

Imine-based Chiroptical Sensing for Analysis of Chiral Amines: From Method Design to Synthetic Application

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Supporting Information

Materials and Methods

All reagents and solvents were purchased from commercial sources and used as received. The aldehyde sensor **HCA** was obtained from Matrix Scientific. All amines and ketone starting materials were purchased from either Sigma Aldrich, Alfa Aesar, or Acros Organics. Enzymes were purchased from Codexis, and PLP cofactor was obtained from Sigma Aldrich. Acetonitrile from Fisher Scientific was sparged with N₂ gas for at least 30 minutes prior to use. Circular dichroism measurements were performed at 25°C on a Jasco J-810 spectropolarimeter, using a Starna 0.1 cm jacketed cell. HPLC-CD measurements were acquired on an Agilent 1100 HPLC instrument, equipped with a Jasco CD 1595 HPLC-CD detector.

Experimental

a) Stock Solutions

The host stock solution was made by dissolving **HCA** (123.11 mg, 0.1 mmol) to 100 mL in acetonitrile. Stock solutions of the guest were made by dissolving the guest [(*R*)-**MBA** (6.44 µL, 0.05 mmol), (*S*)-**MBA** (6.44 µL, 0.05 mmol), (*R*)-**CEA** (7.36

μL , 0.05 mmol), (*S*)-**CEA** (7.36 μL , 0.05 mmol), (*R*)-**CMA** (7.08 μL , 0.05 mmol), (*S*)-**CMA** (7.08 μL , 0.05 mmol), (*R*)-**PPA** (7.20 μL , 0.05 mmol), (*S*)-**PPA** (7.20 μL , 0.05 mmol), (*R*)-**AMH** (7.52 μL , 0.05 mmol), (*S*)-**AMH** (7.52 μL , 0.05 mmol), (*R*)-**MPP** (8.04 μL , 0.05 mmol), (*S*)-**MPP** (8.04 μL , 0.05 mmol), (*R*)-**2-AP** (3.98 μL , 0.05 mmol), (*S*)-**2-AP** (3.98 μL , 0.05 mmol), (*R*)-**2-PG** (6.86 mg, 0.05 mmol), (*S*)-**2-PG** (6.86 mg, 0.05 mmol), (*R*)- **β -MBA** (7.28 μL , 0.05 mmol), (*S*)- **β -MBA** (7.28 μL , 0.05 mmol), and (*S*)-**MPA** (4.46 mg, 0.05 mmol)] to 5 mL in acetonitrile. Each point of the binding and *ee* titration was a separate solution, containing **HCA** (2 mM) and indicated amount of guest (0-8 mM) diluted to 1 mL. The titrations were done this way because of the prohibitive nature of the small cuvette size and the inability to stir its contents.

b) *Samples tested using Iron(II) complex*

Every sample tested contained **HCA** (2 mM) and (*R*)-**MBA** (2 mM) in acetonitrile. To this complex the indicated additives were introduced with the amines. The IBA (isobutylamine), TEA (triethylamine), and Pd(OAc)₂ were at a concentration of 0.5 mM, while (*R*)-1,1-binaphthyl-2,2-diamine (BDA) was at 2.5 mM. The last sample contained 8.3% water by volume.

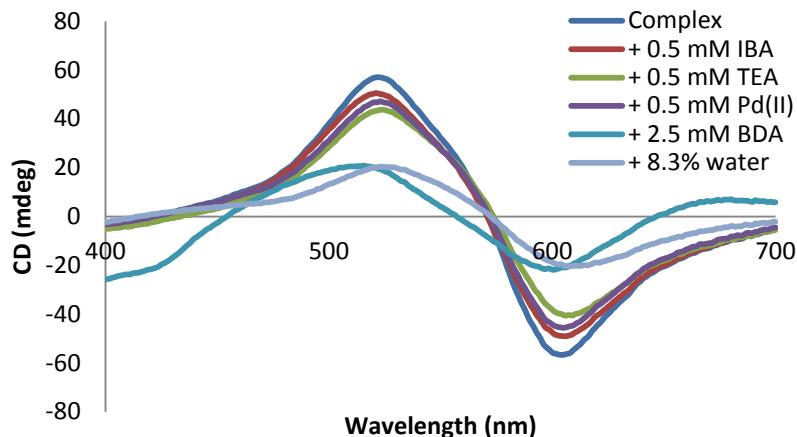


Figure S1. CD signals obtained for **HCA** (2 mM) and **(R)-MBA** (2 mM) with the indicated additive at the noted concentration. Samples were made in acetonitrile, with the CD signal recorded at 25°C.

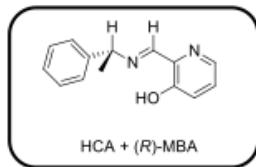
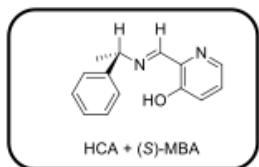
c) Computational method for CD Calculations

Quantum chemical calculations were performed using Gaussian09.¹ Structures of the parent isomer of all structures were used for calculations in addition to tautomers when possible and both cis/trans forms of the imine [all parent isomers modeled with absolute configuration of (*R*) and (*S*)]. Conformational space was exhaustively sampled using three conformer generators (rules based and random displacement) followed by molecular mechanics minimization using MMFF94. The representative conformer sets (140 initial conformers per molecule) were minimized with higher level calculations to provide Boltzmann distributions for each structure at 298.15 K. Density functional theory (DFT) with the B3LYP functional² and the 6-31G** basis set³⁻⁵ was used to identify the lowest energy conformers. All stationary points were confirmed with frequency calculations. To calculate ECD spectra, B3LYP geometries were used as input for M062X⁶ calculations using the 6-31++G**^{7,8} either *in vacuo* or in implicit solvent using Cramer and Truhlar's SMD continuum solvation methodology (solvent = acetonitrile).⁹

Only conformers which contributed more than 1.0% to the total *in vacuo* conformer distribution were sent for implicit solvation minimization or ECD. Time-dependent (TD-DFT) methodology¹⁰ was employed using the keywords: TD=full,singlet,NStates=20 and integral=ultrafinegrid. Spectra were displayed using SpecDis.^{11,12} We have used a $\sigma = 0.3$ eV for band broadening. Final weighting of the conformer specific ECD spectra was done using the Boltzmann percentages calculated using M062X/6-31+G** energies. At that level of theory (*in vacuo* or implicit acetonitrile), neither the cis-imines, nor tautomers contribute to an appreciable level, and for this reason will not be included in the analysis.

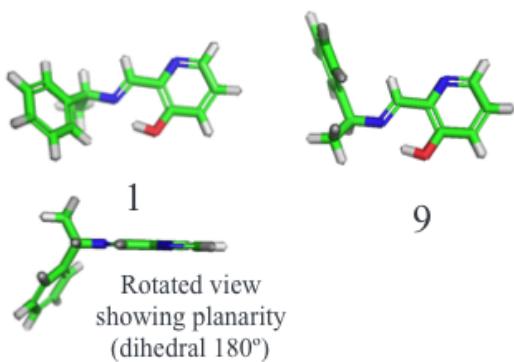
In vacuo and implicit acetonitrile Boltzmann Populations and 3D Conformations:

HCA + S- MBA



Rank	Conformer	Energy	Percent
1	1	0.00	96 (80) [94]
2	9	1.89 (0.83)	4 (20) [6]

Rank	Conformer	Energy	Percent
1	1	0.00	94.5
2	9	1.88	4

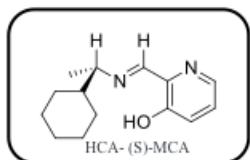


5

Key
B3LYP/6-31G**
(B3LYP/6-31+G**) in acetonitrile
[M062X/6-31+G**] in acetonitrile

Figure S2: Energies calculated at the M062X/6-31+G** level (*in vacuo* and acetonitrile) and reported in relative ΔG in kcal/mol.

HCA + S - CEA



Rank	Conformer	Energy	Percent
1	3	0.00	70 (55)[52]
2	1	0.71 (0.61)	21 (20)[40]
3	5	1.27 (0.51)	8 (23)[2]
4	29	3.10 (2.70)	0 (0) [6]

Key
B3LYP/6-31G**
(B3LYP/6-31+G**) in acetonitrile
[M062X/6-31+G**] in acetonitrile

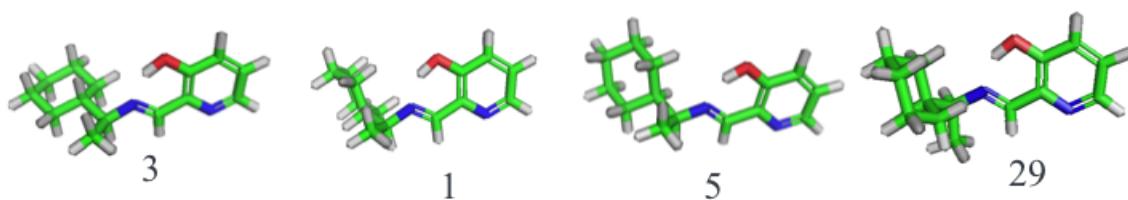
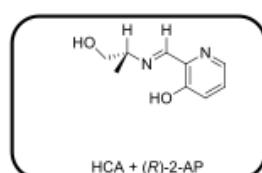
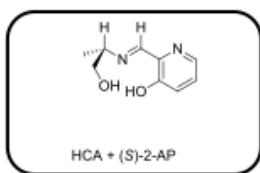


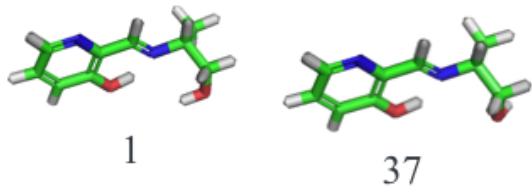
Figure S3: Energies calculated at the M062X/6-31+G** level (*in vacuo* and acetonitrile) and reported in relative ΔG in kcal/mol.

