterization of the compounds:

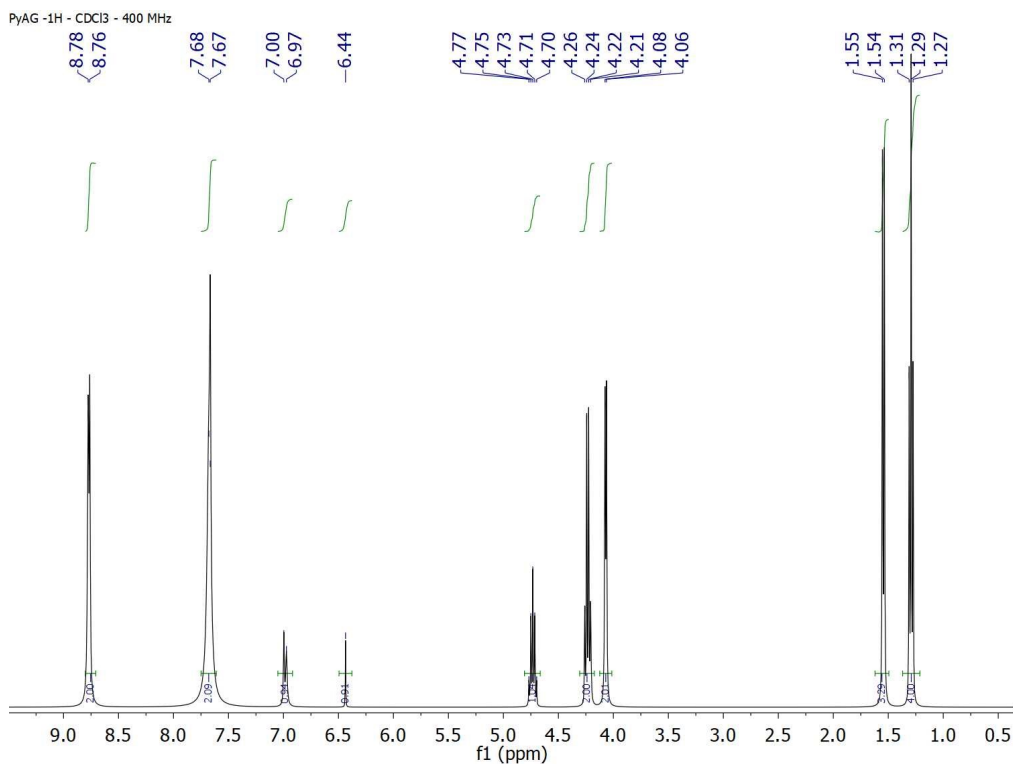


Figure S3: <sup>1</sup>H-NMR of ligand **PyAG** (CDCl<sub>3</sub>, 400 MHz).

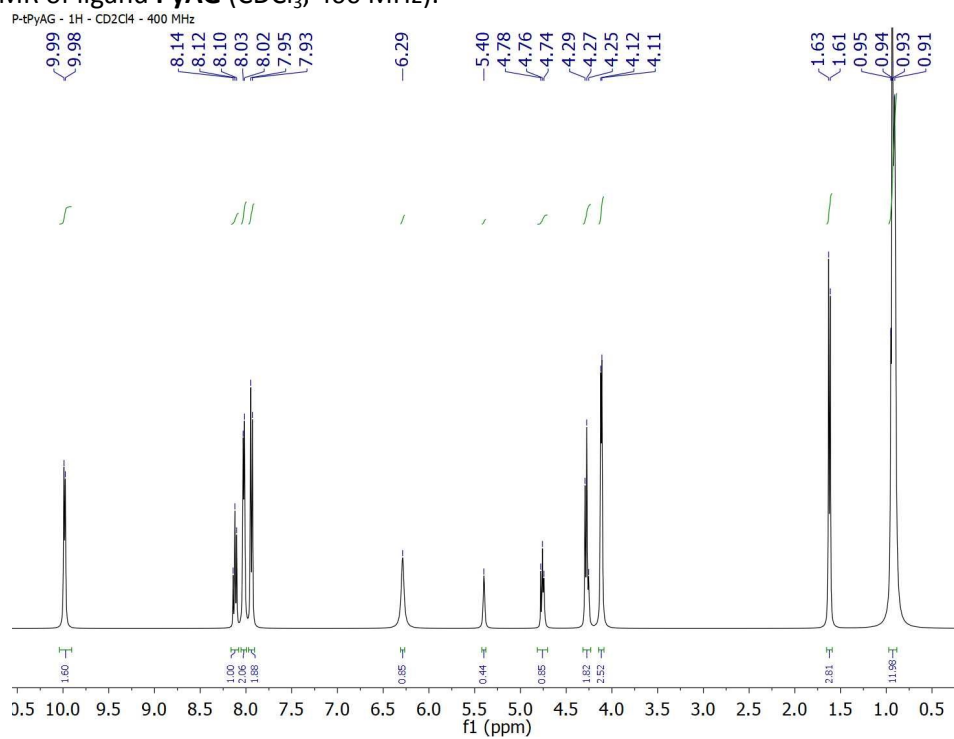


Figure S4: <sup>1</sup>H-NMR of complex **Pt-PyAG** (CD<sub>2</sub>Cl<sub>4</sub>, 400 MHz).

