

Supporting Information for:

**From Red to Blue Shift: Switching the Binding Affinity
from Acceptor to the Donor End by Increasing the π -Bridge
in Push-Pull Chromophores with Coordinative Ends**

Marco Caricato,^a Carmine Coluccini,^a Douglas Vander Griend,^b

*Alessandra Forni,^c and Dario Pasini^{*a,d}*

^a Department of Chemistry, University of Pavia, Viale Taramelli, 10–27100 Pavia, Italy. Fax: +39 0382 987323; Tel: +39 0382 987835; E-mail: dario.pasini@unipv.it Website: www.unipv.it/labt

^b Department of Chemistry & Biochemistry, Calvin College, Grand Rapids, MI 49546-4403- USA.

^c Institute of Molecular Sciences and Technologies (ISTM), CNR, Via Golgi 19, 20133 Milano, Italy

^d INSTM Research Unit, University of Pavia.

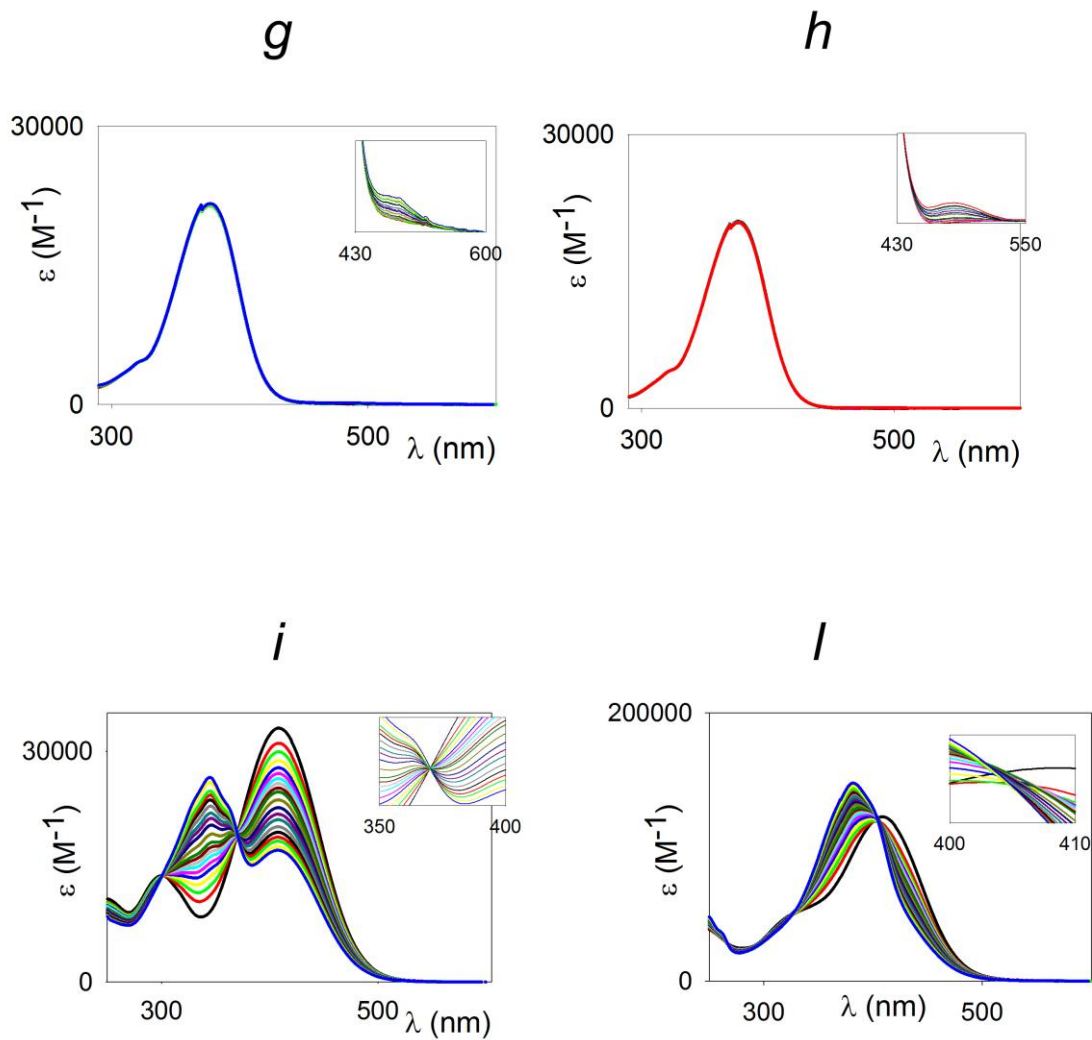


Figure S1. UV/Vis titration experiments with $Er(OTf)_3$ in MeCN for ligands **1** (left, **g** and **h**, with Yb^{3+}), **2** (titration **i**), and **3** (titration **l**).

