Supporting Information for:

Amine dehydrogenases: Efficient biocatalysts for the stereoselective reductive amination of carbonyl compounds

Tanja Knaus,[‡] Wesley Böhmer,[‡] Francesco G. Mutti*

Van 't Hoff Institute for Molecular Sciences, University of Amsterdam, Science Park 904, 1098 XH Amsterdam, Netherlands.

[‡] These authors contributed equally to this work

* Corresponding author: <u>f.mutti@uva.nl</u>

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1. Abbreviations

AmDH	amine dehydrogenase (variant)
Bb-PhAmDH	amine dehydrogenase variant originated from the phenylalanine dehydrogenase from <i>Bacillus badius</i> .
Rs-PhAmDH	amine dehydrogenase variant originated from the phenylalanine dehydrogenase from <i>Rhodoccoccus species</i> .
Ch1-AmDH	chimeric amine dehydrogenase generated through domain shuffling of Bb-PhAmDH variant and L-AmDH variant, the latter originated from the leucine dehydrogenase from <i>Bacillus stearothermophilus</i> .
Cb-FDH	formate dehydrogenase (variant) from Candida boidinii
GDH	glucose dehydrogenase from Bacillus subtilis
ее	enantiomeric excess
ω-TA	ω-transaminase
DCM	dichloromethane
n.a.	not applicable
n.d.	not determined
n.m.	not measureable

2. List of substrates



Figure S1. List of substrates used in this study.

3. General Information

Ketones **1a**, **3a**, **6a**, **8a-11a**, **14a-17a**, **19a-24a**, aldehydes **13a** and **25a** were purchased from Sigma-Aldrich (Steinheim, Germany). Ketone **5a** and aldehyde **7a** were purchased from Alfa Aesar (Shore Road, Heysham, UK). Ketones **2a**, **4a**, **12a**, **18a** were purchased from Acros Organics (Geel, Belgium).

Amines (*R*)-**9b**, *rac*-**16b**, (*S*)-**16b**, *rac*-**10b**, **7b** and **13b** were purchased from Sigma-Aldrich (Steinheim, Germany). Enantiopure (*S*) and (*R*)-configured amines **1b**-**6b**, **8b**, **11b**, **14b**-**24b** and terminal amine **25b** were synthesized by stereoselective amination using established enzymatic methods as reported in literature (employing commercially available stereocomplementary ω -transaminases ATA-113, ATA-117 from Codexis, Redwood City, California, US).[1]

Alcohols **8c**, **10c-12c** were purchased from Sigma-Aldrich (Steinheim, Germany) and alcohol **9c** was purchased from Acros Organics (Geel, Belgium).

Nicotinamide cofactor (NAD⁺) was purchased from Melford Biolaboratories (Chelsworth, Ipswich, UK).

Lysozyme from chicken egg white (3.2 mg, Sigma L6876, lyophilized powder, protein 95%, >40000 U/mg protein) was purchased from Sigma-Aldrich (Steinheim, Germany). Ni²⁺ affinity columns (HisTrap FF, 5 mL) were purchased from GE Healthcare Bio-Sciences (Munich, Germany).

4. Expression and purification of recombinant proteins in E. coli host cells

The amine dehydrogenases Bb-PhAmDH and Ch1-AmDH were expressed and purified as described previously.[2]