HCA + S-2-AP



Rank	Conformer	Energy	Percent
1	1	0.0	95 (80)[62]
2	37	1.73 (0.79)	5 (20)[38]

Rank	Conformer	Energy	Percent
1	1	0.0	96
2	37	1.84	4



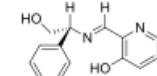
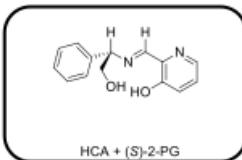
Key
 B3LYP/6-31G**
 (B3LYP/6-31+G**) in acetonitrile
 [M062X/6-31+G**] in acetonitrile

The conformational modeling for this imine is analogous to what was seen for the other imines, and is in accordance with the model outlined in the paper (Figure 3C). The calculated CD signal for this imine, however, incorrectly predicts the sign of the signal (opposite of that observed).

Figure S4: Energies calculated at the M062X/6-31+G** level (*in vacuo* and acetonitrile) and reported in relative ΔG in kcal/mol.

HCA + S-2-PG

Key
 B3LYP/6-31G**
 (B3LYP/6-31+G**) in acetonitrile
 [M062X/6-31+G**] in acetonitrile



Rank	Conformer	Energy	Percent
1	1	0.00	56 (41)[53]
2	5	0.89 ($\rightarrow\#45$)	12.5 (-)[-]
3	10	0.91 (1.07)	12 (7)[12]
4	50	1.42 (0.12)	5 (33)[14]
5	45	1.46 (0.87)	5 (9)[11]
6	12	1.49 (1.66)	4.5 (2)[7]
7	13	1.66 (1.34)	3 (4)[2]

Rank	Conformer	Energy	Percent
1	1	0.00	56
2	5	0.89	12.5
3	57	0.91	12
4	55	1.42	5
5	48	1.46	5
6	11	1.49	4.5
7	12	1.66	3

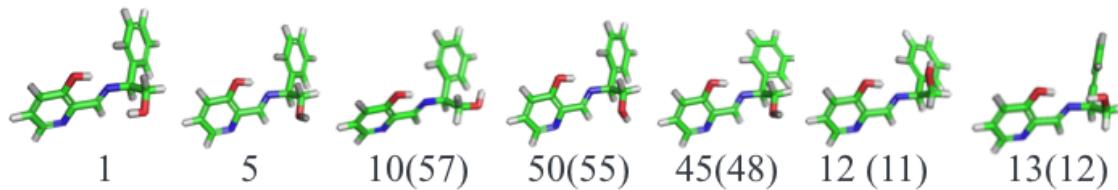
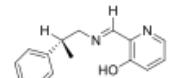
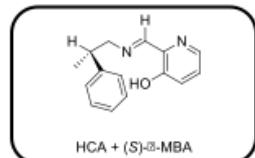


Figure S5: Energies calculated at the M062X/6-31+G** level (*in vacuo* and acetonitrile) and reported in relative ΔG in kcal/mol.

HCA + S- β -MBA

Key

B3LYP/6-31G**
 (B3LYP/6-31+G**) in acetonitrile
 [M062X/6-31+G**] in acetonitrile



HCA + (R)- β -MBA

Rank	Conformer	Energy	Percent
1	3	0.00 (0.21)	26 (25)[45]
2	7	0.02 (0.57)	25 (13)[2]
3	1	0.11 (0.00)	21 (35)[8]
4	52	0.19 (0.38)	19 (19)[19]
5	5	0.91 (1.36)	5 (3)[13]
6	54	1.11 (1.11)	4 (5)[12]

Rank	Conformer	Energy	Percent
1	3	0.00	26
2	7	0.02	25
3	1	0.11	21
4	48	0.19	19
5	5	0.91	5
6	100	1.11	4

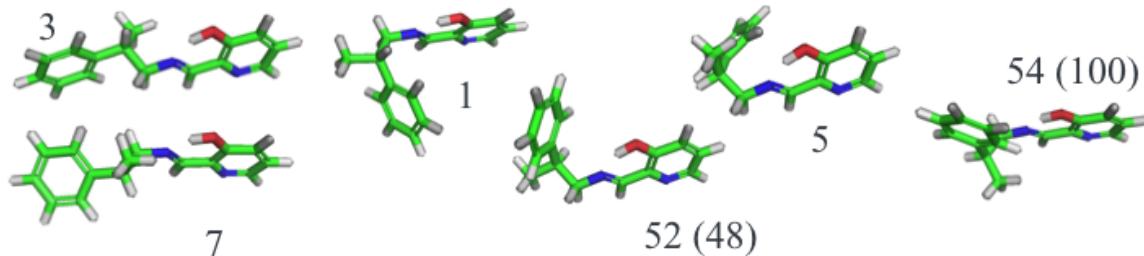
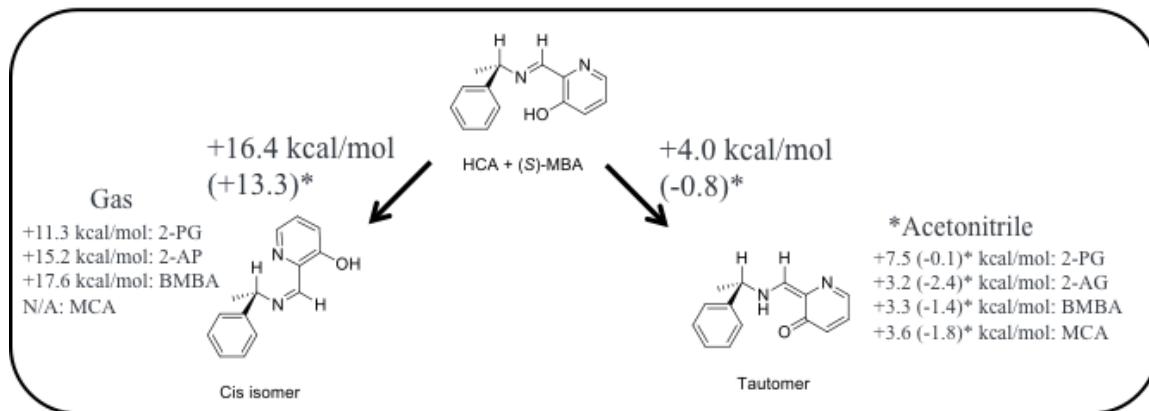


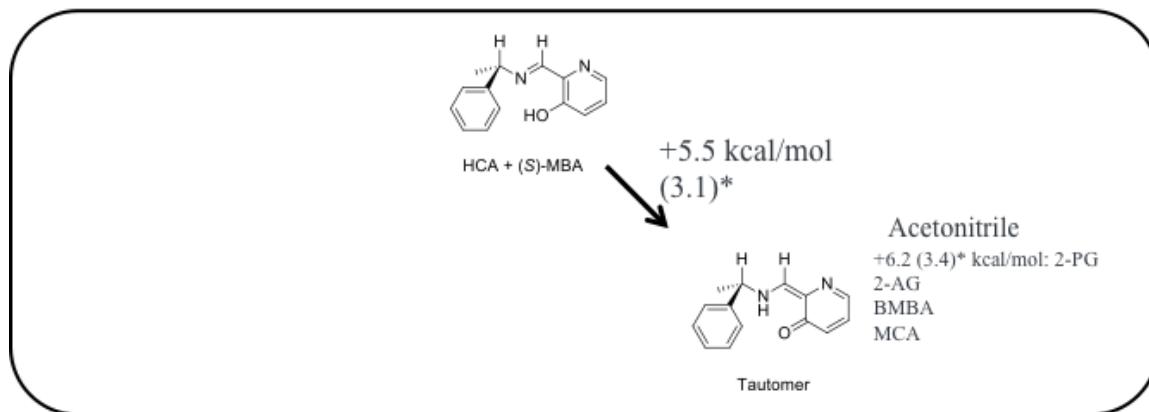
Figure S6: Energies calculated at the M062X/6-31+G** level (*in vacuo* and acetonitrile) and reported in relative ΔG in kcal/mol.

Relative energies of tautomers and cis/trans imines:

B3LYP/6-31+G**



M062X/6-31++G**



Scheme S1: Energies calculated at the B3LYP/6-31+G** or M062X/6-31+G** level (*in vacuo* and acetonitrile) and reported in relative ΔG in kcal/mol.

Minima coordinates (xyz) for *in vacuo* structures (minimization of implicit acetonitrile did not alter coordinates considerably):