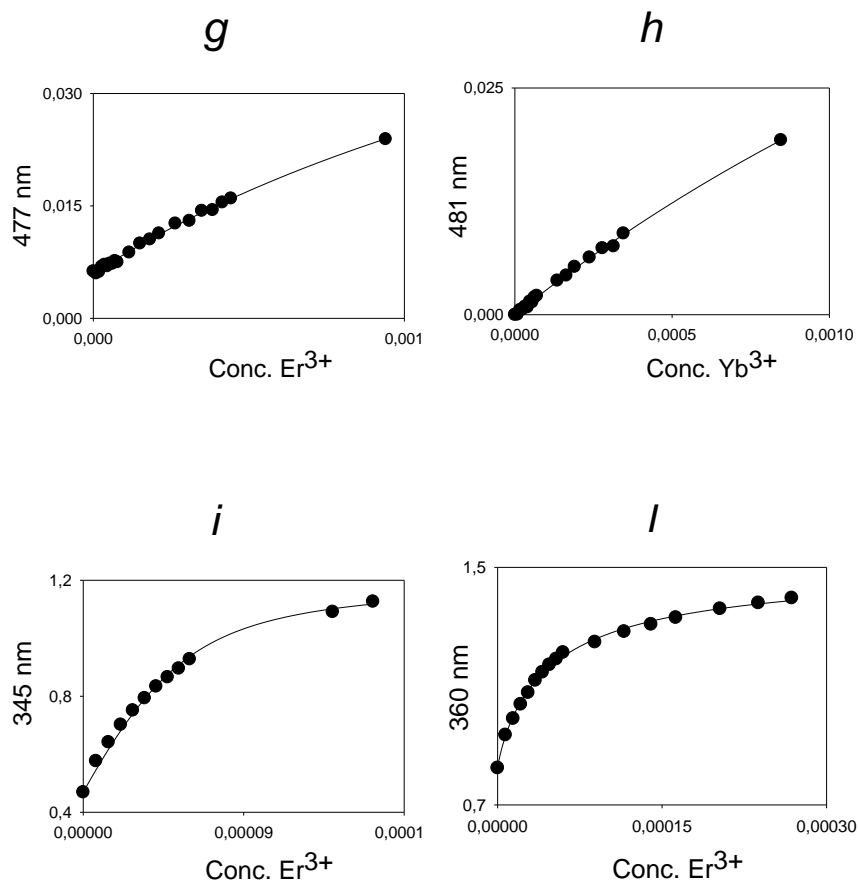


Figure S2. Titration profiles (ascending, wavelenghts indicated on the y axes) and best fit curves corresponding to the titrations shown in Figure S4.

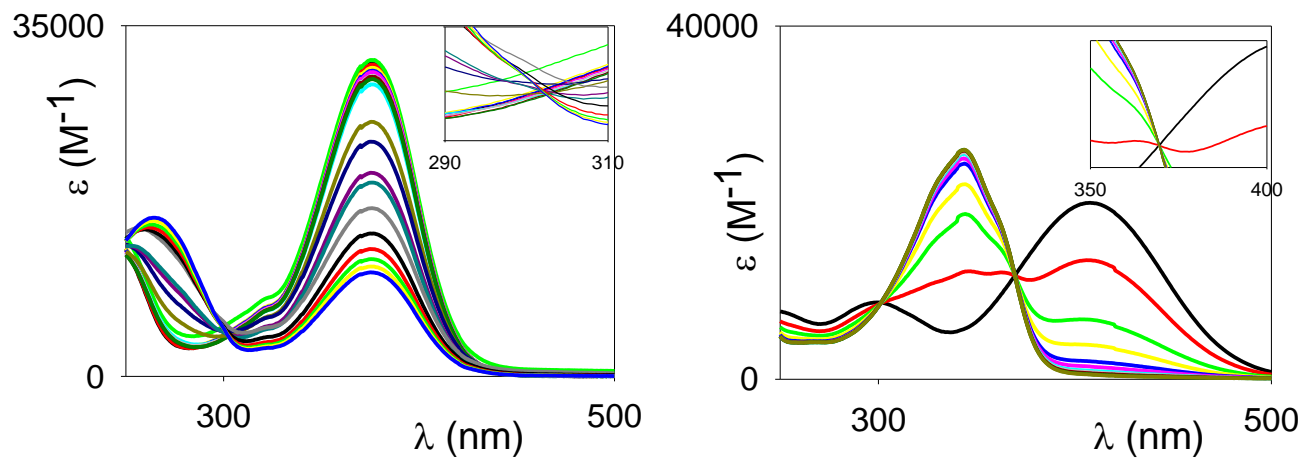


Figure S3. Left: Duplicate titration of **1** with $Sc(OTf)_3$. The isosbestic point is missing. Right: Duplicate titration of **2** with $Sc(OTf)_3$. The isosbestic point is holding.