For recombinant expression of the N-term His6-tagged proteins Rs-PhAmDH and Cb-FDH, 800 mL of LB medium supplemented with the appropriate antibiotic (50 µg/mL kanamycin) were inoculated with 15 mL of an overnight culture of E. coli BL21 DE3 cells harbouring the pET28b plasmid with the genes for the expression of the proteins. Cells were grown at 37 °C until an OD_{600} of 0.6 – 0.9 was reached and expression of protein was induced by the addition of IPTG (0.5 mM final concentration). Protein expression was carried out overnight at 20 °C and after harvesting of the cells (4 °C, 4.5 x 10³ rpm, 15 min), the remaining cell pellet was frozen or directly resuspended in Lysis buffer (50 mM KH₂PO₄, 300 mM NaCl, 10 mM imidazole, pH 8.0) containing lysozyme 1 mg mL⁻¹) and incubated at 4 °C for 35 minutes prior to cell disruption by ultrasonication. After centrifugation (4 $^{\circ}$ C, 14 x 10³ rpm, 1 h) the supernatant was filtered through a 0.45 μm filter and protein purification was performed by Ni-NTA affinity chromatography using pre-packed Ni-NTA HisTrap FF columns (GE Healthcare) according to the manufacturer's instructions. After loading of the filtered lysate, the column was washed with sufficient amounts of washing buffer (50 mM KH₂PO₄, 300 mM NaCl, 25 mM imidazole, pH 8.0), and bound protein was recovered with elution buffer (50 mM KH₂PO₄, 300 mM NaCl, 200 mM imidazole, pH 8.0). The process of purification was analysed by SDS-PAGE and fractions containing sufficient purified protein were pooled and dialyzed over night against potassium phosphate buffer (50 mM, pH 8,). Protein solutions were concentrated and the their concentrations determined spectrophotometrically using an extinction coefficient at 280 nm of 26.6 x 10³ M⁻¹ cm⁻¹ for Rs-PhAmDH and 51.4 x 10³ M⁻¹ cm⁻¹ for Cb-FDH. A protein yield of 40 mg Rs-PhAmDH/L cell culture and 100 mg Cb-FDH/L cell culture was obtained.



Figure S2. SDS-PAGE of purified proteins. Lane 1: PageRuler[™] Unstained Protein Ladder (ThermoFisher Scientific), Iane 2: Cb-FDH, Iane 3: Rs-PhAmDH.

5. Biocatalytic transformations

5.1. <u>Study of the stability of nicotinamide coenzyme at different pH values</u>

The stability of NADH was studied under the following conditions:

- (1) Potassium phosphate buffer (pH 6.5, 50 mM)
- (2) Hepes buffer (pH 8.8, 50 mM)
- (3) Sodium carbonate buffer (pH 10, 50 mM)
- (4) Sodium hydroxide (0.1 N, pH 13)

The decomposition of NADH vs. time was monitored spectrophotometrically at a wavelength of 325 nm.



Figure S3. Stability of NADH at different pH values vs. time; x-axis: time in logarithmic scale; y-axis: absorbance of NADH at 325 nm.

5.2. <u>Reductive amination of 1a by Bb-PhAmDH</u>, **10a** by Rs-PhAmDH and **24a** by Ch1-AmDH in different buffer systems using GDH for NAD⁺/NADH regeneration

In this experiment two buffer systems were used, *i.e.* ammonium chloride buffer (final concentration 1 M, pH 8.7) and ammonium formate buffer (final concentration 1.005 M, pH 8.5).

 NH_4Cl/NH_4OH buffer was prepared by dissolving NH_4Cl (2.85 g, 53 mmol) in water (45 mL). NH_4OH (1.238 mL, 6.4 M) was added and the pH was adjusted with 1 M HCl.

 $HCOONH_4/NH_4OH$ buffer was prepared by dissolving $HCOONH_4$ (3.16 g, 50.1 mmol) in water (45 mL). NH_4OH (0.458 mL, 6.4 M) was added and the pH was adjusted with 1 M formic acid.

Two different stock solutions were prepared containing glucose (60 mM) and GDH (150 U per sample):

Stock solution 1

NAD⁺ (3.5 mg, 0.005 mmol, final concentration 1 mM) was dissolved in NH₄Cl/NH₄OH buffer (4.84 mL). Glucose (37.6 mg, 0.209 mmol) and GDH (300 U mL⁻¹) were dissolved in ammonium chloride buffer (3.27 mL) containing the NAD⁺.

Stock solution 2

NAD⁺ (6.7 mg, 0.01 mmol, final concentration 1 mM) was dissolved in HCOONH₄/NH₄OH buffer (9.24 mL). Glucose (36.9 mg, 0.205 mmol) and GDH (300 U mL⁻¹) were dissolved in ammonium formate buffer (3.21 mL) containing 1 mM NAD⁺.

