## Supporting information for:

# Tandem Driven Dynamic Combinatorial Resolution via Henry – Iminolactone Rearrangement

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### **General methods**

All commercially available starting materials and solvents were of reagent grade and used as received. <sup>1</sup>H and <sup>13</sup>C spectra were recorded with a Bruker Avance 400 instrument or a Bruker DMX 500 instrument at 298K in CD<sub>3</sub>CN or DMSO, using the residual signals: <sup>1</sup>H:  $\delta = 1.94$  ppm; <sup>13</sup>C:  $\delta = 1.32$  ppm and <sup>1</sup>H:  $\delta = 2.50$  ppm; <sup>13</sup>C:  $\delta = 39.52$  ppm respectively. <sup>1</sup>H peak assignments were made by first order analysis of the spectra, supported by standard <sup>1</sup>H-<sup>1</sup>H correlation spectroscopy (COSY). High resolution mass spectra (HRMS) were performed by Instrumentstationen, Kemicentrum, Lund Institute of Technology, Lund, Sweden.

### General procedure for library generation and resolution



The various aldehydes **1-5** (0.15 mmol each) were dissolved in an NMR tube using 750  $\mu$ L CD<sub>3</sub>CN. Subsequently, nitroethane (0.15 mmol) and triethylamine (0.45 mmol) were added and the mixture was left at room temperature. The reaction was followed by <sup>1</sup>H-NMR analysis.

#### Analytical data for compound 12



<sup>1</sup>H NMR (500 MHz, DMSO) δ 1.16 (d, J = 6.94 Hz), 1.56 (d, J = 6.94 Hz), 5.11 (d, J = 2.84 Hz,), 5.29-5.38 (m), 7.50-7.57 (m), 7.62-7.67 (m), 7.70 (d, J = 7.57) 8.86 (s), 9.02 (s); <sup>13</sup>C NMR (125 MHz, DMSO) δ 11.9, 15.2, 57.5, 58.4, 83.0, 83.4, 122.9, 123.1, 123.4, 123.8, 128.8, 129.0, 131.8, 132.1, 132.4, 142.9, 143.0, 169.4, 169.8; HRMS (CI) calcd for  $[C_{10}H_{11}N_2O_3]^+$ : 207.0770, found: 207.0763

### Kinetic analysis of tandem reaction

Kinetic analysis of the tandem reaction with aldehyde **1** was performed using timedependent <sup>1</sup>H-NMR-studies. Each starting material (0.2 mmol) and triethylamine (0.1 mmol) were dissolved in CD<sub>3</sub>CN (600  $\mu$ L), and the reaction followed until completion. The chemical kinetics software package Copasi 4.2 was adopted for fitting the resulting NMR-data to the kinetic model,<sup>1</sup> using the Levenberg-Marquardt method at a tolerance of 1 x 10<sup>-6</sup> for parameter fitting. Estimated kinetic parameters:  $k_1$ : 7.2 x 10<sup>-2</sup> M<sup>-1</sup> min<sup>-1</sup> (SD: 1.4 x 10<sup>-3</sup> M<sup>-1</sup> min<sup>-1</sup>),  $k_{-1}$ : 5.6 x 10<sup>-3</sup> min<sup>-1</sup> (SD: 3.3 x 10<sup>-4</sup> min<sup>-1</sup>),  $k_2$ : 1.4 x 10<sup>-2</sup> min<sup>-1</sup> (SD: 1.2 x 10<sup>-4</sup> min<sup>-1</sup>), where  $k_1$  and  $k_{-1}$  are the rate constants of the forward and reverse Henry reaction, respectively, and  $k_2$  is the rate constant for the consecutive cyclization step.

<sup>&</sup>lt;sup>1</sup> S. Hoops, S. Sahle, R. Gauges, C. Lee, J. Pahle, N. Simus, M. Singhal, L. Xu, P. Mendes and U. Kummer, *Bioinformatics* 2006, **22**, 3067-3074.