Molecule HCA_S_MBA

Conformer 1	Conformer 9
31	31
1 1 gaus C1 2.27438 -0.42185 -0.29393	1 1 gaus C1 -1.92472 -0.40182 -0.08116
2 1 gaus C2 2.56976 0.73760 0.46988	2 1 gaus C2 -2.91758 0.61299 -0.05198
3 1 gaus C3 3.85343 1.29059 0.35067	3 1 gaus C3 -4.26023 0.21414 0.03005
4 1 gaus C4 4.76368 0.68263 -0.50037	4 1 gaus C4 -4.55075 -1.14075 0.07790
5 1 gaus C5 4.38033 -0.46325 -1.21445	5 1 gaus C5 -3.50101 -2.07156 0.04371
6 1 gaus N6 3.16961 -1.00348 -1.11559	6 1 gaus N6 -2.22247 -1.71497 -0.03324
7 1 gaus C7 0.95806 -1.05353 -0.22269	7 1 gaus C7 -0.50292 -0.06674 -0.16804
8 1 gaus N8 0.02038 -0.58710 0.51922	8 1 gaus N8 -0.11087 1.15520 -0.21846
9 1 gaus H9 0.83455 -1.94831 -0.84621	9 1 gaus H9 0.17688 -0.92359 -0.18440
10 1 gaus O10 1.67270 1.30398 1.28689	10 1 gaus O10 -2.61003 1.91459 -0.10043
11 1 gaus C11 -1.27327 -1.27110 0.55087	11 1 gaus C11 1.31026 1.52755 -0.33280
12 1 gaus H12 -1.23803 -2.16016 -0.09865	12 1 gaus H12 1.42353 1.90288 -1.35964
13 1 gaus C13 -2.37445 -0.35415 0.03012	13 1 gaus C13 2.31704 0.40014 -0.14693
14 1 gaus C14 -1.55506 -1.73415 1.99097	14 1 gaus C14 1.56574 2.71445 0.61069
15 1 gaus C15 -2.49401 0.96819 0.47806	15 1 gaus C15 2.53758 -0.18614 1.10866
16 1 gaus C16 -3.52829 1.78210 0.01793	16 1 gaus C16 3.46970 -1.21125 1.26355
17 1 gaus C17 -4.46152 1.28581 -0.89485	17 1 gaus C17 4.20057 -1.66843 0.16469
18 1 gaus C18 -4.34989 -0.02852 -1.34755	18 1 gaus C18 3.98827 -1.09721 -1.08956
19 1 gaus C19 -3.31025 -0.83987 -0.88934	19 1 gaus C19 3.05043 -0.07408 -1.24101
20 1 gaus H20 -1.58654 -0.87734 2.67014	20 1 gaus H20 1.43495 2.42364 1.65704
21 1 gaus H21 -2.51947 -2.24772 2.04067	21 1 gaus H21 2.58472 3.09036 0.48382
22 1 gaus H22 -0.77340 -2.41869 2.33442	22 1 gaus H22 0.86190 3.52343 0.39587
23 1 gaus H23 4.09996 2.17719 0.92546	23 1 gaus H23 -5.03421 0.97421 0.05323
24 1 gaus H24 5.76538 1.08519 -0.61630	24 1 gaus H24 -5.57916 -1.48343 0.14120
25 1 gaus H25 5.07971 -0.95553 -1.88623	25 1 gaus H25 -3.70730 -3.13884 0.08033
26 1 gaus H26 -1.76779 1.36554 1.18043	26 1 gaus H26 1.97453 0.15767 1.97178
27 1 gaus H27 -3.60442 2.80650 0.37109	27 1 gaus H27 3.62661 -1.65311 2.24329
28 1 gaus H28 -5.26635 1.92090 -1.25316	28 1 gaus H28 4.92834 -2.46520 0.28666
29 1 gaus H29 -5.06695 -0.42273 -2.06194	29 1 gaus H29 4.55003 -1.44669 -1.95094
30 1 gaus H30 -3.22485 -1.86161 -1.25147	30 1 gaus H30 2.88859 0.36623 -2.22200
31 1 gaus H31 0.83924 0.75595 1.21925	31 1 gaus H31 -1.61013 1.96633 -0.15765

Molecule HCA_S_2AP

Conformer 1

25
1 1 gaus C1 1.26425 -0.52848 -0.04600
2 1 gaus C2 1.54710 0.83972 0.20380
3 1 gaus C3 2.88934 1.24640 0.18377
4 1 gaus C4 3.86689 0.29848 -0.07671
5 1 gaus C5 3.49097 -1.03415 -0.30871
6 1 gaus N6 2.22544 -1.43996 -0.29354
7 1 gaus C7 -0.11038 -1.02376 -0.04547
8 1 gaus N8 -1.11412 -0.24610 0.14851
9 1 gaus H9 -0.21999 -2.10175 -0.22040
10 1 gaus O10 0.58247 1.73468 0.45721
11 1 gaus C11 -2.46983 -0.79157 0.12930
12 1 gaus H12 -2.43987 -1.87571 -0.07190
13 1 gaus C13 -3.24137 -0.12587 -1.02844
14 1 gaus C14 -3.14479 -0.53585 1.48102
15 1 gaus O15 -3.36276 1.27724 -0.88067
16 1 gaus H16 -3.24472 0.53826 1.65334
17 1 gaus H17 -4.14533 -0.97973 1.49225
18 1 gaus H18 -2.56329 -0.97331 2.29713
19 1 gaus H19 -4.26128 -0.52342 -1.05340
20 1 gaus H20 -2.75480 -0.39080 -1.98012
21 1 gaus H21 3.12709 2.28798 0.37259
22 1 gaus H22 4.91550 0.57891 -0.10013
23 1 gaus H23 4.24301 -1.79282 -0.51241
24 1 gaus H24 -0.28114 1.23230 0.44369
25 1 gaus H25 -2.46527 1.63761 -0.87315

Conformer 37

25
1 1 gaus C1 1.28808 -0.52500 -0.09024
2 1 gaus C2 1.53808 0.84563 0.18902
3 1 gaus C3 2.87587 1.26956 0.22356
4 1 gaus C4 3.87709 0.34041 -0.01317
5 1 gaus C5 3.53058 -0.99293 -0.28183
6 1 gaus N6 2.27107 -1.41680 -0.32096
7 1 gaus C7 -0.07977 -1.03575 -0.14825
8 1 gaus N8 -1.08619 -0.27182 0.07168
9 1 gaus H9 -0.17773 -2.10227 -0.39231
10 1 gaus O10 0.55726 1.72619 0.41286
11 1 gaus C11 -2.43863 -0.80964 -0.00178
12 1 gaus H12 -2.41748 -1.84023 -0.39593
13 1 gaus C13 -3.26026 0.02690 -0.99052
14 1 gaus C14 -3.06799 -0.81800 1.39768
15 1 gaus O15 -3.40713 1.33969 -0.47228
16 1 gaus H16 -3.11321 0.19663 1.79795
17 1 gaus H17 -4.08547 -1.21996 1.35374
18 1 gaus H18 -2.47971 -1.44013 2.07787
19 1 gaus H19 -4.23713 -0.46513 -1.12915
20 1 gaus H20 -2.74543 0.03185 -1.96307
21 1 gaus H21 3.09065 2.31193 0.43482
22 1 gaus H22 4.92155 0.63665 0.00715
23 1 gaus H23 4.30098 -1.73695 -0.47121
24 1 gaus H24 -0.30946 1.22637 0.34380
25 1 gaus H25 -3.82105 1.88732 -1.15017

Molecule HCA_2-PG

Conformer 1

32
1 1 gaus C1 -2.33516 0.07232 0.49746
2 1 gaus C2 -2.61380 -0.67133 -0.67888
3 1 gaus C3 -3.90607 -1.19542 -0.83237
4 1 gaus C4 -4.84051 -0.96266 0.16465
5 1 gaus C5 -4.47250 -0.21321 1.29364
6 1 gaus N6 -3.25447 0.29168 1.45827
7 1 gaus C7 -1.01114 0.64395 0.73183
8 1 gaus N8 -0.04818 0.49731 -0.10751

Conformer 5

32
1 1 gaus C1 -2.37250 0.14019 0.44176
2 1 gaus C2 -2.58623 -0.85921 -0.54341
3 1 gaus C3 -3.87308 -1.40605 -0.65435
4 1 gaus C4 -4.86627 -0.94836 0.19825
5 1 gaus C5 -4.55984 0.04331 1.14272
6 1 gaus N6 -3.34727 0.57506 1.26352
7 1 gaus C7 -1.05824 0.75663 0.61562
8 1 gaus N8 -0.04827 0.40740 -0.09552

9 1 gaus H9 -0.89850 1.19530 1.67335	9 1 gaus H9 -1.00080 1.52803 1.39193
10 1 gaus O10 -1.69304 -0.87946 -1.62926	10 1 gaus O10 -1.60836 -1.28377 -1.35409
11 1 gaus C11 1.24711 1.10581 0.18380	11 1 gaus C11 1.22495 1.08984 0.10621
12 1 gaus H12 1.21112 1.62409 1.15402	12 1 gaus H12 1.19392 1.69259 1.02680
13 1 gaus C13 1.52733 2.17943 -0.89389	13 1 gaus C13 1.45176 2.07664 -1.05205
14 1 gaus C14 2.35891 0.06949 0.21531	14 1 gaus C14 2.37625 0.10029 0.20231
15 1 gaus C15 2.43667 -0.95408 -0.73854	15 1 gaus C15 2.49991 -0.96360 -0.70095
16 1 gaus C16 3.49554 -1.86183 -0.71932	16 1 gaus C16 3.58454 -1.83707 -0.62376
17 1 gaus C17 4.49421 -1.75800 0.25049	17 1 gaus C17 4.56268 -1.65893 0.35631
18 1 gaus C18 4.42567 -0.74182 1.20399	18 1 gaus C18 4.44784 -0.60300 1.26073
19 1 gaus C19 3.36393 0.16320 1.18553	19 1 gaus C19 3.36042 0.26825 1.18313
20 1 gaus O20 0.56659 3.21691 -0.88438	20 1 gaus O20 0.46599 3.09210 -0.95389
21 1 gaus H21 1.59622 1.68747 -1.87597	21 1 gaus H21 1.38681 1.52821 -2.00321
22 1 gaus H22 2.49474 2.64401 -0.68336	22 1 gaus H22 2.46948 2.48614 -0.96463
23 1 gaus H23 -4.13955 -1.76792 -1.72391	23 1 gaus H23 -4.05745 -2.17129 -1.40113
24 1 gaus H24 -5.84949 -1.35408 0.07801	24 1 gaus H24 -5.87311 -1.35069 0.13983
25 1 gaus H25 -5.19129 -0.01912 2.08626	25 1 gaus H25 -5.32429 0.41565 1.82085
26 1 gaus H26 1.65912 -1.05028 -1.48956	26 1 gaus H26 1.73877 -1.11737 -1.45944
27 1 gaus H27 3.53862 -2.65289 -1.46239	27 1 gaus H27 3.66362 -2.66000 -1.32829
28 1 gaus H28 5.31695 -2.46670 0.26526	28 1 gaus H28 5.40531 -2.34139 0.41731
29 1 gaus H29 5.19442 -0.65578 1.96643	29 1 gaus H29 5.20002 -0.45970 2.03110
30 1 gaus H30 3.31257 0.94902 1.93517	30 1 gaus H30 3.27218 1.08537 1.89492
31 1 gaus H31 -0.85469 -0.43585 -1.31670	31 1 gaus H31 -0.78748 -0.77221 -1.09876
32 1 gaus H32 -0.28116 2.82517 -1.13503	32 1 gaus H32 0.46756 3.59916 -1.77471