Biocatalytic reactions

Reaction samples were prepared by combining one of the stock solution above (470 μ L), the substrate (20 mM), and the AmDH (*i.e.* Bb-PhAmDH (115 μ M), Rs-PhAmDH (121 μ M) or Ch1-AmDH (82.1 μ M)). The reactions were run at 30 °C in an incubator for 21 hours (190 rpm). Work-up was performed by the addition of KOH (100 μ L, 10 M), followed by the extraction with dichloromethane (1x600 μ L). After centrifugation, the organic layer was dried with MgSO₄. Conversion and enantiomeric excess were determined as reported in the experimental section of the main manuscript. Analytical methods as well as retention times are reported in paragraph 7.

5.3. <u>Reductive amination of 1a by Bb-PhAmDH</u>, **10a** by Rs-PhAmDH and **24a** by Ch1-AmDH using formate <u>dehydrogenase Cb-FDH as NAD⁺/NADH cofactor recycling enzyme</u>

 $HCOONH_4/NH_4OH$ buffer (1.005 M, pH 8.5) was prepared as explained in paragraph 5.2 containing NAD⁺ (final concentration 1 mM).

Biocatalytic transformations were prepared by combining the buffer/NAD⁺ solution (470 μ L), the Cb-FDH (14 μ L), the substrate (20 mM), and the AmDH (*i.e.* Bb-PhAmDH (115 μ M), Rs-PhAmDH (121 μ M) or Ch1-AmDH (82.1 μ M)). The reactions were run at 30 °C in an incubator for 21 hours (190 rpm). Work-up was performed by the addition of KOH (100 μ L, 10 M), followed by the extraction with dichloromethane (1x600 μ L). After centrifugation, the organic layer was dried with MgSO₄. Conversion and enantiomeric excess were determined as reported in the experimental section of the main manuscript. Analytical methods as well as retention times are reported in paragraph 7 and the results are summarized in Table 1 in the main paper.

5.4. <u>Reductive amination of 1a by Bb-PhAmDH</u>, **10a** by Rs-PhAmDH and **24a** by Ch1-AmDH at varying substrate concentrations using Cb-FDH as cofactor recycling enzyme

Biocatalytic transformations were run under the same reaction conditions as described in 5.3. Substrate concentrations were varied from 30 mM, 40 mM, to 50 mM per sample. The results are reported in Table S1.

<u>Reaction conditions</u>: final volume = 0.5 mL; [NAD⁺] = 1 mM; [substrate] = 30-50 mM; [AmDH] = 80-120 μ M; [Cb-FDH] = 14 μ M; incubation at 190 rpm and 30 °C for 21 h.

Table S1. Reductive amination of **1a**, **10a**, and **24a** by Bb-PhAmDH, Rs-PhAmDH and Ch1-AmDH, respectively, using Cb-FDH for coenzyme recycling in ammonium formate buffer (1.005 M, pH 8.5) at varying substrate concentrations.

entry	enzyme	substrate	substrate [mM]	enzyme [µM]	conversion [%] *	ee%
1	Bb-PhAmDH	1a	30 mM	115	96	>99
2	Bb-PhAmDH	1a	40 mM	115	91	>99
3	Bb-PhAmDH	1a	50 mM	115	88	>99
4	Rs-PhAmDH	24a	30 mM	130	>99	>99
5	Rs-PhAmDH	24a	40 mM	130	>99	>99
6	Rs-PhAmDH	24a	50 mM	130	>99	>99
7	Ch1-AmDH	10a	30 mM	80	>99	>99
8	Ch1-AmDH	10a	40 mM	80	>99	>99
9	Ch1-AmDH	10a	50 mM	80	>99	>99

* Conversion depicted here is the average value obtained from two independent experiments.