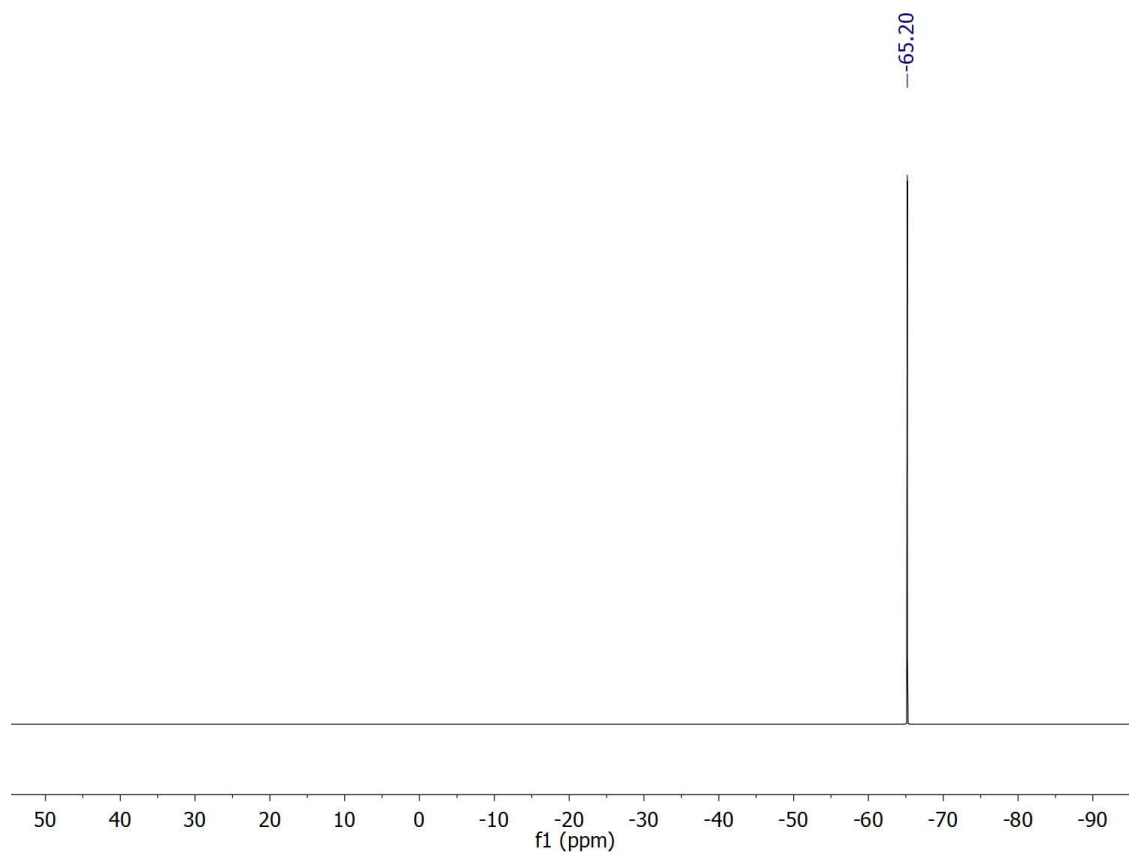


Figure S5:  $^{19}\text{F}$ -NMR of complex **Pt-PyAG** ( $\text{CD}_2\text{Cl}_4$ , 400 MHz).

Self-assembly of the complex in different solvents:

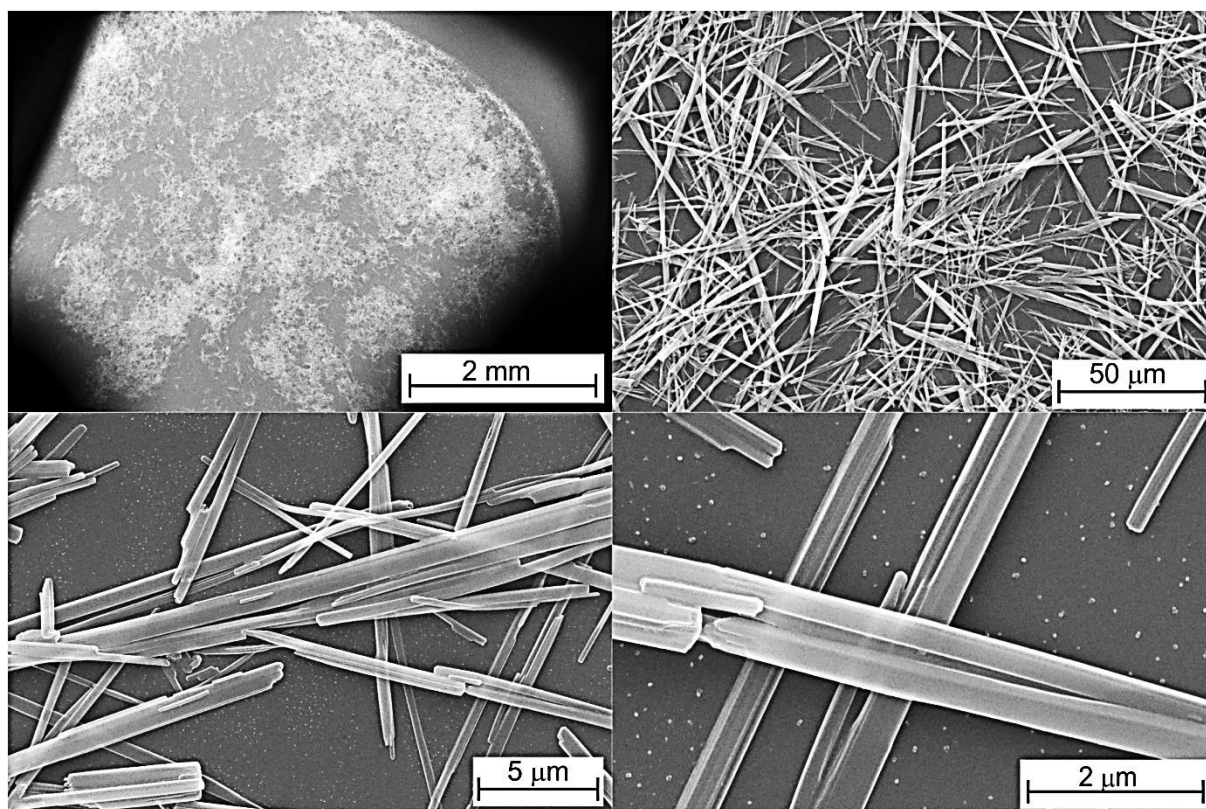


Figure S6: SEM images of the ribbon-like fibers of **Pt-PyAG** in ACN.