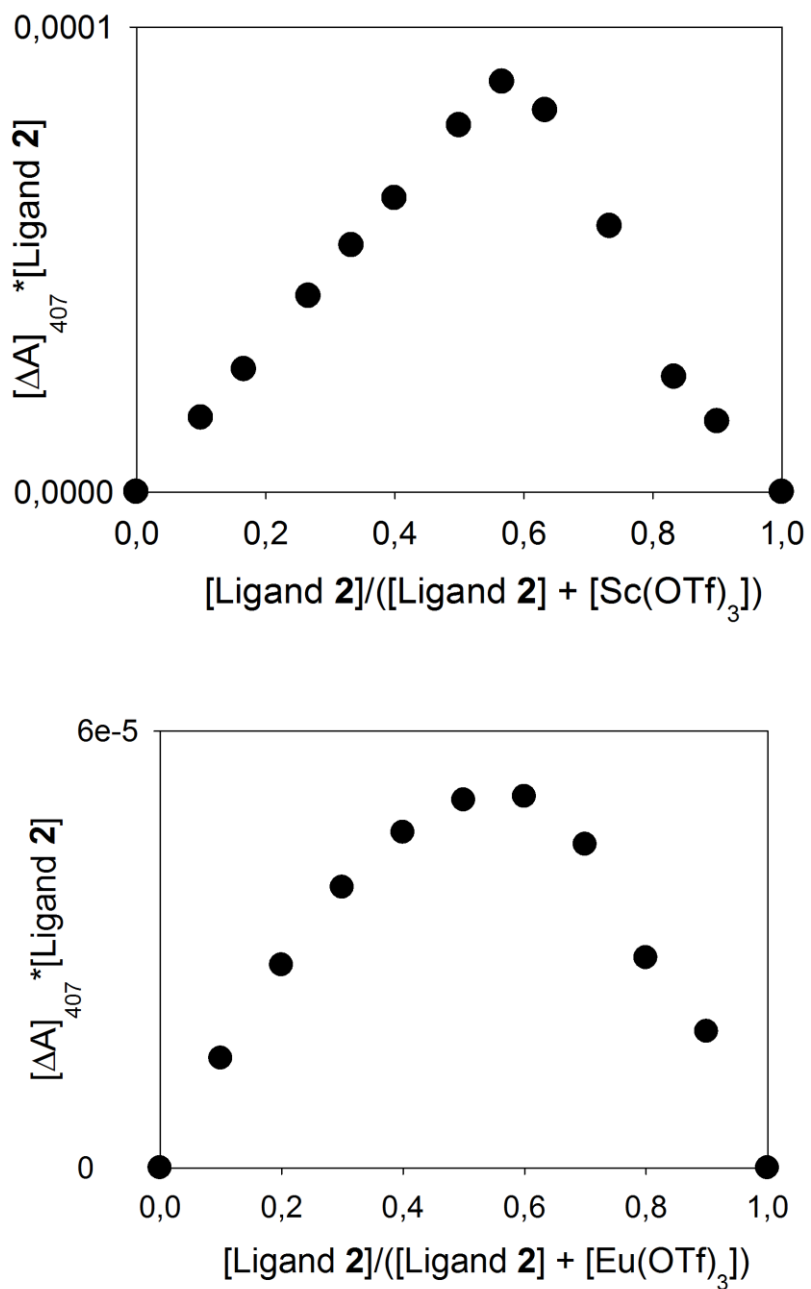


Figure S4. Job plot experiments of **2** with: a) top, $\text{Sc}(\text{OTf})_3$ b) bottom, $\text{Eu}(\text{OTf})_3$. Total concentration of species in each case: $76 \mu\text{M}$ in MeCN.

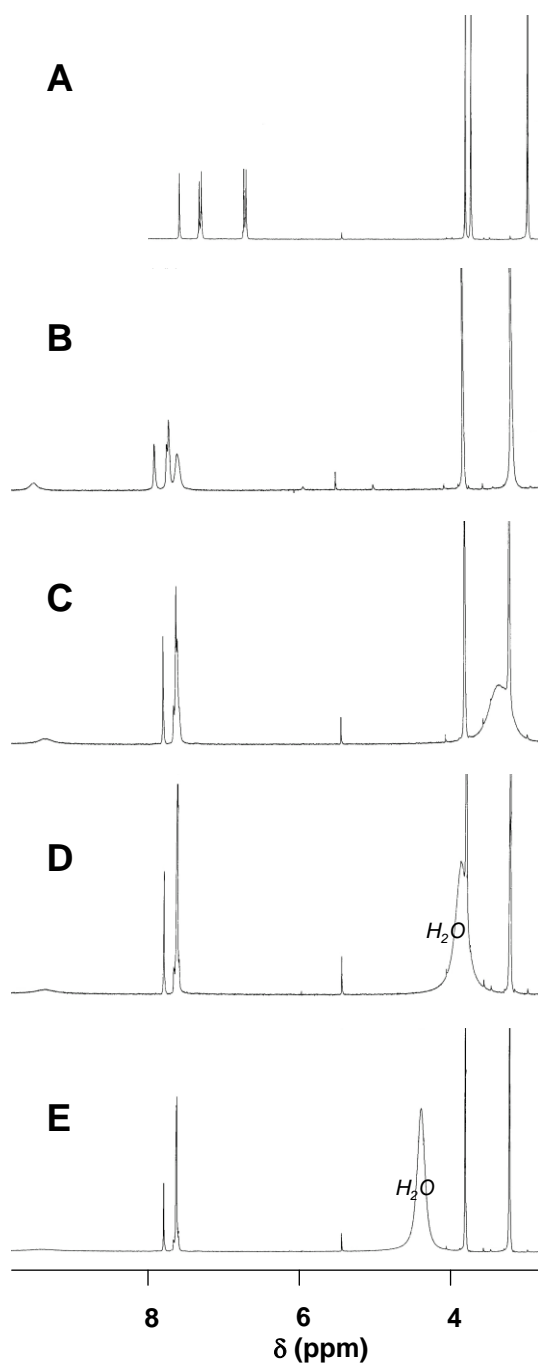


Figure S5. Titration of ligand **1** (0.0126 M in CD_3CN , 300 MHz) with $\text{Sc}(\text{OTf})_3$: A) 0 equivalents; B) 0.3 equivalents; C) 0.6 equivalents; D) 0.8 equivalents; E) 1.3 equivalents. This titration has been reduced for the making of Figure 5 in the main text