5.5. <u>Reductive amination of **10a** by Rs-PhAmDH and **24a** by Ch1-AmDH at varying enzyme concentrations <u>and Cb-FDH as cofactor recycling enzyme</u></u>

Biocatalytic transformations were run under the same reaction conditions as described in 5.4. Enzyme concentrations were varied from 33-115 μ M per sample. The results are reported in Table S2.

entry	enzyme	substrate	enzyme [µM]	conversion [%] *	ee%
1	Rs-PhAmDH	24a	121	>99	>99%
2	Rs-PhAmDH	24a	96	>99	>99%
3	Rs-PhAmDH	24a	73	>99	>99%
4	Rs-PhAmDH	24a	50	>99	>99%
5	Ch1-AmDH	10a	82	99	>99%
6	Ch1-AmDH	10a	66	99	>99%
7	Ch1-AmDH	10a	49	98	>99%
8	Ch1-AmDH	10a	32	95	>99%

Table S2. Reductive amination of **10a**, and **24a** by Rs-PhAmDH and Ch1-AmDH at varying enzyme concentrations using Cb-FDH for coenzyme recycling in ammonium formate buffer (1.005 M, pH 8.5).

* Conversion depicted here is the average value obtained from two independent experiments.

5.6. Time study for the reductive amination of **1a** by Bb-PhAmDH at different temperatures

The reactions were prepared as previously described with a substrate concentration of 50 mM and an enzyme concentration of 46 μ M. The progress of the reaction was monitored at different temperatures (from 30 to 60 °C) vs. time (1h, 2h, 3h, 5h, 8h, 16h, 21h, 24h, etc.). Every biocatalytic transformation was performed in duplicate and the results were averaged. At 60 °C no measurable conversion could be observed. Conversion and enantiomeric excess were determined as described in paragraph 7 and the results are summarized in Table S3.

<u>Reaction conditions</u>: final volume = 0.5 mL; ammonium formate buffer (1.005 M, pH 8.7); [NAD⁺] = 1 mM; [substrate] = 50 mM; [Bb-PhAmDH] = 46 μ M; [Cb-FDH] = 14 μ M; incubation at 190 rpm.

entry	substrate	time [h]	20 °C	30 °C	40 °C	50 °C
1	1a	1	3	6	8.4	7
2	1a	2	5	10	19	10
3	1a	3	7	14	29	12
4	1a	5	9	21	43	14
5	1a	8	10	25	46	12
6	1a	16	25	52	72	n.d.
7	1a	18	n.d.	n.d.	n.d.	19
8	1a	21	37		84	n.d.
9	1a	24	37	63	83	21
10	1a	end	79	94	87	n.d.

Table S3. Conversions [%] for the reductive amination of 1a by Bb-PhAmDH at different temperatures vs. time.

Conversion depicted here is the average value obtained from two independent experiments.

The reactions were prepared as described in paragraph 5.4 using a substrate concentration of 50 mM and an enzyme concentration of 48 μ M. The progress of the reaction was monitored at different temperatures (from 30 to 70 °C) vs. time (1h, 2h, 3h, 5h, 8h, 16h, 21h, 24h, etc.). Every biocatalytic transformation was performed in duplicate and the results were averaged. At 70 °C no measurable conversion could be observed. Conversion and enantiomeric excess were determined as described in paragraph 7 and the results are summarized in Table S4.

<u>Reaction conditions</u>: final volume = 0.5 mL; ammonium formate buffer (1.005 M, pH 8.5); [NAD⁺] = 1 mM; [substrate] = 50 mM; [Rs-PhAmDH] = 48 μ M; [Cb-FDH] = 14 μ M; incubation at 190 rpm.

entry	substrate	time [h]	20 °C	30 °C	40 °C	50 °C	60 °C
1	24a	1	83	80	83	83	73
3	24a	2	91	94	93	92	80
5	24a	3	98	99	94	95	83
7	24a	5	>99	>99	>99	96	83
9	24a	8	>99	>99	>99	96	86
11	24a	16	>99	>99	>99	n.d.	n.d.
13	24a	18	n.d.	n.d.	n.d.	96	76
14	24a	21	>99	>99	>99	n.d.	n.d.
16	24a	24	>99	>99	>99	98	92
18	24a	30	n.d.	n.d.	n.d.	98	93
19	24a	end	>99	>99	>99	n.d.	n.d.