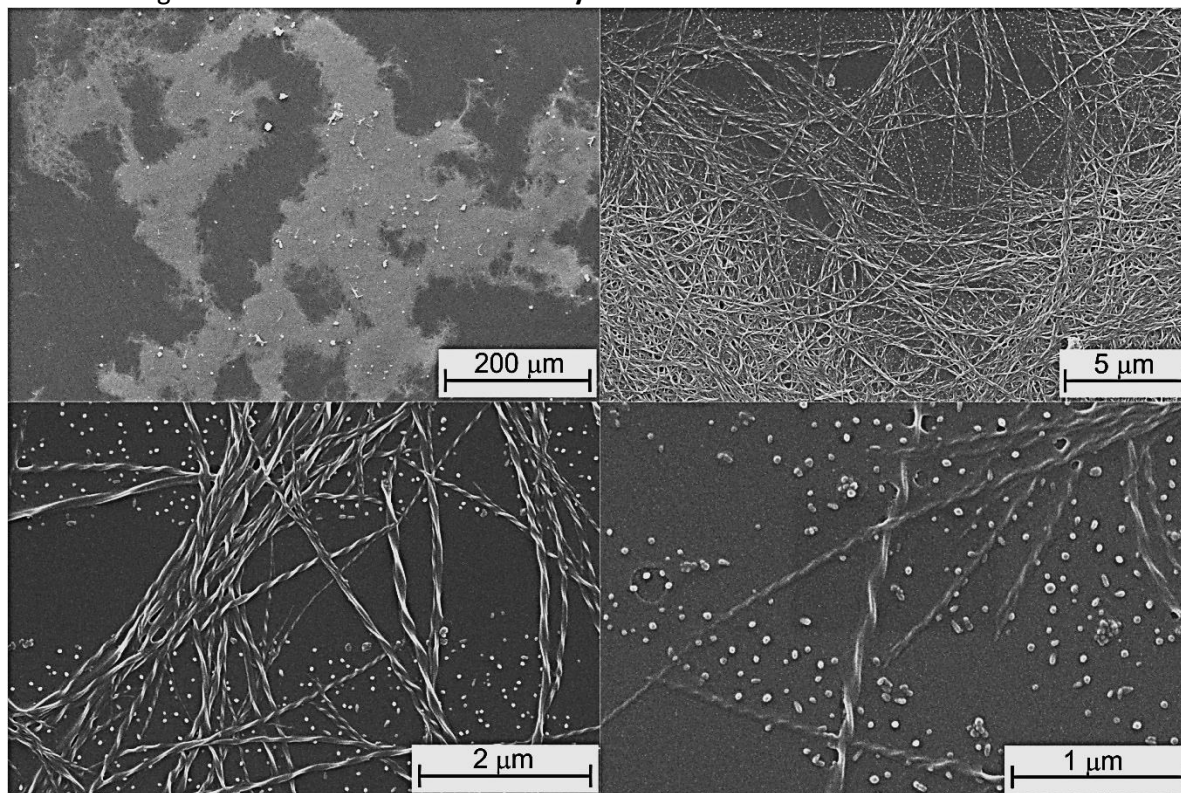


Figure S7: SEM images of the twisted fibers of **Pt-PyAG** in TCE.

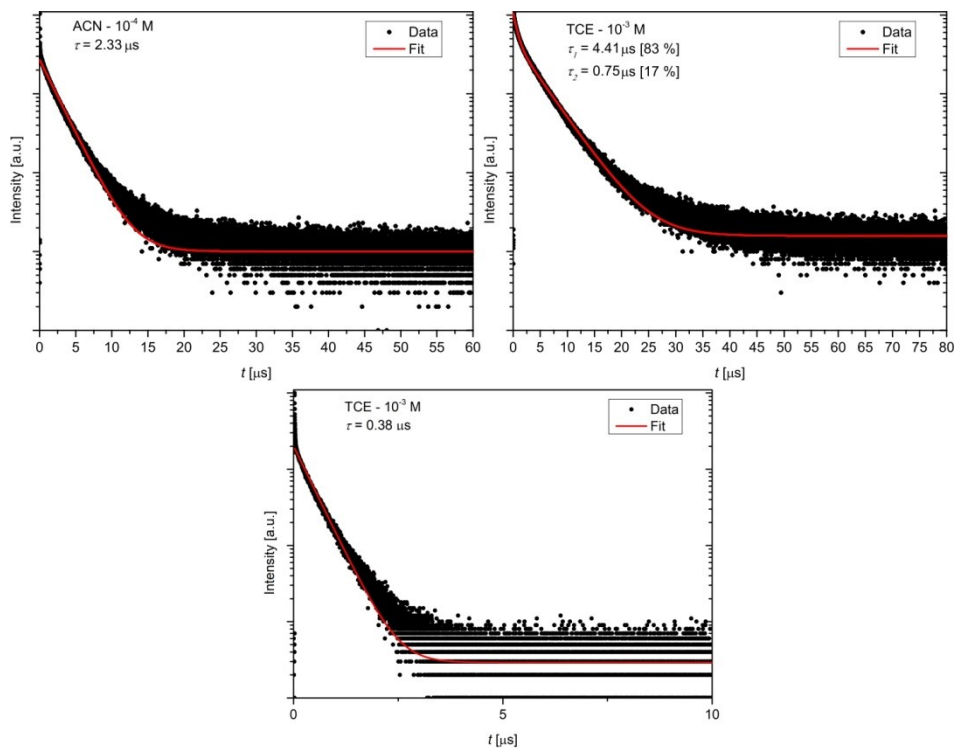


Figure S8: Excited-state lifetime decays of **Pt-PyAG** in ACN ( $10^{-4}$  M) and TCE ( $10^{-3}$  M) ( $\lambda_{exc} = 375$  nm;  $\lambda_{em} = 465$  nm) (top) ; and of **Pt-PyAG** in TCE ( $10^{-3}$  M,  $\lambda_{exc} = 375$  nm;  $\lambda_{em} = 575$  nm) (bottom). Decays were fitted with an exponential using a tailfit function.

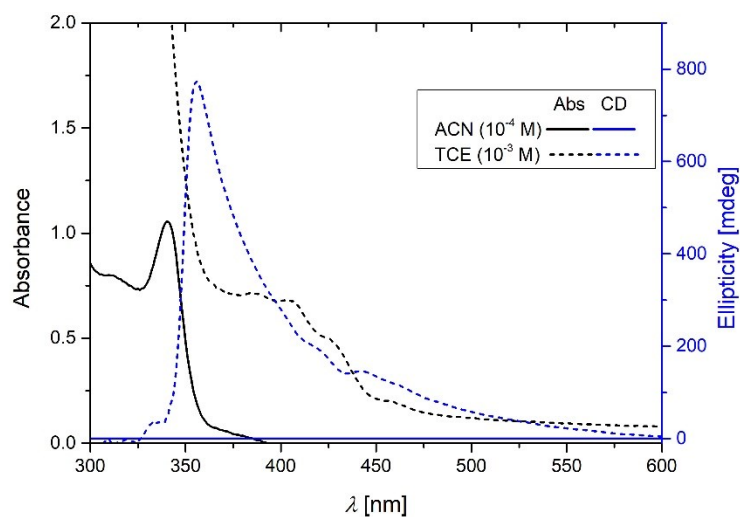


Figure S9: Absorption and CD spectra of **Pt-PyAG** in ACN ( $10^{-4}$  M) and TCE ( $10^{-3}$  M).