Conformer 10

32
 1 1 gaus C1 2.47706 0.25789 -0.45596
 2 1 gaus C2 2.78713 -0.48988 0.71023
 3 1 gaus C3 4.10430 -0.94739 0.86388
 4 1 gaus C4 5.03134 -0.64847 -0.12250
 5 1 gaus C5 4.63157 0.10073 -1.24066
 6 1 gaus N6 3.38939 0.54321 -1.40580
 7 1 gaus C7 1.12529 0.75957 -0.68874
 8 1 gaus N8 0.16948 0.53733 0.14012
 9 1 gaus H9 0.98783 1.32877 -1.61673
 10 1 gaus O10 1.87242 -0.76210 1.65033
 11 1 gaus C11 -1.15499 1.07415 -0.13225
 12 1 gaus H12 -1.15823 1.65274 -1.06894
 13 1 gaus C13 -1.51047 2.06038 1.01594
 14 1 gaus C14 -2.20111 -0.02778 -0.23913
 15 1 gaus C15 -3.37356 0.21100 -0.97199
 16 1 gaus C16 -4.38192 -0.75240 -1.03970

Conformer 50

32
 1 1 gaus C1 -2.38860 0.15802 0.41799
 2 1 gaus C2 -2.57721 -0.93461 -0.46784
 3 1 gaus C3 -3.86435 -1.48326 -0.56682
 4 1 gaus C4 -4.88151 -0.93646 0.20049
 5 1 gaus C5 -4.59850 0.14377 1.05061
 6 1 gaus N6 -3.38620 0.67850 1.15894
 7 1 gaus C7 -1.07732 0.78354 0.57292
 8 1 gaus N8 -0.04488 0.36867 -0.06694
 9 1 gaus H9 -1.04325 1.62258 1.27839
 10 1 gaus O10 -1.57686 -1.44621 -1.19615
 11 1 gaus C11 1.21601 1.07618 0.09739
 12 1 gaus H12 1.18787 1.69849 1.00845
 13 1 gaus C13 1.41115 2.03828 -1.10283
 14 1 gaus C14 2.38749 0.11431 0.20577
 15 1 gaus C15 3.36692 0.30815 1.18639
 16 1 gaus C16 4.47439 -0.53728 1.26756

17 1 gaus C17 -4.22992 -1.97177 -0.37941	17 1 gaus C17 4.61492 -1.59222 0.36582
18 1 gaus C18 -3.06354 -2.22065 0.34613	18 1 gaus C18 3.64250 -1.79529 -0.61532
19 1 gaus C19 -2.05796 -1.25653 0.41930	19 1 gaus C19 2.53804 -0.94782 -0.69594
20 1 gaus O20 -2.76059 2.69090 0.82757	20 1 gaus O20 0.39757 3.02208 -1.18932
21 1 gaus H21 -0.76085 2.85709 1.03746	21 1 gaus H21 1.36356 1.46312 -2.03190
22 1 gaus H22 -1.45546 1.51872 1.97209	22 1 gaus H22 2.41494 2.48162 -1.03215
23 1 gaus H23 4.36263 -1.52129 1.74765	23 1 gaus H23 -4.03007 -2.31875 -1.23888
24 1 gaus H24 6.05913 -0.98733 -0.03525	24 1 gaus H24 -5.88934 -1.33703 0.14802
25 1 gaus H25 5.34437 0.34698 -2.02419	25 1 gaus H25 -5.38218 0.58646 1.66112
26 1 gaus H26 -3.48994 1.15317 -1.50068	26 1 gaus H26 3.25881 1.12377 1.89745
27 1 gaus H27 -5.28030 -0.55157 -1.61624	27 1 gaus H27 5.22204 -0.37459 2.03847
28 1 gaus H28 -5.01006 -2.72510 -0.43561	28 1 gaus H28 5.47333 -2.25441 0.42922
29 1 gaus H29 -2.93298 -3.17084 0.85601	29 1 gaus H29 3.74231 -2.61701 -1.31853
30 1 gaus H30 -1.14935 -1.46476 0.97369	30 1 gaus H30 1.78308 -1.11927 -1.45696
31 1 gaus H31 1.02095 -0.33196 1.35094	31 1 gaus H31 -0.76054 -0.91618 -0.97198
32 1 gaus H32 -3.44381 2.00819 0.88544	32 1 gaus H32 0.52775 3.65204 -0.46825

Conformer 45

32
 1 1 gaus C1 2.36455 0.13306 -0.46973
 2 1 gaus C2 2.61116 -0.73682 0.62481
 3 1 gaus C3 3.90350 -1.26319 0.76552
 4 1 gaus C4 4.86992 -0.91187 -0.16470
 5 1 gaus C5 4.53242 -0.04269 -1.21367
 6 1 gaus N6 3.31418 0.46781 -1.36449
 7 1 gaus C7 1.04069 0.71520 -0.68234
 8 1 gaus N8 0.05237 0.43553 0.08662
 9 1 gaus H9 0.95549 1.39471 -1.53820
 10 1 gaus O10 1.65907 -1.05779 1.51145
 11 1 gaus C11 -1.23593 1.06836 -0.14885
 12 1 gaus H12 -1.21648 1.63727 -1.09208
 13 1 gaus C13 -1.49240 2.09053 0.97306
 14 1 gaus C14 -2.36920 0.05068 -0.21068
 15 1 gaus C15 -3.56503 0.40361 -0.85093
 16 1 gaus C16 -4.64147 -0.48132 -0.89355
 17 1 gaus C17 -4.53544 -1.73953 -0.29793
 18 1 gaus C18 -3.34659 -2.10255 0.33467
 19 1 gaus C19 -2.27028 -1.21437 0.37940
 20 1 gaus O20 -0.52769 3.12294 0.84641
 21 1 gaus H21 -1.42225 1.57244 1.94078
 22 1 gaus H22 -2.51736 2.47651 0.86843
 23 1 gaus H23 4.11299 -1.92998 1.59545
 24 1 gaus H24 5.88012 -1.30208 -0.08606

Conformer 12

32
 1 1 gaus C1 2.38927 -0.14213 -0.57257
 2 1 gaus C2 2.68900 0.03773 0.80449
 3 1 gaus C3 3.98576 -0.28147 1.23622
 4 1 gaus C4 4.90119 -0.75158 0.30762
 5 1 gaus C5 4.51235 -0.89245 -1.03401
 6 1 gaus N6 3.29078 -0.59554 -1.46544
 7 1 gaus C7 1.06079 0.16800 -1.09388
 8 1 gaus N8 0.12260 0.57852 -0.32119
 9 1 gaus H9 0.92967 0.02636 -2.17474
 10 1 gaus O10 1.79131 0.49707 1.68399
 11 1 gaus C11 -1.18501 0.90135 -0.86826
 12 1 gaus H12 -1.16572 0.87182 -1.97063
 13 1 gaus C13 -1.55154 2.35227 -0.45788
 14 1 gaus C14 -2.24962 -0.07316 -0.37801
 15 1 gaus C15 -2.18540 -0.65109 0.89805
 16 1 gaus C16 -3.20817 -1.48985 1.34681
 17 1 gaus C17 -4.30734 -1.75999 0.53162
 18 1 gaus C18 -4.37789 -1.19020 -0.74111
 19 1 gaus C19 -3.35647 -0.35393 -1.19033
 20 1 gaus O20 -1.65126 2.53272 0.93849
 21 1 gaus H21 -2.48204 2.62926 -0.97806
 22 1 gaus H22 -0.76000 3.02696 -0.79808
 23 1 gaus H23 4.23738 -0.15155 2.28360
 24 1 gaus H24 5.91210 -1.00791 0.60979

25 1 gaus H25 5.27612 0.24632 -1.95274	25 1 gaus H25 5.21657 -1.25727 -1.77817
26 1 gaus H26 -3.65100 1.37833 -1.32587	26 1 gaus H26 -1.31955 -0.46666 1.52478
27 1 gaus H27 -5.55874 -0.19128 -1.39786	27 1 gaus H27 -3.14071 -1.93584 2.33491
28 1 gaus H28 -5.37039 -2.43313 -0.33344	28 1 gaus H28 -5.09985 -2.41483 0.88138
29 1 gaus H29 -3.25150 -3.08271 0.79312	29 1 gaus H29 -5.22498 -1.40155 -1.38725
30 1 gaus H30 -1.34391 -1.51214 0.85754	30 1 gaus H30 -3.41523 0.08132 -2.18514
31 1 gaus H31 0.83460 -0.56506 1.22910	31 1 gaus H31 0.95227 0.68861 1.17237
32 1 gaus H32 -0.53989 3.65151 1.65347	32 1 gaus H32 -2.35542 1.95116 1.25933

Conformer 13

32
 1 1 gaus C1 2.34047 -0.24549 -0.47038
 2 1 gaus C2 2.58975 0.07327 0.89005
 3 1 gaus C3 3.87251 -0.17932 1.39812
 4 1 gaus C4 4.82654 -0.72482 0.55319
 5 1 gaus C5 4.48560 -1.01111 -0.77849
 6 1 gaus N6 3.27667 -0.77969 -1.27939
 7 1 gaus C7 1.03096 -0.00602 -1.07123
 8 1 gaus N8 0.06929 0.53307 -0.41109
 9 1 gaus H9 0.93086 -0.31986 -2.11795
 10 1 gaus O10 1.64884 0.59684 1.68782
 11 1 gaus C11 -1.22532 0.75246 -1.06330
 12 1 gaus H12 -1.17070 0.43600 -2.11731
 13 1 gaus C13 -1.49532 2.27597 -1.07348
 14 1 gaus C14 -2.30002 -0.08493 -0.38100
 15 1 gaus C15 -2.83521 0.26198 0.86821
 16 1 gaus C16 -3.80689 -0.54125 1.46509
 17 1 gaus C17 -4.25419 -1.70141 0.83019
 18 1 gaus C18 -3.72554 -2.05513 -0.41126
 19 1 gaus C19 -2.75422 -1.25126 -1.00897
 20 1 gaus O20 -1.35888 2.89184 0.19504
 21 1 gaus H21 -2.52137 2.45946 -1.40450
 22 1 gaus H22 -0.81424 2.73559 -1.80717
 23 1 gaus H23 4.08367 0.05692 2.43576
 24 1 gaus H24 5.82923 -0.93282 0.91383
 25 1 gaus H25 5.21913 -1.44168 -1.45610
 26 1 gaus H26 -2.50092 1.17133 1.35407
 27 1 gaus H27 -4.21678 -0.25805 2.43040
 28 1 gaus H28 -5.01035 -2.32424 1.29926
 29 1 gaus H29 -4.06771 -2.95430 -0.91547
 30 1 gaus H30 -2.34482 -1.53316 -1.97623
 31 1 gaus H31 0.81451 0.65863 1.14347
 32 1 gaus H32 -0.46661 2.68532 0.50788