Table S4. Conversions [%] for the reductive amination of 24a by Rs-PhAmDH at different temperatures vs. time.

Conversion depicted here is the average value obtained from two independent experiments.

5.8. Time study for the reductive amination of 10a by Ch1-AmDH at different temperatures

The reactions were prepared as previously described with a substrate concentration of 50 mM substrate and an enzyme concentration of 33 μ M. The conversion was monitored at different temperatures (from 30 to 60 °C) vs. time (1h, 2h, 3h, 5h, 8h, 16h, 21h, 24h, etc.). Every biocatalytic transformation was performed in duplicate and the results were averaged. A preliminary time study at 70 °C provided mediocre conversions and therefore this temperature was not thoroughly analysed (data at 18 h and 48 h are available). Conversion and enantiomeric excess were determined as described in paragraph 7 and the results are summarized in Table S5.

<u>Reaction conditions</u>: final volume = 0.5 mL; ammonium formate buffer (1.005 M, pH 8.5); [NAD⁺] = 1 mM; [substrate] = 50 mM; [Ch1-AmDH] = 33 μ M; [Cb-FDH] = 14 μ M; incubation at 190 rpm.

entry	substrate	time [h]	20 °C	30 °C	40 °C	50 °C	60 °C	70 °C
1	10a	1	23	38	58	58	61	n.d.
2	10a	2	38	61	80	73	74	n.d.
3	10a	3	56	78	90	79	82	n.d.
4	10a	5	69	90	94	93	82	n.d.
5	10a	8	80	94	97	90	84	n.d.
6	10a	16	86	98	98	n.d.	n.d.	n.d.
7	10a	18	n.d.	n.d.	n.d.	96	92	8
8	10a	21	98	98	99	n.d.	n.d.	n.d.
9	10a	24	98	97	>99	n.d.	93	n.d.
10	10a	30	n.d.	n.d.	n.d.	98	97	n.d.
11	10a	end	>99	>99	>99	>99	>99	<10

 Table S5. Conversions [%] for the reductive amination of 10a by Ch1-AmDH at different temperatures over time.

Conversion depicted here is the average value obtained from two independent experiments.

5.9. <u>Reductive amination of a library of ketones and aldehydes by Bb-PhAmDH, Rs-PhAmDH and Ch1-</u> <u>AmDH</u>

The reactions were prepared and performed following the optimal reaction conditions as described in the experimental section of the main manuscript. The main results are reported in the manuscript: tables 2-5. Substrates that were tested and found not to be accepted or only accepted poorly are reported in Table S6.

Table S6. Attempts of reductive amination on substrates that were not converted or converted at a very moderate extent using Bb-PhAmDH, Rs-PhAmDH, and Ch1-AmDH.

substrate	enzyme	enzyme [µM]	time [h]	conversion [%]	ee% (R)
	Ch1-AmDH	32.2	24	8	n.d.
2-butanone	Rs-PhAmDH	51.4	24	4	n.d.
	Ch1-AmDH	32.2	24	n.m.	n.a.
butanal	Rs-PhAmDH	51.4	24	n.m.	n.a.
O H	Ch1-AmDH	32.2	24	n.m.	n.a.
Senzaldehyde	Rs-PhAmDH	51.4	24	n.m.	n.a.
 0 !!	Ch1-AmDH	32.2	24	n.m.	n.d.
		32.2	48	n.m.	n.d.
Me	Rs-PhAmDH	51.4	24	n.m.	n.d.
o-methylacetophenone		51.4	48	n.m.	n.d.
0 	Ch1-AmDH	32.2	24	n.m.	n.d.
		32.2	48	n.m.	n.d.
но	Rs-PhAmDH	51.4	24	n.m.	n.d.
hydroxyacetophenone		51.4	48	n.m.	n.m.
	Ch1-AmDH	91.8	48	8	n.d.
propiophenone	Rs-PhAmDH	102.6	48	n.m.	n.d.
	Ch1-AmDH	91.8	48	2	n.d.
valerophenone (butyl phenyl ketone)	Rs-PhAmDH	102.6	48	2	n.d.
	Ch1-AmDH	91.8	48	n.m.	n.d.
Left butyrophenone	Rs-PhAmDH	102.6	48	1	n.d.