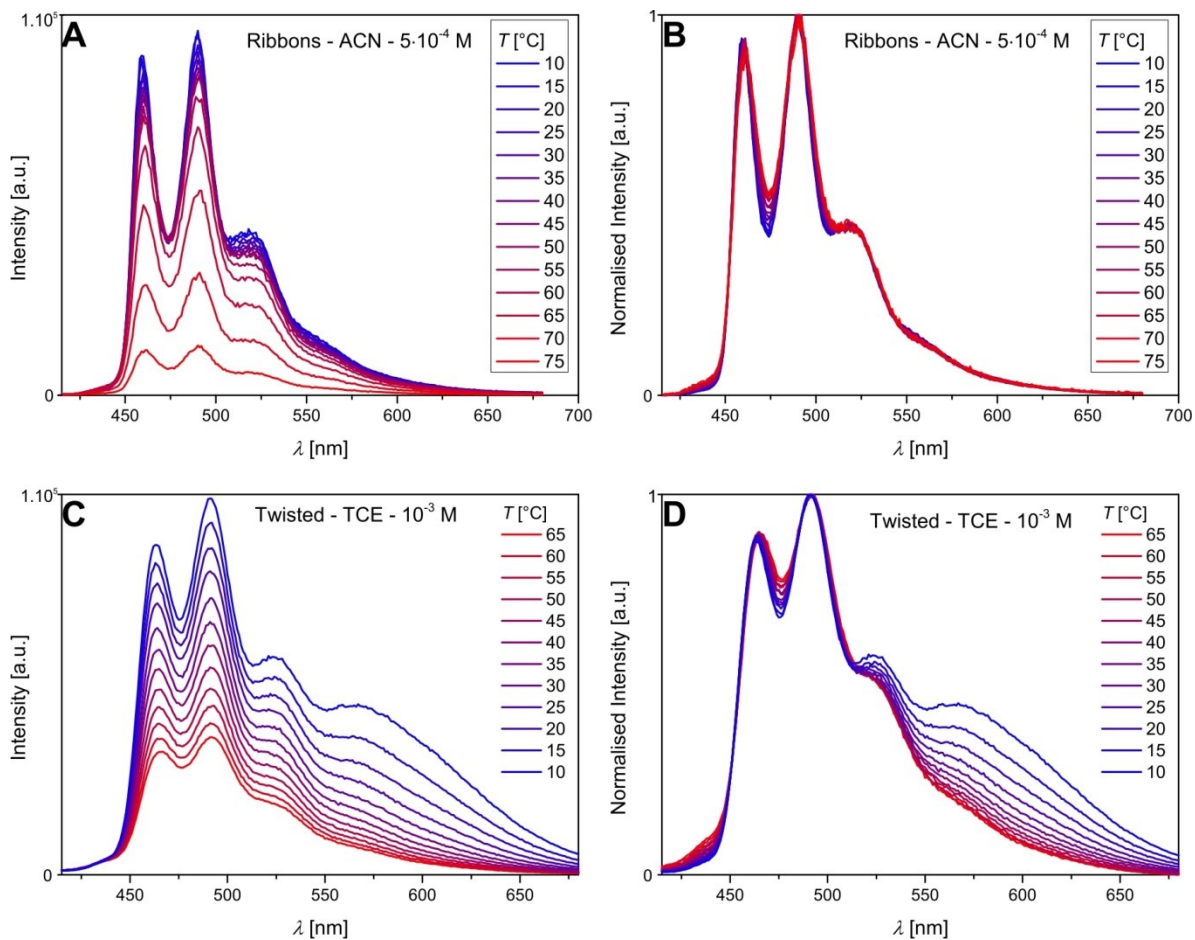


Figure S10: Temperature-dependent emission spectra and normalized spectra of the ribbons (A&B) and the twisted fibers (C&D) ( $\lambda_{exc} = 350$  nm).

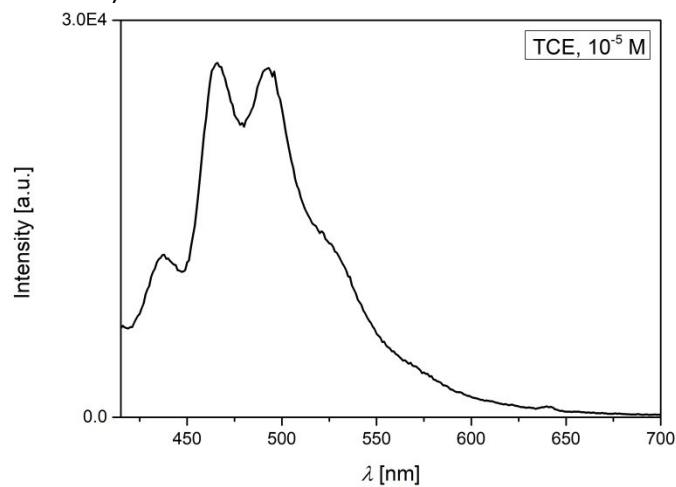


Figure S11: Emission spectrum of the molecularly dissolved Pt-PyAG in TCE at  $10^{-5}$  M ( $\lambda_{exc} = 350$  nm) (very weak emission).