Molecule HCA_BMBA

Conformer 3

34
 1 1 gaus C1 -2.97266 -0.45551 -0.23929
 2 1 gaus C2 -3.41886 0.88295 -0.07996
 3 1 gaus C3 -4.79531 1.09807 0.08662
 4 1 gaus C4 -5.64509 0.00265 0.08853
 5 1 gaus C5 -5.11051 -1.28478 -0.07592
 6 1 gaus N6 -3.81036 -1.51085 -0.23618
 7 1 gaus C7 -1.55443 -0.75762 -0.41996
 8 1 gaus N8 -0.66171 0.16531 -0.43657
 9 1 gaus H9 -1.31292 -1.82129 -0.54272
 10 1 gaus O10 -2.57761 1.92399 -0.08438
 11 1 gaus C11 0.73497 -0.18993 -0.62473
 12 1 gaus C12 1.62053 0.34549 0.52775
 13 1 gaus H13 1.43459 1.42528 0.58562
 14 1 gaus C14 3.09253 0.14927 0.19412
 15 1 gaus C15 1.22927 -0.27202 1.88024
 16 1 gaus C16 3.66525 -1.13004 0.13059
 17 1 gaus C17 5.01162 -1.29797 -0.19256
 18 1 gaus C18 5.81463 -0.18730 -0.45789
 19 1 gaus C19 5.25936 1.09079 -0.39816
 20 1 gaus C20 3.91091 1.25347 -0.07659
 21 1 gaus H21 1.35662 -1.36014 1.87756
 22 1 gaus H22 1.84978 0.13360 2.68445
 23 1 gaus H23 0.18248 -0.05891 2.11446
 24 1 gaus H24 1.07590 0.26707 -1.56191
 25 1 gaus H25 0.86245 -1.27969 -0.72371
 26 1 gaus H26 -5.15795 2.11327 0.20942
 27 1 gaus H27 -6.71537 0.13429 0.21541
 28 1 gaus H28 -5.76023 -2.15693 -0.07743
 29 1 gaus H29 3.05697 -2.00627 0.33845
 30 1 gaus H30 5.43441 -2.29777 -0.23558
 31 1 gaus H31 6.86352 -0.31785 -0.70739
 32 1 gaus H32 5.87446 1.96295 -0.60081
 33 1 gaus H33 3.48610 2.25341 -0.03170
 34 1 gaus H34 -1.65865 1.55066 -0.21659

Conformer 7

34
 1 1 gaus C1 2.93079 -0.56094 -0.21731
 2 1 gaus C2 3.46084 0.73655 0.01079
 3 1 gaus C3 4.84040 0.84862 0.24052
 4 1 gaus C4 5.61196 -0.30325 0.23349
 5 1 gaus C5 4.99768 -1.54319 -0.00247
 6 1 gaus N6 3.69296 -1.67195 -0.22230
 7 1 gaus C7 1.50324 -0.75296 -0.46239
 8 1 gaus N8 0.68228 0.23457 -0.47674
 9 1 gaus H9 1.18932 -1.79078 -0.63434
 10 1 gaus O10 2.69280 1.83287 0.00996
 11 1 gaus C11 -0.73020 -0.01585 -0.70882
 12 1 gaus C12 -1.59718 0.38682 0.51192
 13 1 gaus H13 -1.25375 -0.22638 1.35514
 14 1 gaus C14 -3.05442 0.03245 0.25172
 15 1 gaus C15 -1.40709 1.86407 0.89636
 16 1 gaus C16 -3.80429 0.69851 -0.72951
 17 1 gaus C17 -5.13570 0.35899 -0.96818
 18 1 gaus C18 -5.74602 -0.65513 -0.22787
 19 1 gaus C19 -5.01308 -1.32615 0.75089
 20 1 gaus C20 -3.68004 -0.98427 0.98435
 21 1 gaus H21 -1.68718 2.53156 0.07425
 22 1 gaus H22 -2.02952 2.11851 1.75909
 23 1 gaus H23 -0.36423 2.06865 1.15188
 24 1 gaus H24 -0.91546 -1.07303 -0.95177
 25 1 gaus H25 -1.04035 0.58115 -1.57613
 26 1 gaus H26 5.26646 1.83078 0.41678
 27 1 gaus H27 6.68246 -0.25192 0.40759
 28 1 gaus H28 5.58569 -2.45803 -0.01256
 29 1 gaus H29 -3.34813 1.49435 -1.31237
 30 1 gaus H30 -5.69782 0.88854 -1.73223
 31 1 gaus H31 -6.78344 -0.91831 -0.41212
 32 1 gaus H32 -5.47729 -2.11593 1.33470
 33 1 gaus H33 -3.11604 -1.51214 1.74961
 34 1 gaus H34 1.75882 1.52611 -0.18481

Conformer 1

34
 1 1 gaus C1 -2.17284 -0.17970 -0.56972

Conformer 52

34
 1 1 gaus C1 2.61383 0.52829 -0.08925

2 1 gaus C2 -2.70163 0.48150 0.71304	2 1 gaus C2 2.45116 -0.87752 -0.20778
3 1 gaus C3 -3.94668 0.06829 1.05342	3 1 gaus C3 3.59544 -1.68000 -0.07849
4 1 gaus C4 -4.59509 0.87200 0.12818	4 1 gaus C4 4.81667 -1.06775 0.15679
5 1 gaus C5 -3.99341 1.11271 -1.11676	5 1 gaus C5 4.87772 0.33079 0.25995
6 1 gaus N6 -2.81456 0.60232 -1.45924	6 1 gaus N6 3.80730 1.10999 0.14085
7 1 gaus C7 -0.87939 -0.71296 -0.99176	7 1 gaus C7 1.46944 1.42836 -0.21119
8 1 gaus N8 -0.18563 -1.48124 -0.23236	8 1 gaus N8 0.28538 0.98810 -0.43762
9 1 gaus H9 -0.55104 -0.41303 -1.99472	9 1 gaus H9 1.69755 2.49642 -0.09646
10 1 gaus O10 -2.05538 -1.26134 1.58831	10 1 gaus O10 1.26299 -1.44852 -0.43283
11 1 gaus C11 1.09991 -1.97351 -0.69368	11 1 gaus C11 -0.81768 1.92678 -0.53432
12 1 gaus C12 2.25140 -1.52226 0.23753	12 1 gaus C12 -1.93396 1.60320 0.48680
13 1 gaus H13 1.96152 -1.81502 1.25428	13 1 gaus H13 -1.46402 1.60981 1.47846
14 1 gaus C14 2.42754 -0.01024 0.22935	14 1 gaus C14 -2.53016 0.21875 0.27211
15 1 gaus C15 3.54708 -2.27158 -0.12022	15 1 gaus C15 -3.00356 2.71026 0.46553
16 1 gaus C16 2.08919 0.74989 1.35558	16 1 gaus C16 -2.35644 -0.78592 1.23177
17 1 gaus C17 2.23942 2.13765 1.36084	17 1 gaus C17 -2.90411 -2.05743 1.05246
18 1 gaus C18 2.73047 2.79245 0.23165	18 1 gaus C18 -3.63780 -2.34698 -0.09734
19 1 gaus C19 3.06802 2.04879 -0.90066	19 1 gaus C19 -3.81696 -1.35646 -1.06492
20 1 gaus C20 2.91745 0.66229 -0.90011	20 1 gaus C20 -3.26809 -0.08798 -0.88079
21 1 gaus H21 3.86442 -2.06553 -1.14784	21 1 gaus H21 -3.48073 2.79110 -0.51687
22 1 gaus H22 4.36250 -1.97273 0.54419	22 1 gaus H22 -3.78803 2.50312 1.19863
23 1 gaus H23 3.40935 -3.35403 -0.02607	23 1 gaus H23 -2.56357 3.68476 0.70299
24 1 gaus H24 1.30692 -1.65617 -1.72793	24 1 gaus H24 -1.23429 1.86107 -1.54823
25 1 gaus H25 1.06179 -3.07070 -0.68544	25 1 gaus H25 -0.47533 2.96332 -0.38491
26 1 gaus H26 -4.36870 -0.14931 2.02903	26 1 gaus H26 3.49411 -2.75674 -0.16581
27 1 gaus H27 -5.55986 1.31313 0.35978	27 1 gaus H27 5.72055 -1.66023 0.26154
28 1 gaus H28 -4.48591 1.73966 -1.85652	28 1 gaus H28 5.82578 0.83061 0.44504
29 1 gaus H29 1.70055 0.24802 2.23798	29 1 gaus H29 -1.78332 -0.56963 2.12980
30 1 gaus H30 1.97062 2.70534 2.24711	30 1 gaus H30 -2.75386 -2.82052 1.81072
31 1 gaus H31 2.84814 3.87209 0.23196	31 1 gaus H31 -4.06459 -3.33526 -0.24082
32 1 gaus H32 3.45002 2.54886 -1.78623	32 1 gaus H32 -4.38509 -1.57187 -1.96550
33 1 gaus H33 3.18760 0.10034 -1.79045	33 1 gaus H33 -3.41906 0.66949 -1.64576
34 1 gaus H34 -1.20209 -1.54190 1.14538	34 1 gaus H34 0.58820 -0.71230 -0.49084