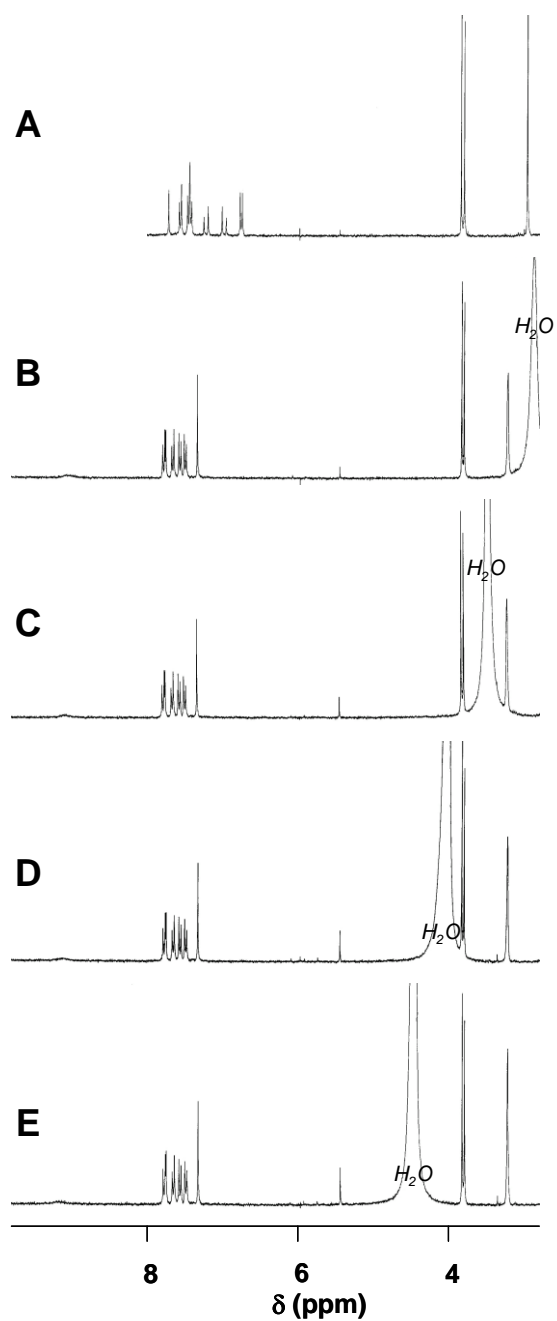
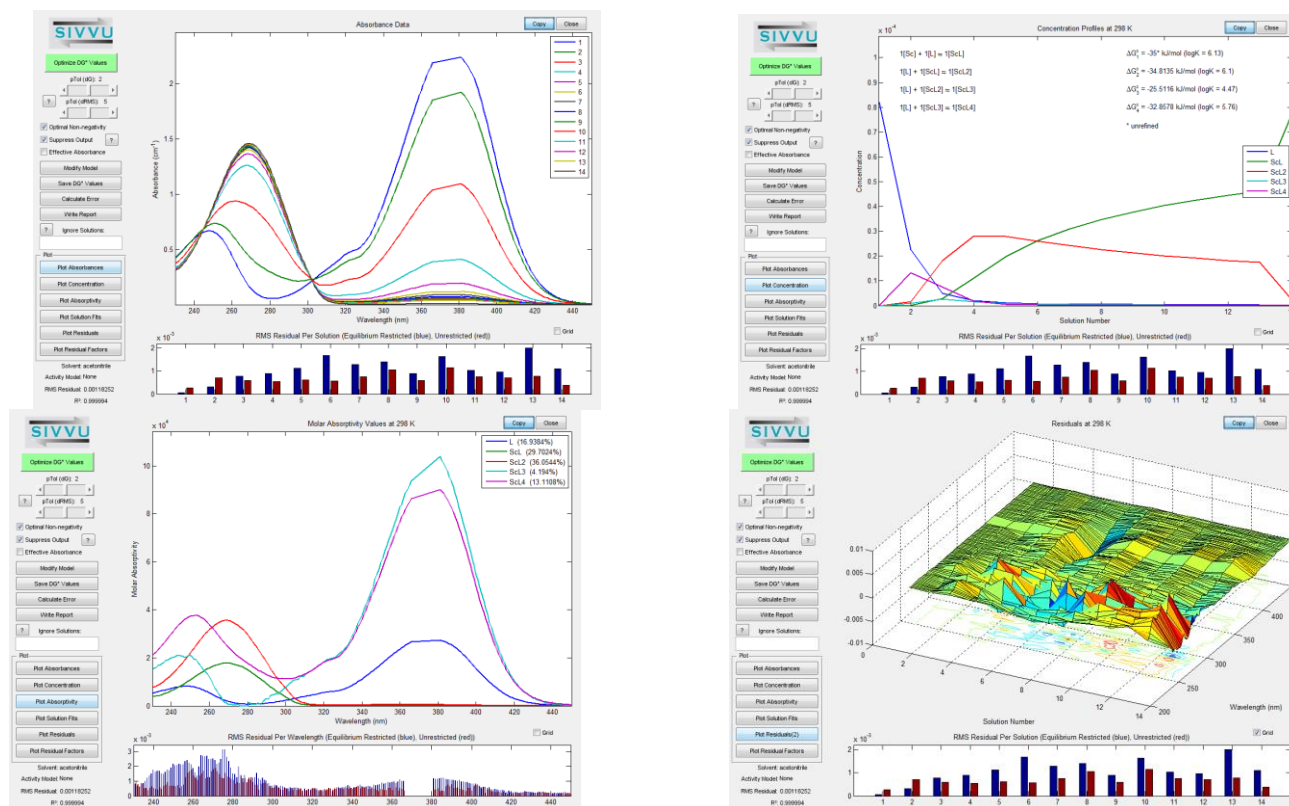


Figure S6. Titration of ligand **2** (0.007 M in CD_3CN) with $\text{Sc}(\text{OTf})_3$: A) 0 equivalents; B) 0.3 equivalents; C) 0.6 equivalents; D) 1.1 equivalents; E) 1.9 equivalents. This titration has been reduced for the making of Figure 6 in the main text

Table S1. Titration of Ligand **1** with Sc(OTf)₃ (titration *a* in Figure 3)



Optimization Summary:

Data at 298 K

Non-negativity was enforced with optimization (not truncation).