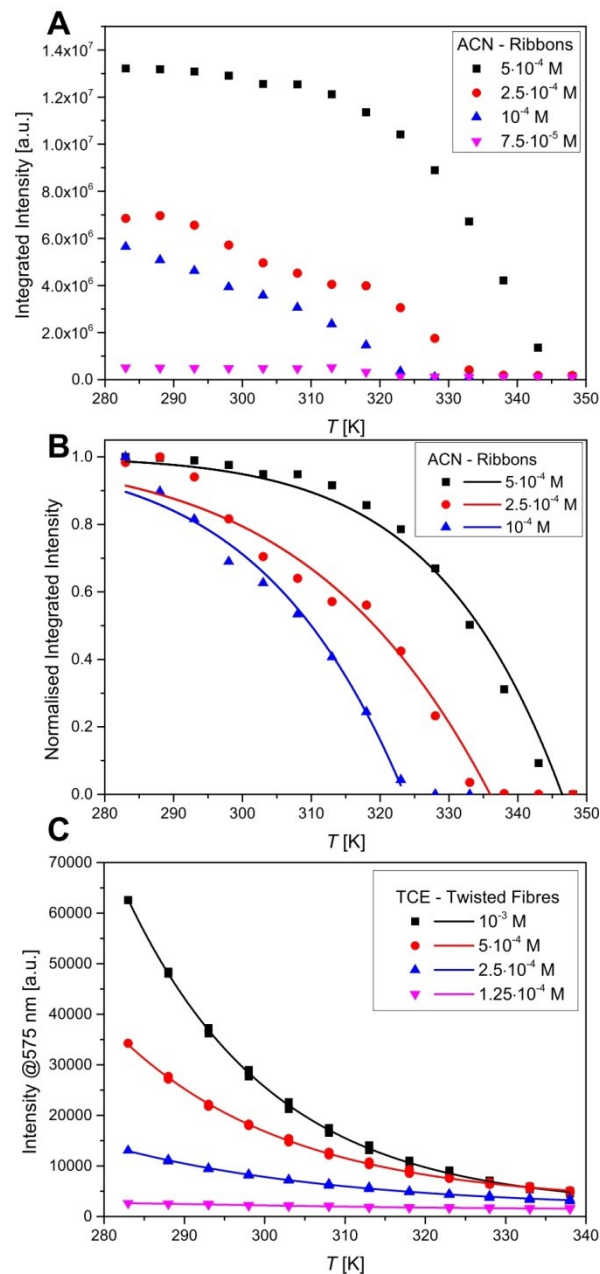


Figure S12. A. Integrated emission intensity vs. temperature for the ribbons at different concentrations; B. Normalized emission intensity vs. temperature (symbols) with the exponential fits (line) for the nanoribbons; C. Integrated emission intensity vs. temperature (symbols) with the sigmoidal fits (line) for the twisted fibers. The fitting of the data presented in Figure S11B was performed using the following equation:

$$y = 1 - a * \exp\left(-\frac{b}{x}\right)$$

The fitting of the data presented in Figure S11C was performed using the following equation:

$$y = A2 + (A1 - A2) / \left(1 + \frac{\exp(x - x0)}{dx}\right)$$

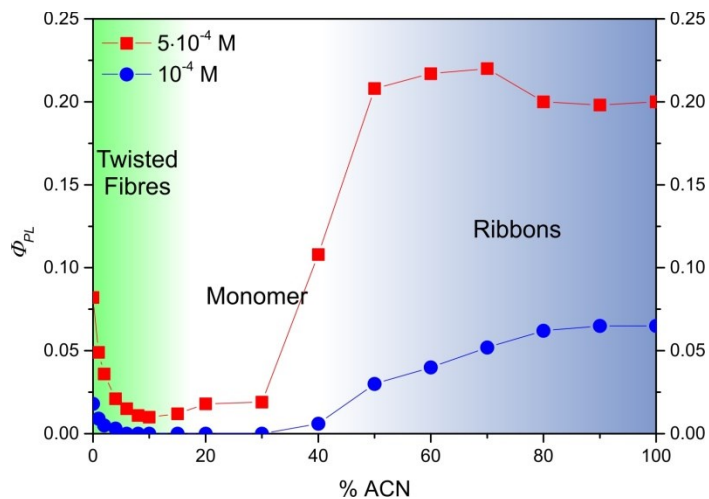


Figure S13. Quantum yield ( $\Phi_{exc} = 350$  nm) vs. solvent composition (TCE/ACN) at different concentrations.

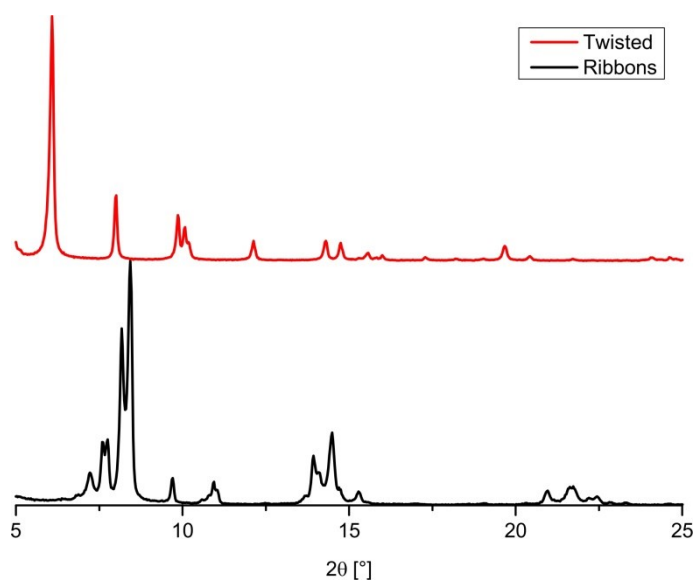


Figure S14. Powder X-ray diffraction patterns of the ribbons (black line) and the twisted fibers (red) of **Pt-PyAG**.



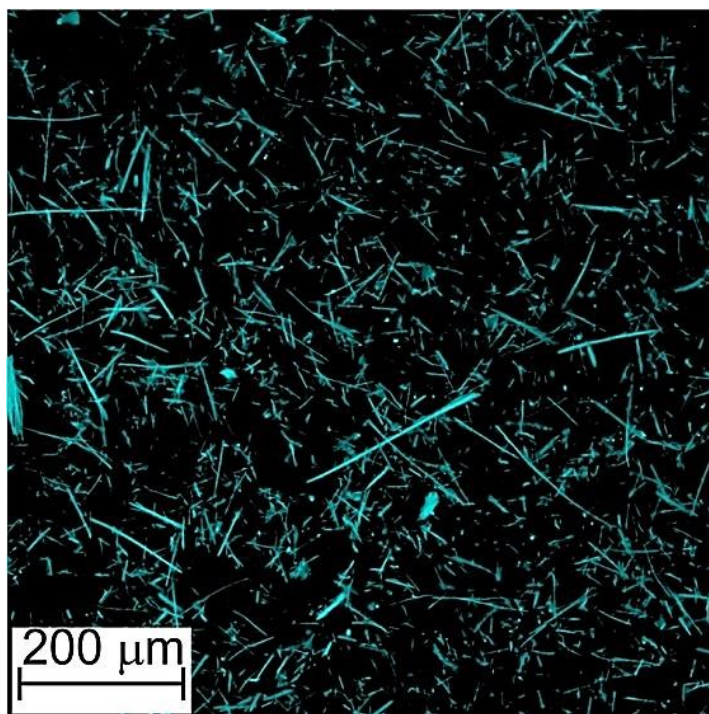


Figure S15. Confocal fluorescence microscopy image of the nanoribbons in lambda mode ( $\lambda_{exc} = 405 \text{ nm}$ ).