Conformer 5

34
 1 1 gaus C1 -2.19190 0.01878 0.64034
 2 1 gaus C2 -2.61925 -0.42900 -0.63740
 3 1 gaus C3 -3.81542 0.09522 -1.14887
 4 1 gaus C4 -4.51873 1.01472 -0.38544
 5 1 gaus C5 -4.01810 1.39538 0.86929
 6 1 gaus N6 -2.88482 0.91371 1.37065
 7 1 gaus C7 -0.94608 -0.47139 1.22579

Conformer 54

34
 1 1 gaus C1 2.61884 -0.43198 -0.23421
 2 1 gaus C2 2.42466 0.97128 -0.14092
 3 1 gaus C3 3.55046 1.77249 0.10141
 4 1 gaus C4 4.78720 1.16030 0.23629
 5 1 gaus C5 4.88056 -0.23578 0.12668
 6 1 gaus N6 3.82686 -1.01353 -0.10209
 7 1 gaus C7 1.49202 -1.32939 -0.47948

8 1 gaus N8 -0.22022 -1.34591 0.62809	8 1 gaus N8 0.29499 -0.88744 -0.62058
9 1 gaus H9 -0.67861 -0.03869 2.19791	9 1 gaus H9 1.74380 -2.39667 -0.53445
10 1 gaus O10 -1.91795 -1.31867 -1.35309	10 1 gaus O10 1.21941 1.53934 -0.27526
11 1 gaus C11 1.02317 -1.78283 1.23595	11 1 gaus C11 -0.78892 -1.82404 -0.85574
12 1 gaus C12 2.24508 -1.62083 0.29186	12 1 gaus C12 -1.91342 -1.72947 0.21178
13 1 gaus H13 3.09181 -2.02174 0.86459	13 1 gaus H13 -2.61555 -2.52896 -0.05900
14 1 gaus C14 2.55944 -0.15998 -0.00001	14 1 gaus C14 -2.68857 -0.42052 0.13095
15 1 gaus C15 2.10554 -2.47694 -0.97836	15 1 gaus C15 -1.38096 -2.04052 1.61936
16 1 gaus C16 3.63039 0.46788 0.65017	16 1 gaus C16 -2.19018 0.78157 0.65540
17 1 gaus C17 3.93585 1.80856 0.41227	17 1 gaus C17 -2.91840 1.96681 0.54603
18 1 gaus C18 3.16975 2.54968 -0.48732	18 1 gaus C18 -4.16306 1.97475 -0.08515
19 1 gaus C19 2.09920 1.93887 -1.14235	19 1 gaus C19 -4.67331 0.78669 -0.60830
20 1 gaus C20 1.79676 0.59840 -0.90163	20 1 gaus C20 -3.94063 -0.39575 -0.49890
21 1 gaus H21 1.26057 -2.16152 -1.59584	21 1 gaus H21 -0.63882 -1.30631 1.94468
22 1 gaus H22 3.00998 -2.40669 -1.58944	22 1 gaus H22 -2.19515 -2.04206 2.34949
23 1 gaus H23 1.95071 -3.52973 -0.71826	23 1 gaus H23 -0.90213 -3.02588 1.64172
24 1 gaus H24 0.92233 -2.85114 1.47135	24 1 gaus H24 -0.41440 -2.86015 -0.88678
25 1 gaus H25 1.21503 -1.24886 2.17897	25 1 gaus H25 -1.22499 -1.59577 -1.83613
26 1 gaus H26 -4.15929 -0.23185 -2.12459	26 1 gaus H26 3.42485 2.84762 0.17592
27 1 gaus H27 -5.44894 1.43931 -0.75064	27 1 gaus H27 5.67844 1.75140 0.42387
28 1 gaus H28 -4.55471 2.11515 1.48311	28 1 gaus H28 5.84125 -0.73525 0.22860
29 1 gaus H29 4.23679 -0.10354 1.34939	29 1 gaus H29 -1.22201 0.80061 1.14429
30 1 gaus H30 4.77371 2.27076 0.92664	30 1 gaus H30 -2.50919 2.88600 0.95529
31 1 gaus H31 3.40483 3.59279 -0.67777	31 1 gaus H31 -4.72988 2.89760 -0.16686
32 1 gaus H32 1.49523 2.50724 -1.84398	32 1 gaus H32 -5.64286 0.77748 -1.09836
33 1 gaus H33 0.95654 0.14294 -1.41566	33 1 gaus H33 -4.34894 -1.31781 -0.90668
34 1 gaus H34 -1.13124 -1.57884 -0.78795	34 1 gaus H34 0.56960 0.80168 -0.46606

Molecule HCA_CEA

Conformer 3

37
 1 1 gaus C1 -2.45675 0.10936 -0.46876
 2 1 gaus C2 -2.80176 -0.13106 0.88746
 3 1 gaus C3 -4.10065 -0.58498 1.16148
 4 1 gaus C4 -4.97693 -0.77512 0.10386
 5 1 gaus C5 -4.54485 -0.51010 -1.20475
 6 1 gaus N6 -3.31881 -0.07956 -1.48659
 7 1 gaus C7 -1.12184 0.58392 -0.83063
 8 1 gaus N8 -0.21697 0.79900 0.05377
 9 1 gaus H9 -0.95460 0.74074 -1.90418
 10 1 gaus O10 -1.93713 0.05981 1.89149

Conformer 1

37
 1 1 gaus C1 -2.31601 0.23627 -0.41307
 2 1 gaus C2 -2.48949 -0.38090 0.85397
 3 1 gaus C3 -3.71404 -1.01576 1.11015
 4 1 gaus C4 -4.68743 -1.00815 0.12264
 5 1 gaus C5 -4.42470 -0.36935 -1.09909
 6 1 gaus N6 -3.27112 0.23691 -1.36301
 7 1 gaus C7 -1.06373 0.91024 -0.75219
 8 1 gaus N8 -0.08246 0.96789 0.07329
 9 1 gaus H9 -1.02571 1.35703 -1.75427
 10 1 gaus O10 -1.53334 -0.37082 1.79106

11 1 gaus C11 1.09645 1.29642 -0.35456	11 1 gaus C11 1.14911 1.65473 -0.30796
12 1 gaus H12 1.15439 1.32504 -1.45696	12 1 gaus H12 1.05658 2.02143 -1.34491
13 1 gaus C13 2.19441 0.33185 0.16237	13 1 gaus C13 2.35505 0.67793 -0.28187
14 1 gaus C14 1.24009 2.72929 0.18160	14 1 gaus C14 1.33893 2.87134 0.60985
15 1 gaus C15 3.61564 0.82256 -0.18099	15 1 gaus C15 2.22779 -0.40543 -1.36992
16 1 gaus C16 4.70014 -0.15390 0.30271	16 1 gaus C16 3.45128 -1.33340 -1.40791
17 1 gaus C17 4.47541 -1.57280 -0.23519	17 1 gaus C17 3.71577 -1.96982 -0.03601
18 1 gaus C18 3.06767 -2.07298 0.11308	18 1 gaus C18 3.84296 -0.89785 1.05541
19 1 gaus C19 1.98463 -1.09889 -0.37317	19 1 gaus C19 2.61473 0.02631 1.09087
20 1 gaus H20 1.23883 2.73490 1.27660	20 1 gaus H20 1.35209 2.57773 1.66288
21 1 gaus H21 2.16524 3.19379 -0.16761	21 1 gaus H21 2.28009 3.38147 0.38035
22 1 gaus H22 0.40367 3.34573 -0.16000	22 1 gaus H22 0.52049 3.58421 0.47293
23 1 gaus H23 -4.38506 -0.77505 2.19117	23 1 gaus H23 -3.86764 -1.49449 2.07165
24 1 gaus H24 -5.98916 -1.12558 0.28143	24 1 gaus H24 -5.64619 -1.49005 0.28854
25 1 gaus H25 -5.21658 -0.65267 -2.04815	25 1 gaus H25 -5.17526 -0.35137 -1.88597
26 1 gaus H26 3.79917 1.80914 0.25691	26 1 gaus H26 2.08264 0.06661 -2.35060
27 1 gaus H27 4.69426 -0.17990 1.40169	27 1 gaus H27 4.33505 -0.75585 -1.71485
28 1 gaus H28 5.23496 -2.25598 0.16323	28 1 gaus H28 4.62054 -2.58846 -0.07058
29 1 gaus H29 2.98465 -2.18983 1.20298	29 1 gaus H29 4.74370 -0.29608 0.86674
30 1 gaus H30 0.99551 -1.46477 -0.08042	30 1 gaus H30 2.75409 0.79313 1.86124
31 1 gaus H31 -1.08452 0.38382 1.47902	31 1 gaus H31 -0.76105 0.13780 1.40491
32 1 gaus H32 1.99371 -1.06944 -1.47370	32 1 gaus H32 1.73218 -0.55666 1.38419
33 1 gaus H33 2.09970 0.30090 1.25916	33 1 gaus H33 3.23384 1.29390 -0.53025
34 1 gaus H34 3.69871 0.94378 -1.27167	34 1 gaus H34 1.32710 -1.00282 -1.17502
35 1 gaus H35 5.68932 0.21600 0.00741	35 1 gaus H35 3.30901 -2.11007 -2.16881
36 1 gaus H36 4.59945 -1.57038 -1.32763	36 1 gaus H36 2.88509 -2.64407 0.21588
37 1 gaus H37 2.89591 -3.06626 -0.31840	37 1 gaus H37 3.98381 -1.36747 2.03620

Conformer 5

37
 1 1 gaus C1 2.53081 -0.44478 -0.27955
 2 1 gaus C2 2.78428 0.74865 0.44721
 3 1 gaus C3 4.06397 1.31505 0.34903
 4 1 gaus C4 5.01115 0.68667 -0.44517
 5 1 gaus C5 4.66785 -0.49207 -1.12505
 6 1 gaus N6 3.46121 -1.04522 -1.04657
 7 1 gaus C7 1.21810 -1.08671 -0.22919
 8 1 gaus N8 0.25537 -0.60018 0.46606
 9 1 gaus H9 1.11931 -2.00409 -0.82431
 10 1 gaus O10 1.85161 1.33332 1.20925
 11 1 gaus C11 -1.04470 -1.26847 0.47448
 12 1 gaus H12 -0.98463 -2.19169 -0.12745
 13 1 gaus C13 -2.09541 -0.35278 -0.21218