Activity Coefficients Model: None.

Species with Fixed Molar Absorptivity Curves: None.

Solutions ignored: None.

Optimized Values (kJ/mol): $\Delta G^{\circ}_1 = -35(\text{unrefined})$; $\Delta G^{\circ}_2 = -34.8(1)$; $\Delta G^{\circ}_3 = -25.5(1)$; $\Delta G^{\circ}_4 = -32.9(1)$;

Equilibrium Restricted RMS Residual (6 chemical factors): 0.0011557

Unrestricted RMS Residual (6 mathematical factors): 0.0005969

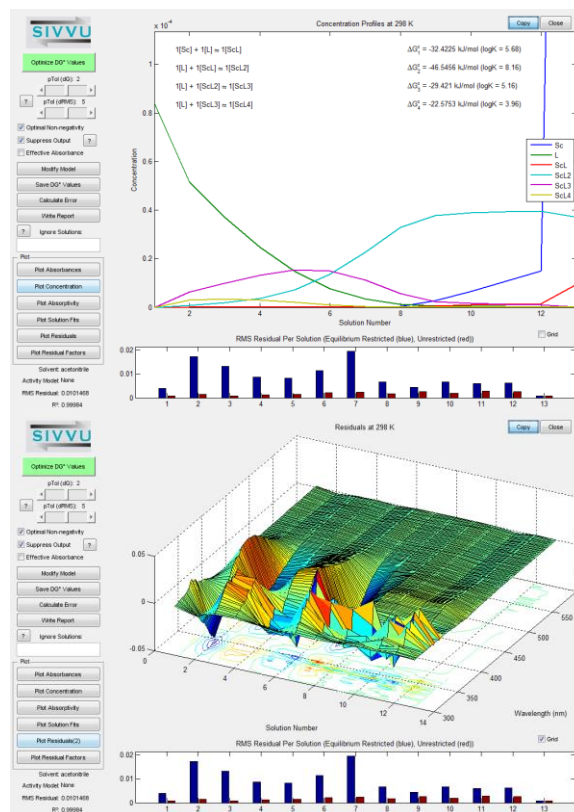
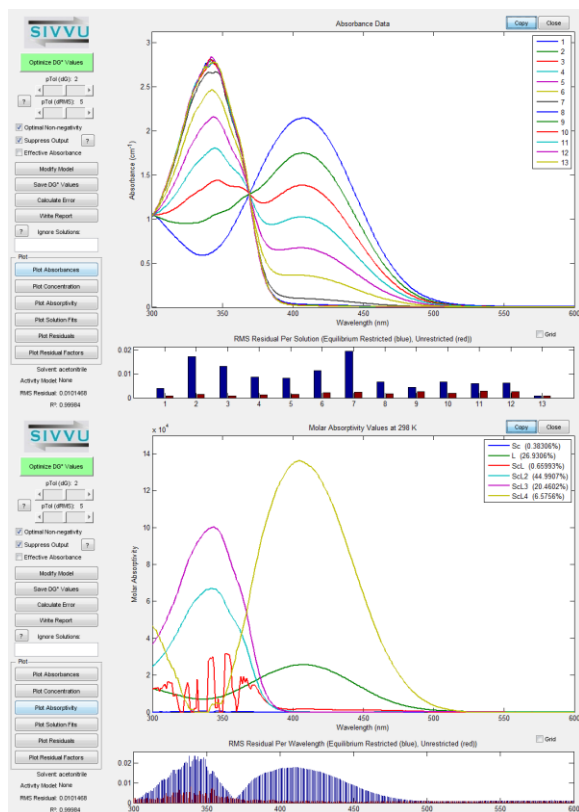
Restricted Data Reconstruction (6 chemical factors): 99.752%

Unrestricted Data Reconstruction (6 mathematical factors): 99.8181%

Remaining Error Imbedded in Absorbance Values: 0.0010009

R²: 99.9994%

Table S2. Titration of Ligand **2** with Sc(OTf)₃ (titration *c* in Figure 3)



Optimization Summary:

Data at 298 K

Non-negativity was enforced with optimization (not truncation).

Activity Coefficients Model: None.

Species with Fixed Molar Absorptivity Curves: None.

Solutions ignored: None.

Optimized Values (kJ/mol): $\Delta G^{\circ}_1 = -32.4(2)$; $\Delta G^{\circ}_2 = -46.5(1)$; $\Delta G^{\circ}_3 = -29.4(1)$; $\Delta G^{\circ}_4 = -22.6(1)$;