5.10.<u>Additional data set for substrates that are moderately converted or not converted by some of the</u> <u>amine dehydrogenases from this study</u>

Table S7. Reductive amination of phenyl-propanone derivatives with Bb-PhAmDH. Reaction conditions: final volume = 0.5 mL; ammonium formate buffer (1.005 M, pH 8.5); [NAD⁺] = 1 mM; [substrate] = 50 mM; [Cb-FDH] = 14 μ M; incubation at 190 rpm, 30 °C.

entry	substrate	enzyme [µM]	time [h]	conversion substrate [%]	ee% (R)
1	2 a	51	48	10	>99
2	3a	51	48	21	>99
3	4a	51	48	3	n.d.
4	5a	51	48	7	>99
5	6a	51	48	no conv.	-
6	21a	51	48	8	>99

n.d. = not determined due to too low conversion

Table S8. Additional data for the reductive amination of substrates with Ch1-AmDH. Reaction conditions: final volume = 0.5 mL; ammonium formate buffer (1.005 M, pH 8.5); [NAD⁺] = 1 mM; [substrate] = 50 mM; [Cb-FDH] = 14 μ M; incubation at 190 rpm, 30 °C.

entry	substrate	enzyme [µM]	time[h]	conversion substrate[%]	ee% (R)
1	18 a	32	48	2	n.d.
2	21a	32	24	14	>99
3	22a	92	48	4	>99
4	23a	92	48	1	n.d.
6	25a	92	48	70	n.a.

n.d. = not determined due to too low conversion

n.a. = not applicable

6. NMR spectra (recorded on a Brucker AMX 400 (400 Mhz, ¹H) in CDCl₃)

Figure S4. 1H-NMR of the preparative synthesis of (R)-4j by Rs-PhAmDH (CDCl3, 400 Mhz).



<u>DB1701-30m-B</u>: constant pressure 13.5 psi, T injector 300 °C, split ratio 40:1, T initial 60 °C, hold 6.5 min; gradient 20 °C/min up to 100 °C, hold 1 min, gradient 20 °C/min up to 280 °C, hold 1 min.

<u>DB1701-60m</u>: constant pressure 13.5 psi, T injector 300 °C, split ratio 40:1, T initial 80 °C, hold 6.5 min, gradient 5 °C/min up to 160 °C, hold 2 min; gradient 20 °C/min up to 280 °C, hold 1 min.

<u>DEX-CB-A:</u> constant flow 1.4 mL/min, T injector 250 °C, split ratio 40:1, T initial 100 °C, hold 2 min; gradient 1 °C/min up to130 °C, hold 5 min; gradient 10 °C/min up to 170 °C, hold 10 min.; gradient 10 °C/min up to 180 °C, hold 1 min.

<u>DEX-CB-B:</u> constant flow 1.4 ml/min, T injector 250 °C, split ratio 40:1, T initial 100 °C, hold 2 min; gradient1 °C/min up to 118 °C, hold 5 min; gradient 10 °C/min up to 170 °C hold 10 min, gradient 10 °C/min up to 180 °C, hold 1 min.