Conformer 29

37
 1 1 gaus C1 -2.32002 0.40475 0.07808
 2 1 gaus C2 -2.42191 -0.90782 -0.45436
 3 1 gaus C3 -3.62247 -1.60487 -0.25222
 4 1 gaus C4 -4.64326 -0.98313 0.45096
 5 1 gaus C5 -4.45064 0.31873 0.93790
 6 1 gaus N6 -3.32086 0.99689 0.75781
 7 1 gaus C7 -1.09849 1.19299 -0.09110
 8 1 gaus N8 -0.08249 0.71747 -0.71560
 9 1 gaus H9 -1.13600 2.19357 0.34956
 10 1 gaus O10 -1.42038 -1.48053 -1.13309
 11 1 gaus C11 1.16023 1.46982 -0.90134
 12 1 gaus H12 1.30490 1.50446 -1.99176
 13 1 gaus C13 2.35816 0.64492 -0.34667

14 1 gaus C14 -1.37754	-1.66166	1.92088	14 1 gaus C14 1.14996	2.91844	-0.39779
15 1 gaus C15 -2.31523	1.00127	0.48893	15 1 gaus C15 2.29621	0.40573	1.17390
16 1 gaus C16 -3.30116	1.88249	-0.29505	16 1 gaus C16 3.52617	-0.36730	1.67861
17 1 gaus C17 -4.63805	1.16561	-0.53208	17 1 gaus C17 3.71752	-1.69031	0.92378
18 1 gaus C18 -4.42929	-0.19492	-1.21333	18 1 gaus C18 3.77261	-1.46011	-0.59306
19 1 gaus C19 -3.44110	-1.07195	-0.42783	19 1 gaus C19 2.53611	-0.69428	-1.08793
20 1 gaus H20 -1.40417	-0.78540	2.57426	20 1 gaus H20 1.00880	2.98959	0.68486
21 1 gaus H21 -2.34455	-2.16869	1.97947	21 1 gaus H21 2.10507	3.39396	-0.63915
22 1 gaus H22 -0.61489	-2.34355	2.30821	22 1 gaus H22 0.35886	3.50144	-0.87987
23 1 gaus H23 4.27898	2.22730	0.89571	23 1 gaus H23 -3.72130	-2.60932	-0.65052
24 1 gaus H24 6.01104	1.09860	-0.54272	24 1 gaus H24 -5.58524	-1.49448	0.62479
25 1 gaus H25 5.39659	-1.00052	-1.75216	25 1 gaus H25 -5.23913	0.82437	1.49065
26 1 gaus H26 -1.35943	1.52194	0.60890	26 1 gaus H26 1.38747	-0.16454	1.40768
27 1 gaus H27 -2.85588	2.14664	-1.26470	27 1 gaus H27 3.43350	-0.55224	2.75546
28 1 gaus H28 -5.30610	1.79313	-1.13405	28 1 gaus H28 2.88047	-2.36364	1.15626
29 1 gaus H29 -4.04169	-0.03585	-2.22951	29 1 gaus H29 3.85652	-2.41714	-1.12141
30 1 gaus H30 -3.28089	-2.02289	-0.95231	30 1 gaus H30 2.60893	-0.51565	-2.16857
31 1 gaus H31 1.03066	0.76205	1.14272	31 1 gaus H31 -0.67993	-0.80190	-1.16290
32 1 gaus H32 -3.88639	-1.32210	0.54481	32 1 gaus H32 1.64478	-1.31471	-0.93167
33 1 gaus H33 -1.68192	-0.13667	-1.20964	33 1 gaus H33 3.25172	1.25436	-0.55361
34 1 gaus H34 -2.71384	0.83393	1.49898	34 1 gaus H34 2.21681	1.35701	1.71268
35 1 gaus H35 -3.46486	2.82653	0.23798	35 1 gaus H35 4.42254	0.25565	1.54682
36 1 gaus H36 -5.14120	1.01156	0.43329	36 1 gaus H36 4.62850	-2.19508	1.26695
37 1 gaus H37 -5.38705	-0.71719	-1.32450	37 1 gaus H37 4.67820	-0.88738	-0.83951

Calculation of CD Spectra:

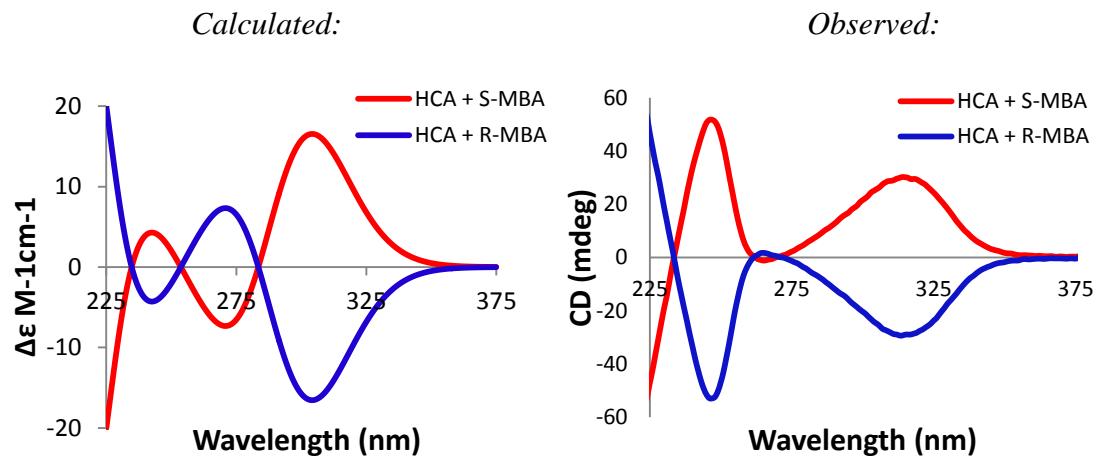


Figure S7: Calculated (left) and observed (right) CD spectra for the imine complexes formed between **HCA** (2 mM) and each enantiomer of **MBA** (2 mM).

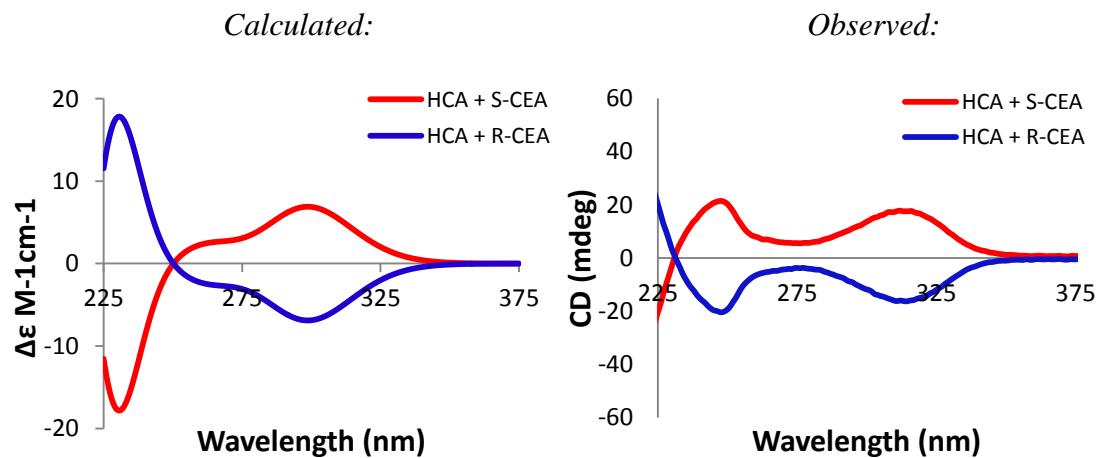


Figure S8: Calculated (left) and observed (right) CD spectra for the imine complexes formed between **HCA** (2 mM) and each enantiomer of **CEA** (2 mM).

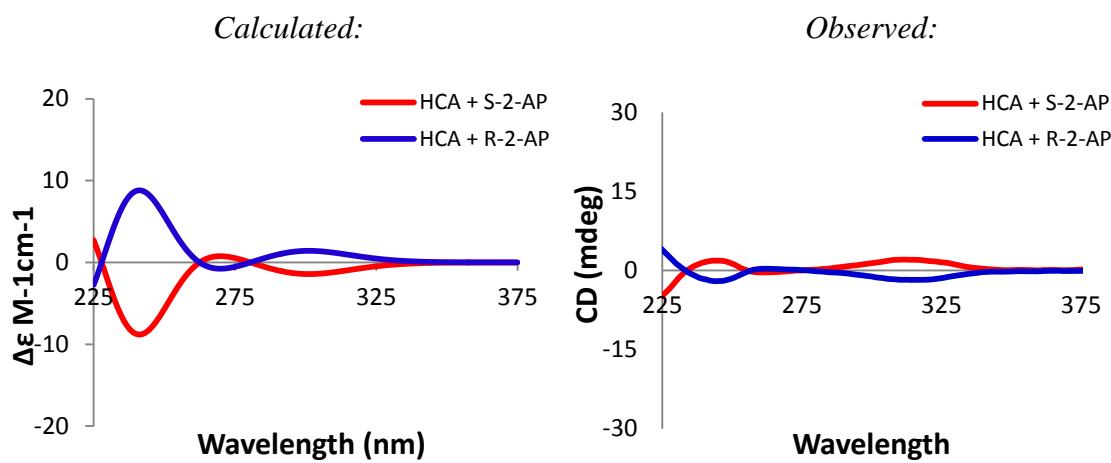


Figure S9: Calculated (left) and observed (right) CD spectra for the imine complexes formed between **HCA** (2 mM) and each enantiomer of **2-AP** (2 mM).