Equilibrium Restricted RMS Residual (6 chemical factors): 0.010147

Unrestricted RMS Residual (6 mathematical factors): 0.0019111

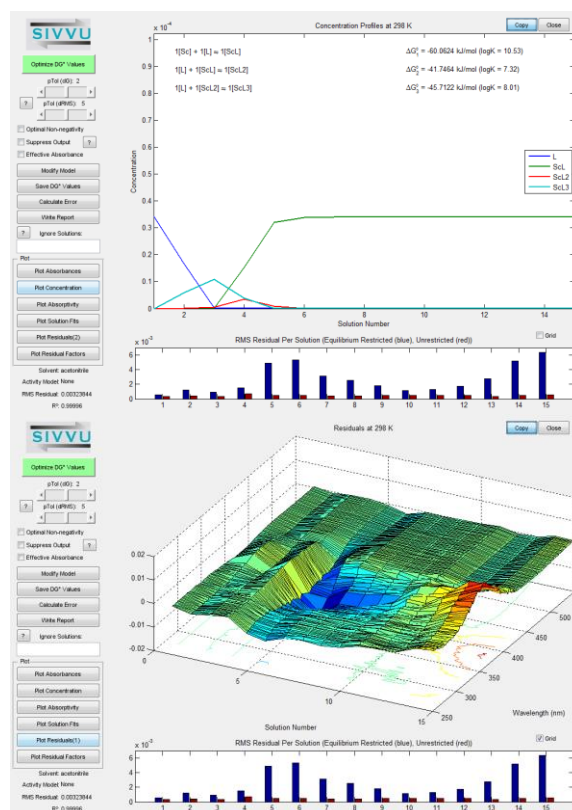
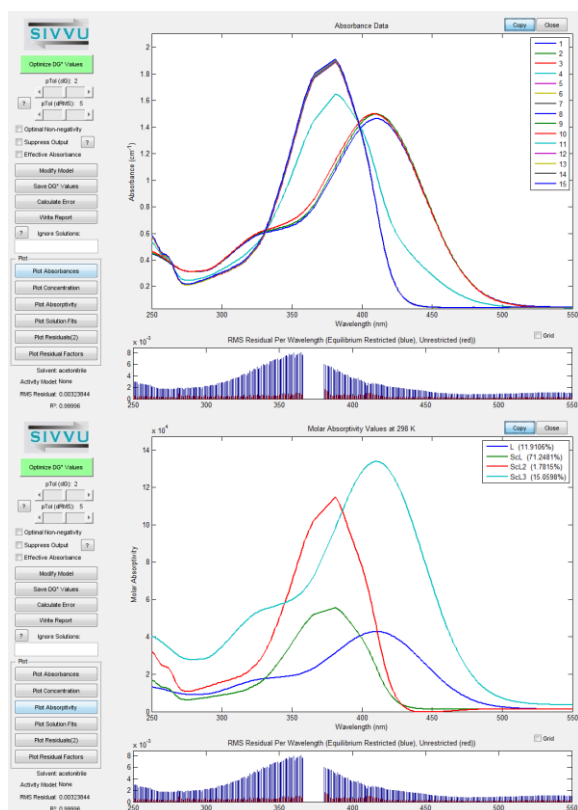
Restricted Data Reconstruction (6 chemical factors): 99.3834%

Unrestricted Data Reconstruction (6 mathematical factors): 99.6497%

Remaining Error Imbedded in Absorbance Values: 0.0093941

R²: 99.984%

Table S3. Titration of Ligand **3** with Sc(OTf)₃ (titration *e* in Figure 3)



Optimization Summary:

Data at 298 K

Non-negativity was enforced with optimization (not truncation).

Activity Coefficients Model: None.

Species with Fixed Molar Absorptivity Curves: None.

Solutions ignored: None.

Optimized Values (kJ/mol): $\Delta G^{\circ}_1 = -60.1(3)$; $\Delta G^{\circ}_2 = -41.7(2)$; $\Delta G^{\circ}_3 = -45.7(1)$;

Equilibrium Restricted RMS Residual (4 chemical factors): 0.0032382

Unrestricted RMS Residual (4 mathematical factors): 0.00045912

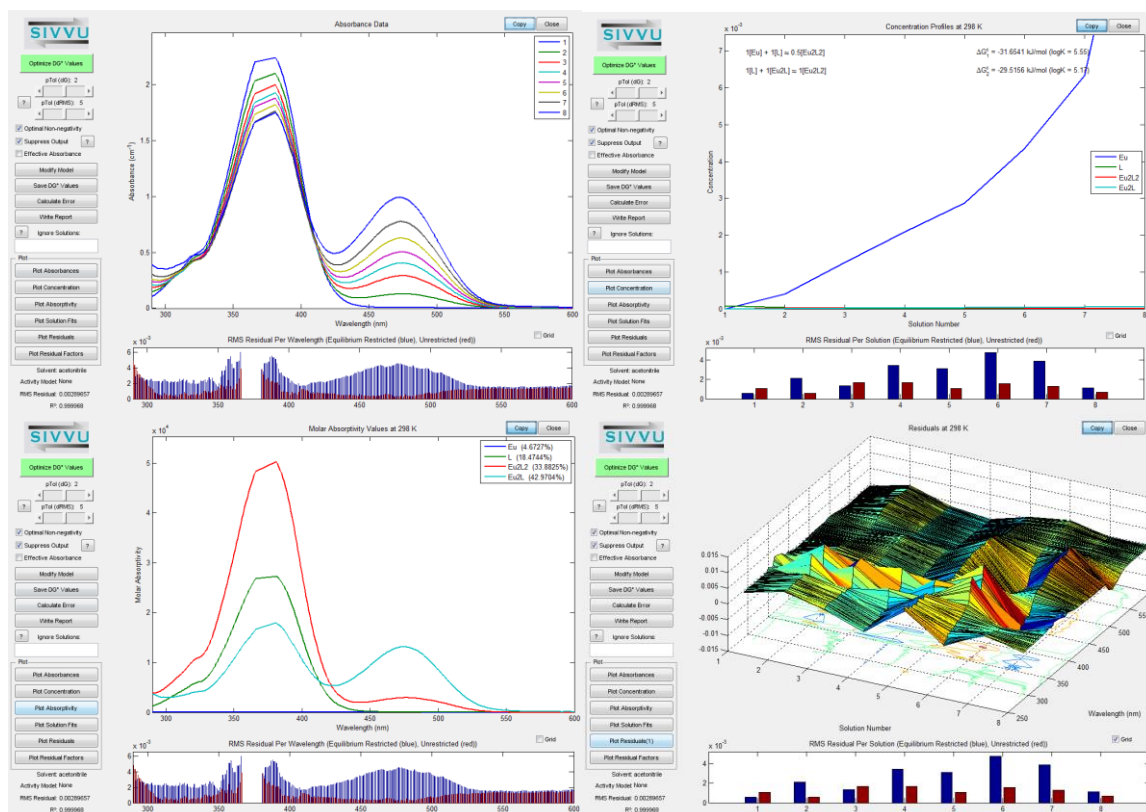
Restricted Data Reconstruction (4 chemical factors): 99.7735%