7.2. <u>Retention times</u>

Table S9. GC retention times for measuring the conversion of substrates 1-25a and 1-25b.

number	retention time [min]	number	retention time [min]	number	retention time [min]	GC method
1a	21.8			1c	21.9	DB1701-60m
2a	27.7	2b	26.5			DB1701-60m
3a	28.4	3b	27.6			DB1701-60m
4a	28.7	4b	27.8			DB1701-60m
5a	24.4	5b	22.5			DB1701-60m
6a	22.3	6b	20.1			DB1701-60m
7a	17.7	7b	18.6			DB1701-60m
8a	3.0	8b	2.6			DB1701-30m-B
9a	4.7	9b	3.7			DB1701-30m-B
10a	4.8	10b	3.9	10c	5.0	DB1701-30m-A
11a	7.7	11b	6.0	11c	8.1	DB1701-30m-A
12a	3.7	12b	3.1			DB1701-30m-B
13a	2.6	13b	2.8	13c	3.9	DB1701-30m-B
14a	13.3	14b	11.7	14c	13.0	DB1701-30m-A
15a	22.0	15b	19.7			DB1701-60m
16a	10.7	16b	9.3	16c	11.0	DB1701-30m-A
17a	10.6	17b	9.8	17c	11.7	DB1701-30m-A
18a	14.3	18b	14.0	18c	15.4	DB1701-30m-A
19a	10.4	19b	10.0	19c	11.9	DB1701-30m-A
20a	4.6	20b	3.8			DB1701-60m
21 a	24.1	21b	22.6			DB1701-60m
22a	15.6	22b	15.0			DB1701-60m
23a	16.2	23b	15.5			DB1701-60m
24a	24.9	24b	23.3	24c	25.3	DB1701-60m
25a	13.0	25b	14.6	25c	14.6	DB1701-60m

number	retention time [min]	number	retention time [min]	GC method
(S)- 1b	30.8	(R)- 1b	31.3	DEX-CB-A
(S)- 2b	30.9	(<i>R</i>)- 2b	32.0	DEX-CB-A
(S)- 3b	36.1	(<i>R</i>)- 3b	36.4	DEX-CB-A
(S)- 4b	37.4	(R)- 4b	37.7	DEX-CB-A
(S)- 5b	32.2	(<i>R</i>)- 5b	32.3	DEX-CB-A
(S)- 6b	30.4	(R)- 6b	30.7	DEX-CB-A
(S)- 8b	13.1	(R)- 8b	14.1	DEX-CB-B
(S)- 9b	14.4	(R)- 9b	15.6	DEX-CB-B
(S)- 10b	16.3	(R)- 10b	17.7	DEX-CB-A
(S)- 11b	23.9	(R)- 11b	25.2	DEX-CB-A
(S)- 12b	14.4	(R)- 12b	14.7	DEX-CB-B
(S)- 14b	39.5	(R)- 14b	40.0	DEX-CB-A
(S)- 15b	30.6	(R)- 15b	30.9	DEX-CB-A
(S)- 16b	32.8	(R)- 16b	34.5	DEX-CB-A
(S)- 18b	43.0	(R)- 18b	44.4	DEX-CB-A
(S)- 19b	34.1	(R)- 19b	36.2	DEX-CB-A
(S)- 20b	13.7	(R)- 20b	14.9	DEX-CB-A
(S)- 21b	31.5	(R)- 21b	31.6	DEX-CB-A
(S)- 22b	42.0	(R)- 22b	42.1	DEX-CB-A
(S)- 23b	44.1	(R)- 23b	44.3	DEX-CB-A
(S)- 24b	43.1	(R)- 24b	43.5	DEX-CB-A

 Table S10. GC retention times for measuring the enantiomeric excess of substrates 1-24b.

7.3. GC chromatograms

Reference compounds 1a and 1c



Reductive amination of 1a



Enantiomeric excess of 1b



Reference compounds 2a and 2b



Reductive amination of 2a



Enantiomeric excess of 2b



Reference compounds 3a and 3b



Reductive amination of 3a



Enantiomeric excess of 3b



Reference compounds 4a and 4b



Reductive amination of 4a



Enantiomeric excess of 4b



Reference compounds 5a and 5b



Reductive amination of 5a



Enantiomeric excess of 5b



Reference compounds 6a and 6b



Reductive amination of 6a



Enantiomeric excess of 6b



Reference compounds 7a and 7b



Reductive amination of 7a



Reference compounds 8a and 8b



Reductive amination of 8a



Enantiomeric excess of 8b



Reference compounds 9a and 9b



Reductive amination of 9a



Enantiomeric excess of 9b



Reference compounds 10a, 10b and 10c



Reductive amination of 10a



Enantiomeric excess of 10b

(the order of the elution of (S)-10b and (R)-10b with Chromopack Chiracel Dex-CB capillary column is known from literature [1,2]).