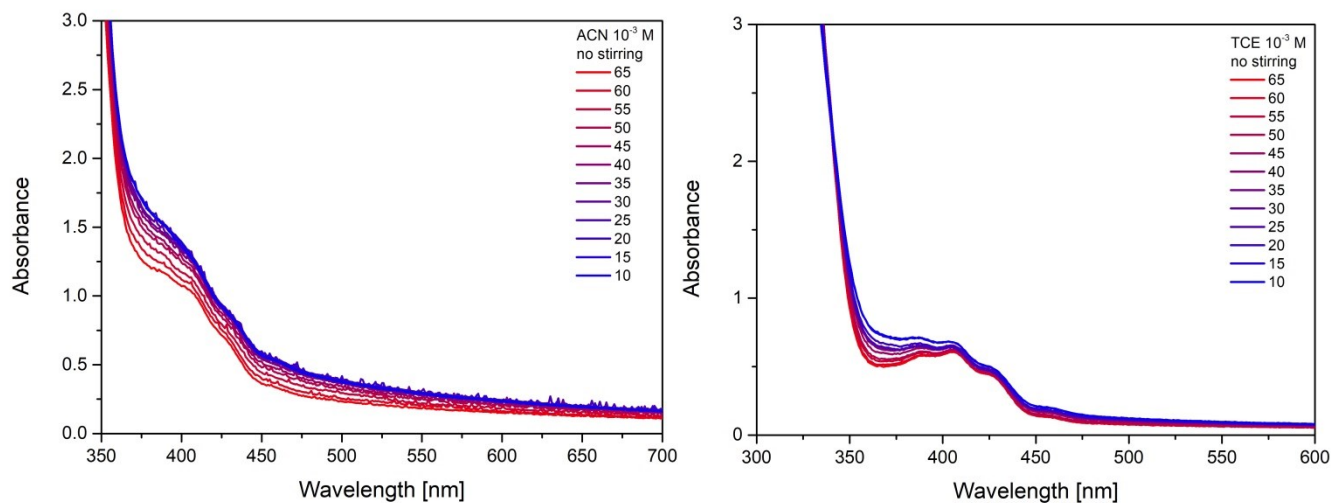


Figure S16. Temperature-dependent absorption spectra of Pt-PyAG in ACN (top) and TCE (bottom)

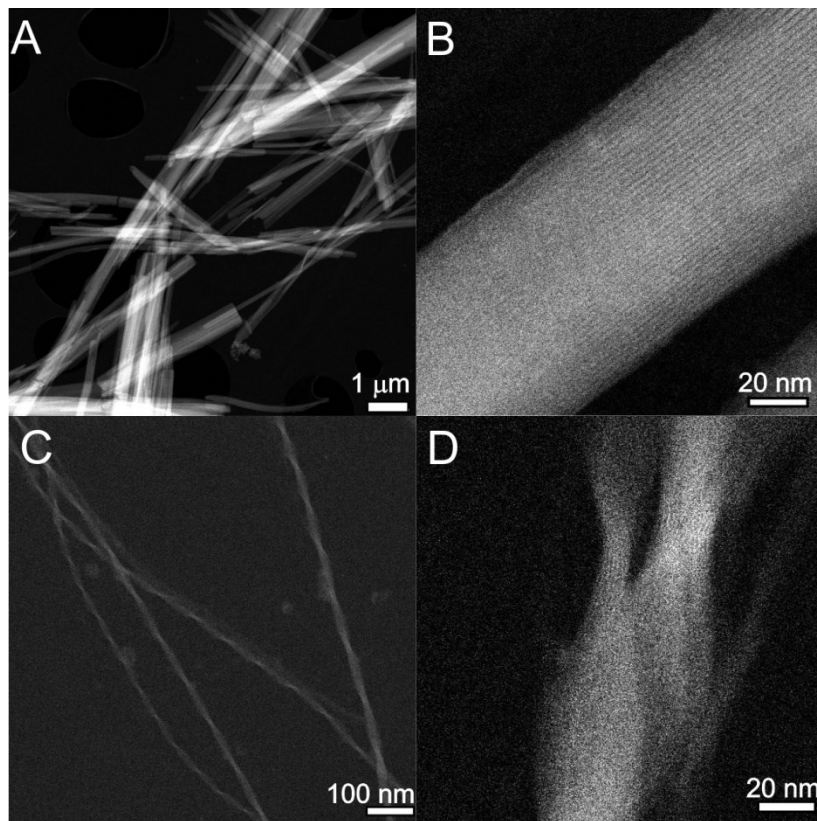


Figure S17. ADF-STEM images of the nanoribbons (A&B) and the twisted fibers (C&D)

### Extended details on AA and CG models parametrization

#### Details of all atom models parametrization

The computational All-Atom (AA) model of Pt-PyAG was parametrized according to the general AMBER force field (GAFF) <sup>1</sup>, by using the AMBERtools 17 <sup>2</sup>, while the missing parameters related to the atoms coordinating to the Pt atom were obtained following the procedure of the Metal Center Parameter Builder (MCPB) <sup>3</sup>. Here the system was considered neutral and the wavefunction was set in its singlet state. After running a preliminary geometrical optimization using the PM6 semi empirical method<sup>4,5</sup> the models were optimized at the B3LYP level of theory <sup>6</sup>, by using 6-31G\* basis set (BS) for the elements of the first three periods of the periodic table while for the Pt densities the LanL2DZ BS was used.

The Gaussian09 program was used for this procedure <sup>7</sup>. From this conformation the RESP partial charges <sup>8</sup> of Pt-PyAG were carried out. The Van Der Waals (VdW) parameters of the Pt atom were those of <sup>9</sup>, while those of the other atoms were taken from GAFF. The calculation of bonded parameters (stretching and bending force constants) of the metal coordinations were based on the Hessian matrix, using the Seminario's method <sup>10</sup>. Torsion force constants were set to 0 as in ref. <sup>3</sup>.

The AA models for the various solvents, ACN and TCE, were obtained accordingly.

## Coarse Grained parameters *.itp* GROMACS file format

Here below we report the *.itp* file (GROMACS format – energies in  $\text{kJ mol}^{-1}$ ) for the developed CG models used in this work. The SCX CG beads in the Pt-PyAG cores are *de facto* SC5 MARTINI beads, where the interactions SCX-SCX has been optimized to  $\epsilon = 2.0 \text{ kJ/mol}$  (instead of  $2.625 \text{ kJ/mol}$  for the original SC5-SC5) in order to reproduce the AA free energy profile of the core-core interaction, obtained by means of metadynamics simulations (Figure S18).