Unrestricted Data Reconstruction (4 mathematical factors): 99.8377%

Remaining Error Imbedded in Absorbance Values: 0.0019527

R²: 99.996%

Table S4. Titration of Ligand **1** with Eu(OTf)₃ (titration **b** in Figure 3)



Optimization Summary:

Data at 298 K

Non-negativity was enforced with optimization (not truncation).

Activity Coefficients Model: None.

Species with Fixed Molar Absorptivity Curves: None.

Solutions ignored: None.

Optimized Values (kJ/mol): $\Delta G^{\circ}_1 = -31.65(6)$; $\Delta G^{\circ}_2 = -29.52(5)$;

Equilibrium Restricted RMS Residual (4 chemical factors): 0.0028966

Unrestricted RMS Residual (4 mathematical factors): 0.0012714

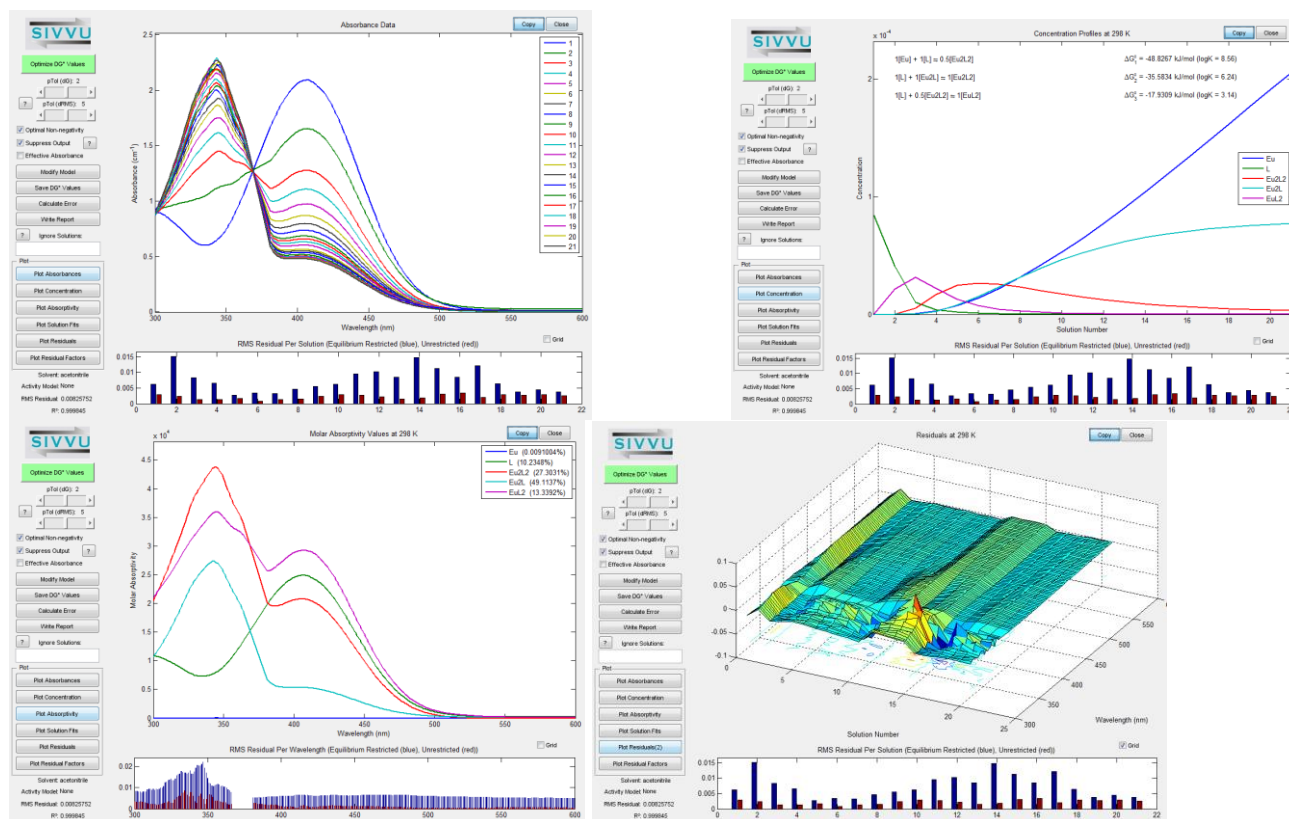
Restricted Data Reconstruction (4 chemical factors): 99.701%

Unrestricted Data Reconstruction (4 mathematical factors): 99.7264%

Remaining Error Imbedded in Absorbance Values: 0.0028966

R²: 99.9968%

Table S5. Titration of Ligand **2** with Eu(OTf)₃ (titration *d* in Figure 3)



Optimization Summary:

Data at 298 K

Non-negativity was enforced with optimization (not truncation).