Reference compounds 11a, 11b and 11c



Reductive amination of 11a



Enantiomeric excess of 11b



Reference compounds 12a, 12b and 12c



Reductive amination of 12a



Enantiomeric excess of 12b



Reference compounds 13a, 13b



Reductive amination of 13a



Reference compounds 14a, 14b and 14c



Reductive amination of 14a



Enantiomeric excess of 14b

FID1 A, Front Signal (Wesley/160309_Deta1\160115_WB_WB019821822(ee)_2\Am7S.D)	N			
Reference compound	(S)- 14b			
0	40	42	· · · ·	44 m
FID1 A. Front Signal (Wesley/160309_Data1/160115_WB_WB019&21&22(ee)_2/Am7R.D)				
Reference compound	(R)-14	lb		
0-bm, , , , , , , , , , , , , , , , , , ,	39 40	41 42	43	44 m
FID1 A, Front Signal (Wesley/160309_Data1/160115_W8_W8019&21&22(ee)_2/Ch7CD)				
Reaction sample	(R)-14	ŀb		
36 37 38	39 40	41 42	43	44 mi
•				

Reference compounds 15a, 15b



Reductive amination of 15a



Enantiomeric excess of 15b



Reference compounds 16a, 16b and 16c



Reductive amination of 16a



Enantiomeric excess of 16b



Reference compounds 17a, 17b and 17c



Reductive amination of 17a



Reference compounds 18a, 18b and 18c



Reductive amination of 18a



Enantiomeric excess of 18b



Reference compounds 19a, 19b and 19c



Reductive amination of 19a



Enantiomeric excess of 19b



Reference compounds 20a, 20b



Reductive amination of 20a



Enantiomeric excess of 20b



Reference compounds 21a, 21b



Reductive amination of 21a



Enantiomeric excess of 21b



Reference compounds 22a, 22b



Reductive amination of 22a



Enantiomeric excess of 22b



Reference compounds 23a, 23b



Reductive amination of 23a



Enantiomeric excess of 23b



Reference compounds 24a, 24b and 24c



Reductive amination of 24a



Enantiomeric excess of 24b



Reference compounds 25a, 25c

FID1 A, Front Signal (Wesley/16030	9_Data1\160114_WB_WB021&22\K30.D)		
pA	Ř.		
300 -	f ar-		
200	25a		
100 -			
0 -			
	12 13	14 15	18 min
EID1 & Emot Signal (Masket (6010	9 Delet1160114 WB WB021822/0420 D		
pA-	5_08811100114_VI5_VI002102210100.0j	ĩ	
300-		2	
200		25-	
200		250	
100-			
0-			· · · · · · · · · ·
	12 13	14 15	16 min
4			

Reductive amination of 25a

0 0 50	25a 25b	[™] 25c	Ch1-AmDH + 25 a
0 - FID1 A, Front Signal (Wesley\160309_Data 1\16	12 13 00114_WB_WB021622VRb0A.D	14 15	18
10 mm	4 25	b	Rs-PhAmDH + 25a

8. References

1. Koszelewski, D., et al., Asymmetric Synthesis of Optically Pure Pharmacologically Relevant Amines Employing ω-Transaminases. *Adv. Synth. Catal.*, **2008**, *350*, 2761-2766.

2. Mutti, F.G., et al., Conversion of alcohols to enantiopure amines through dual-enzyme hydrogenborrowing cascades. *Science*, **2015**, *349*, 1525-1529.