CG model for the **Pt-PyAG** monomer:

```
Pt-PyAG
[ moleculetype ]
;name nrexcl
TRMR 2

[ atoms ]
;nr type resi res atom cgnr charge
1 SCX 1 HEA C1 1 0.0
2 SCX 1 HEA C2 2 0.0
3 SCX 1 HEA C3 3 0.0
4 SCX 1 HEA C4 4 0.0
5 SNO 1 HEA N1 5 0.0
6 C2 1 HEA P1 6 0.0
7 SCX 1 HEA C6 7 0.0
8 SNO 1 HEA N2 8 0.0
9 C2 1 HEA P2 9 0.0
10 SNO 1 Pt0 Pt 10 0.0
11 SCX 1 TAI C7 11 0.0
12 SCX 1 TAI C8 12 0.0
13 P1 1 TAI O1 13 0.0
14 P4 1 TAI O2 14 0.0
15 P5 1 TAI O3 15 0.0
16 EO 1 TAI O4 16 0.0

[ constraints ]
;
[ bonds ]
;ai aj funct r k
1 2 1 0.18 25000.00
1 3 1 0.18 25000.00
2 4 1 0.27 25000.00
3 7 1 0.27 25000.00
4 5 1 0.17 25000.00
7 8 1 0.17 25000.00
4 6 1 0.28 25000.00
7 9 1 0.28 25000.00
12 13 1 0.24 25000.00
11 13 1 0.24 25000.00
```

3 10 1 0.30 25000.00  
2 10 1 0.30 25000.00  
5 10 1 0.27 25000.00  
8 10 1 0.27 25000.00  
10 11 1 0.30 16560.28  
10 12 1 0.30 16560.28  
2 3 1 0.17 25000.00  
11 12 1 0.17 25000.00  
13 14 1 0.41 14412.18

14 15 1 0.37 6616.01  
15 16 1 0.30 7678.43

[ angles ]

;ai aj ak funct theta cth  
3 2 4 2 154.63 2000.00  
2 3 7 2 154.63 2000.00  
1 2 4 2 140.99 2000.00  
1 3 7 2 140.99 2000.00  
1 2 10 2 134.32 2000.00  
1 3 10 2 134.32 2000.00  
4 2 10 2 82.96 2000.00  
7 3 10 2 82.96 2000.00  
2 4 5 2 91.50 2000.00  
3 7 8 2 91.50 2000.00  
2 4 6 2 167.03 283.17  
3 7 9 2 167.03 283.17  
5 4 6 2 95.80 1988.74  
8 7 9 2 95.80 1988.74  
4 5 10 2 114.89 1634.55  
7 8 10 2 114.89 1634.55  
5 10 3 2 102.49 2000.00  
8 10 2 2 102.49 2000.00  
8 10 3 2 69.15 2000.00  
5 10 2 2 69.15 2000.00  
3 10 11 2 206.55 475.52  
3 10 12 2 206.55 475.52  
2 10 11 2 206.55 475.52  
2 10 12 2 206.55 475.52  
5 10 11 2 93.77 40.07  
5 10 12 2 93.77 40.07  
8 10 11 2 93.77 40.07  
8 10 12 2 93.77 40.07  
10 11 13 2 138.23 704.92  
10 12 13 2 138.23 704.92  
12 13 14 2 151.70 16.48  
11 13 14 2 151.70 16.48  
8 10 5 2 167.95 426.01  
13 14 15 2 93.74 38.87  
14 15 16 2 134.15 41.44

[ dihedrals ]

;i	j	k	l	func	phase	kd	pn
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4	2	3	7	9	-177.73	2.17	2
3	2	4	5	9	179.56	0.53	4
3	2	4	6	9	-6.50	0.38	1
1	2	4	5	9	-177.35	0.64	6
1	2	4	6	9	177.50	0.46	2
10	2	4	5	9	-0.42	5.00	1
10	2	4	5	9	179.12	1.33	2
10	2	4	6	9	176.11	0.50	2
2	3	7	8	9	-178.24	0.50	4
2	3	7	9	9	-9.01	0.36	1
1	3	7	8	9	173.11	0.60	6
1	3	7	9	9	174.24	0.46	2
10	3	7	8	9	0.21	5.00	1
10	3	7	8	9	-179.63	1.33	2
10	3	7	9	9	170.59	0.52	2
2	4	5	10	9	1.00	5.00	1
2	4	5	10	9	-177.94	1.36	2
6	4	5	10	9	6.32	0.60	5
3	7	8	10	9	-0.87	5.00	1
3	7	8	10	9	178.31	1.35	2
9	7	8	10	9	0.99	0.60	5
10	12	13	14	9	-164.54	0.27	2
10	11	13	14	9	170.45	0.31	2
12	13	14	15	9	-110.75	0.46	1
12	13	14	15	9	-51.54	0.21	2
11	13	14	15	9	-116.46	0.47	1
11	13	14	15	9	-66.95	0.24	2
13	14	15	16	9	-3.16	0.14	1
13	14	15	16	9	-11.97	0.18	2
1	3	10	5	9	178.79	0.64	6
1	3	10	8	9	-179.00	5.00	1
1	3	10	8	9	-177.96	1.37	2
1	3	10	11	9	-23.36	0.10	2
1	3	10	12	9	-35.02	0.14	3
7	3	10	5	9	-179.82	5.00	1
7	3	10	5	9	-179.63	1.36	2
7	3	10	8	9	-0.04	5.00	1
7	3	10	8	9	179.93	1.29	2
7	3	10	11	9	-22.45	0.08	1
7	3	10	11	9	-39.53	0.06	2
7	3	10	12	9	12.23	0.19	6
1	2	10	5	9	-179.73	5.00	1
1	2	10	5	9	-179.49	1.38	2
1	2	10	8	9	-179.90	0.69	6
1	2	10	11	9	177.41	0.12	5
1	2	10	12	9	-164.09	0.13	5
4	2	10	5	9	0.32	5.00	1
4	2	10	5	9	-179.35	1.29	2

```

4 2 10 8 9 -179.87 5.00 1
4 2 10 8 9 -179.73 1.36 2
4 2 10 11 9 168.93 0.11 3
4 2 10 12 9 122.41 0.15 3
4 5 10 3 9 -0.59 5.00 1
4 5 10 3 9 178.76 1.41 2
4 5 10 2 9 -0.88 5.00 1
4 5 10 2 9 178.18 1.35 2
4 5 10 8 9 179.50 0.66 2
4 5 10 11 9 -20.33 0.29 5
4 5 10 12 9 7.84 0.32 5
7 8 10 3 9 0.54 5.00 1
7 8 10 3 9 -178.97 1.34 2
7 8 10 2 9 0.66 5.00 1
7 8 10 2 9 -178.69 1.41 2
7 8 10 5 9 179.97 0.67 2
7 8 10 11 9 3.22 0.35 5
7 8 10 12 9 -2.56 0.31 5
3 10 11 13 9 143.46 0.13 1
2 10 11 13 9 -43.30 0.15 3
5 10 11 13 9 159.69 0.21 2
8 10 11 13 9 154.99 0.21 2
3 10 12 13 9 -7.90 0.12 3
2 10 12 13 9 154.90 0.14 5
5 10 12 13 9 173.27 0.20 2
8 10 12 13 9 -179.39 0.20 2

```

CG model for different solvents:

All solvents have been parametrized in order to respect the overall polarity, and polarity anisotropic/isotropic features, of the native solvent molecules, which is particularly important in this case. OCT has been parametrized, as in standard MARTINI, using C1 beads. TCE molecules has been parametrized as two C4 MARTINI beads. ACN has been parametrized as one SC1 and one SP4 beads (while this gives rise to ACN CG molecules that are slightly larger than the AA ones, this was necessary to respect the key polarity features of ACN, possessing a hydrophobic tail and a hydrophilic head, which can interact with the amino acid tails of the monomers).