Activity Coefficients Model: None.

Species with Fixed Molar Absorptivity Curves: None.

Solutions ignored: None.

Optimized Values (kJ/mol): $\Delta G^{\circ}_1 = -48.8(1)$; $\Delta G^{\circ}_2 = -35.6(1)$; $\Delta G^{\circ}_3 = -17.9(2)$;

Equilibrium Restricted RMS Residual (5 chemical factors): 0.0082575

Unrestricted RMS Residual (5 mathematical factors): 0.0022966

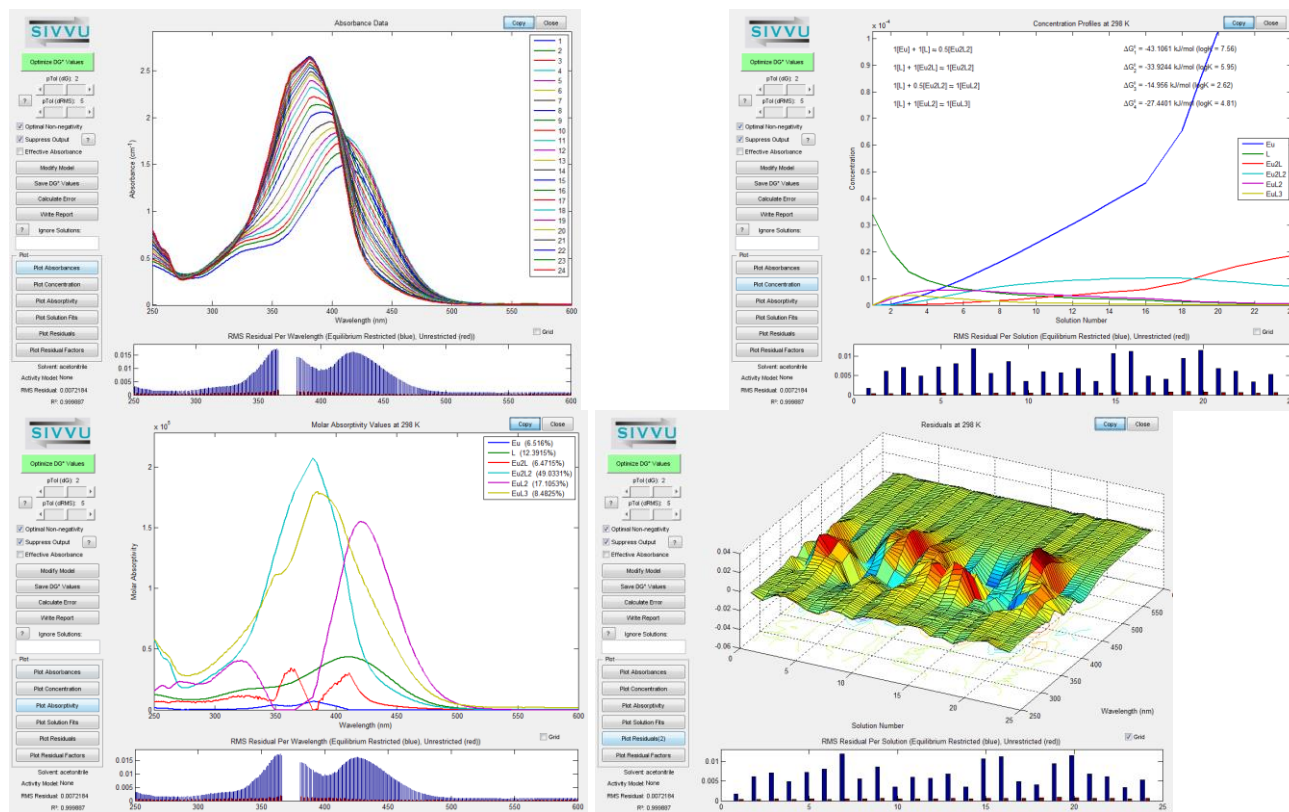
Restricted Data Reconstruction (5 chemical factors): 98.8921%

Unrestricted Data Reconstruction (5 mathematical factors): 99.3284%

Remaining Error Imbedded in Absorbance Values: 0.0046161

R²: 99.9845%

Table S6. Titration of Ligand **3** with Eu(OTf)₃ (titration *f* in Figure 3)



Optimization Summary:

Data at 298 K

Non-negativity was enforced with optimization (not truncation).

Activity Coefficients Model: None.

Species with Fixed Molar Absorptivity Curves: None.

Solutions ignored: None.

Optimized Values (kJ/mol): $\Delta G^{\circ}_1 = -43.1(1)$; $\Delta G^{\circ}_2 = -33.9(1)$; $\Delta G^{\circ}_3 = -15.0(2)$; $\Delta G^{\circ}_4 = -27.4(2).9$;

Equilibrium Restricted RMS Residual (6 chemical factors): 0.0072184

Unrestricted RMS Residual (6 mathematical factors): 0.00055748

Restricted Data Reconstruction (6 chemical factors): 99.847%

Unrestricted Data Reconstruction (6 mathematical factors): 99.7912%

Remaining Error Imbedded in Absorbance Values: 0.0041675

R²: 99.9887%