TCE

[moleculetype]

; molname nrexcl

TCE 1

[atoms]

; id type resnr residu atom cgnr charge

1 C4 1 TCE CX 1 0

2 C4 1 TCE CX 2 0

[bonds]

; ij funct length force.c.

1 2 1 0.47 1250

ACN

```
[moleculetype]
;molname  nrexcl
ACN      1
```

```
[atoms]
;id  type  resnr  residu  atom  cgnr  charge
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 2  SC1   1    ACN   C1   2    0
```

```
[constraints]
;ij  funct  length
 1 2  1    0.27
```

Additional data from the molecular simulations

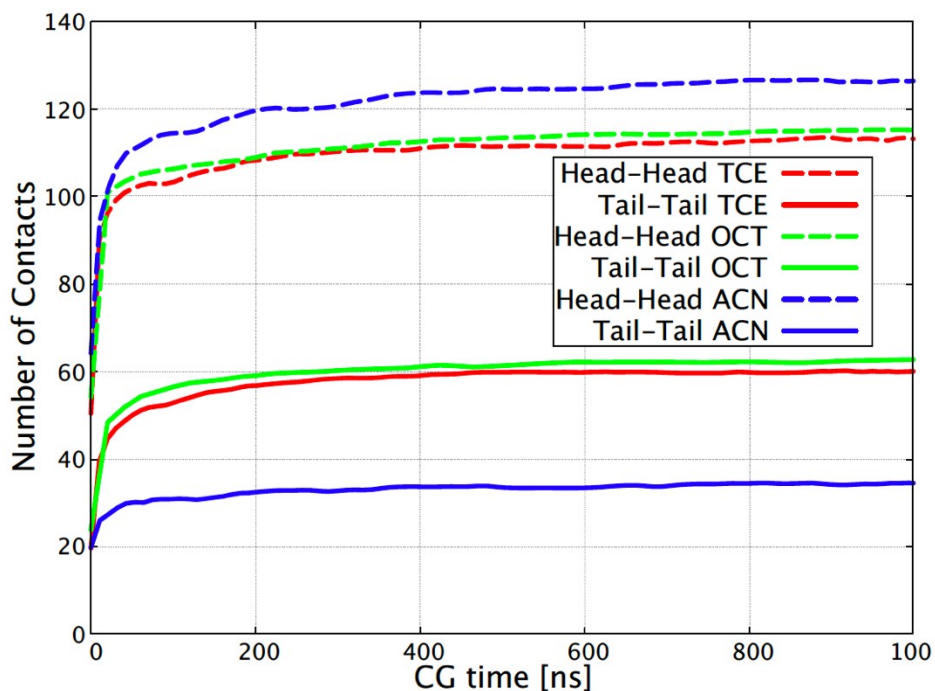


Figure S18: Number of contacts between the monomers Pt-heads (head-head) and between the peptide tails (tail-tail) in TCE, OCT and ACN obtained from CG-MD self-assembling simulations. The results show that the interactions between the monomers heads are relatively stronger in ACN than in TCE and OCT. On the contrary, the tail-tail interactions are stronger in TCE and OCT than in ACN.

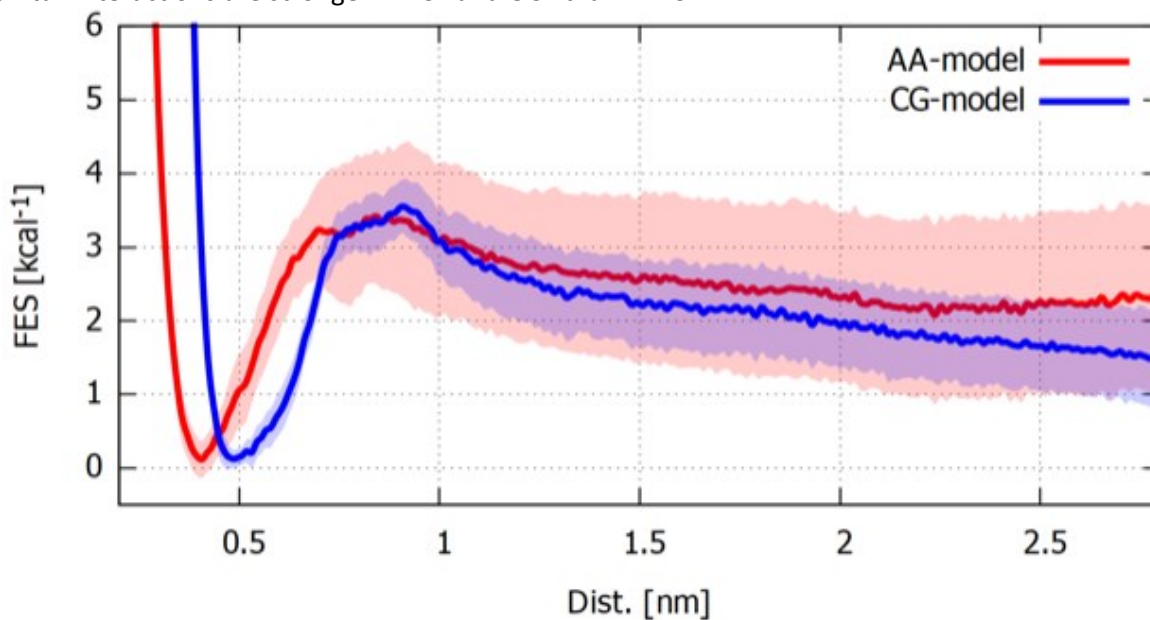


Figure S19: Free energy profile of head-head interaction obtained from AA and CG metadynamics simulations, showing consistent head-head stacking strength, and used to parametrize consistent CG models for the monomers.



## References:

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