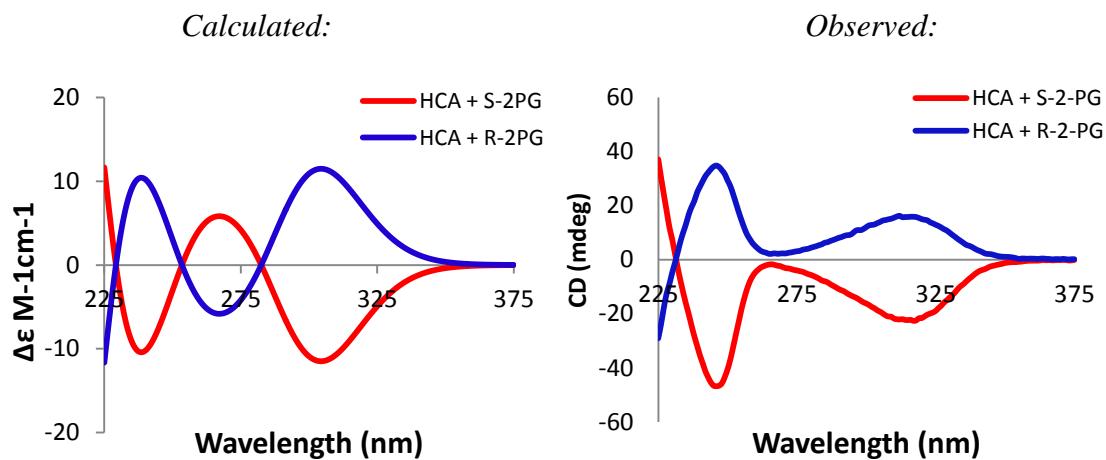


Figure S10: Calculated (left) and observed (right) CD spectra for the imine complexes formed between **HCA** (2 mM) and each enantiomer of **2-PG** (2 mM).

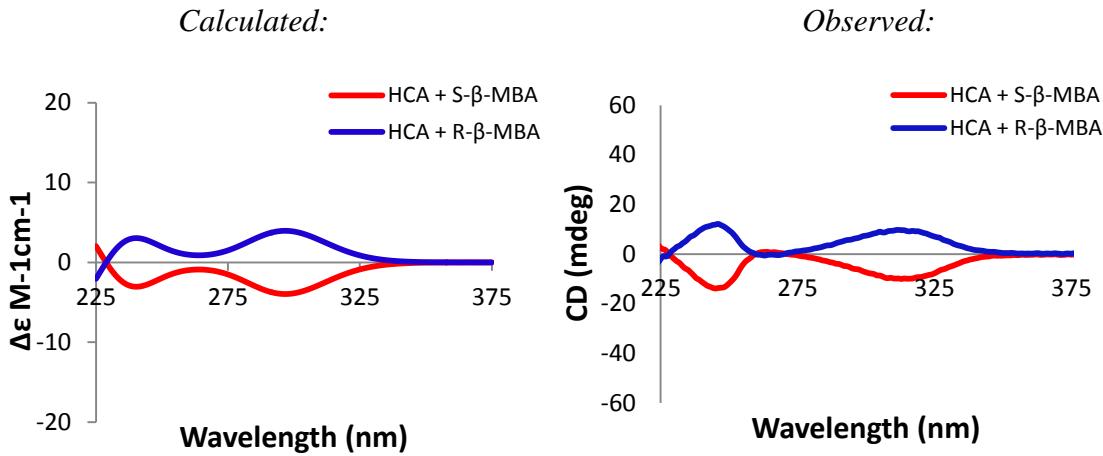


Figure S11: Calculated (left) and observed (right) CD spectra for the imine complexes formed between **HCA** (2 mM) and each enantiomer of **β-MBA** (2 mM).

d) *Unknown ee Calculations: Stand-Alone CD Spectrophotometer*

MBA:

Eight test solutions of 1 mL were independently made for the **MBA** guest (2 mM total amine content per vial) with **HCA** (2 mM) in acetonitrile. These solutions were transferred to the 0.1 cm jacketed CD cell, which was maintained at 25°C by a water circulation bath, and the CD spectrum recorded. Two standards were also created, representing either pure (*R*)-**MBA** or (*S*)-**MBA** (2 mM) with **HCA** (2 mM). These standards were used to create a 2-point calibration curve,¹³ which is pictured below. The best-fit trendline of this plot was used to relate the measured CD signal at 317 nm of the unknown guest to the *ee* of the sample. The results of this analysis, along with the errors, are also shown below in **Figure S12** and **Table S1**.

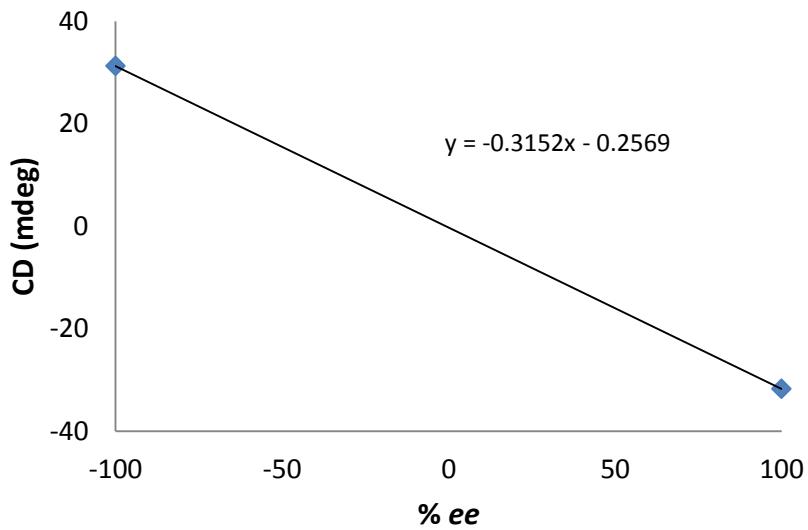


Figure S12. Calibration curve for **MBA** (2 mM) and **HCA** (2 mM) in acetonitrile at 25°C, measured by the stand alone CD spectrophotometer.

Unknown	CD _{317nm}	% ee _{calc}	% ee _{actual}	% Error
1	-28.0	90.7	90.0	0.7
2	11.1	-35.2	-40.0	4.8
3	-5.3	17.3	20.0	2.7
4	23.2	-74.3	-75.0	0.7
5	4.1	-13.0	-10.0	3.0
6	26.2	-83.9	-85.0	1.1
7	-9.9	32.2	35.0	2.8
8	-0.02	0.4	0.0	0.4

Table S1. Results of the stand alone CD spectrophotometer analysis of the eight unknown samples of **MBA**. The average error was determined to be 2.0%.

MPP:

Eight test solutions of 1 mL were independently made for the **MPP** guest (2 mM total amine content per vial) with **HCA** (2 mM) in acetonitrile. These solutions were transferred to the 0.1 cm jacketed CD cell, which was maintained at 25°C by a water circulation bath, and the CD spectrum recorded. Two standards were also created, representing either pure (*R*)-**MPP** or (*S*)-**MPP** (2 mM) with **HCA** (2 mM). These standards were used to create a 2-point calibration curve,¹³ which is pictured below. The best-fit trendline of this plot was used to relate the measured CD signal at 317 nm of the unknown guest to the *ee* of the sample. The results of this analysis, along with the errors, are also shown below in **Figure S13** and **Table S2**.

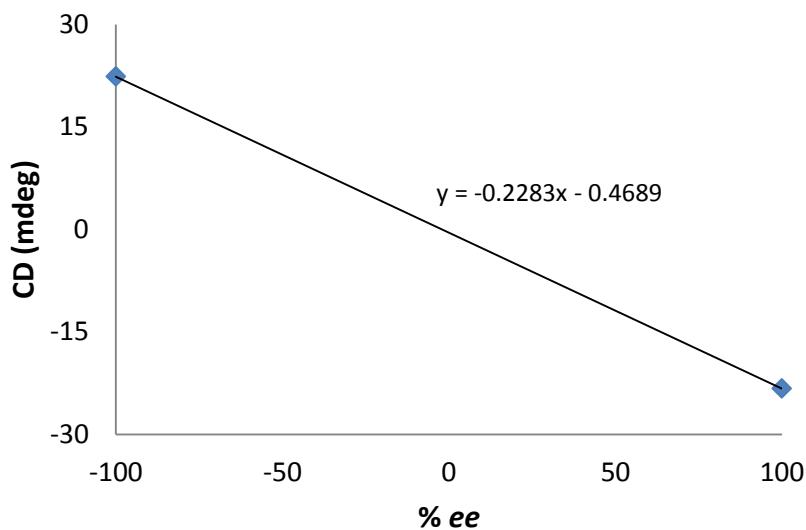


Figure S13. Calibration curve for **MPP** (2 mM) and **HCA** (2 mM) in acetonitrile at 25°C, measured by the stand alone CD spectrophotometer.

Unknown	CD _{317nm} (mdeg)	% ee _{calc}	% ee _{actual}	% Error
1	-18.5	79.0	80.0	1.0
2	-8.9	37.0	38.5	1.5
3	20.4	-91.5	-90.0	1.5
4	1.34	-7.9	0.0	7.9
5	-5.4	21.6	25.0	3.4
6	-3.4	12.7	15.0	2.3
7	12.4	-56.6	-50.0	6.6
8	10.9	-50.0	-45.1	5.0

Table S2. Results of the stand alone CD spectrophotometer analysis of the eight unknown samples of **MPP**. The average error was determined to be 3.6%.

AMH:

Eight test solutions of 1 mL were independently made for the **AMH** guest (2 mM total amine content per vial) with **HCA** (2 mM) in acetonitrile. These solutions were transferred to the 0.1 cm jacketed CD cell, which was maintained at 25°C by a water circulation bath, and the CD spectrum recorded. Two standards were also created, representing either pure (*R*)-**AMH** or (*S*)-**AMH** (2 mM) with **HCA** (2 mM). These standards were used to create a 2-point calibration curve,¹³ which is pictured below. The best-fit trendline of this plot was used to relate the measured CD signal at 317 nm of the unknown guest to the *ee* of the sample. The results of this analysis, along with the errors, are also shown below in **Figure S14** and **Table S3**.

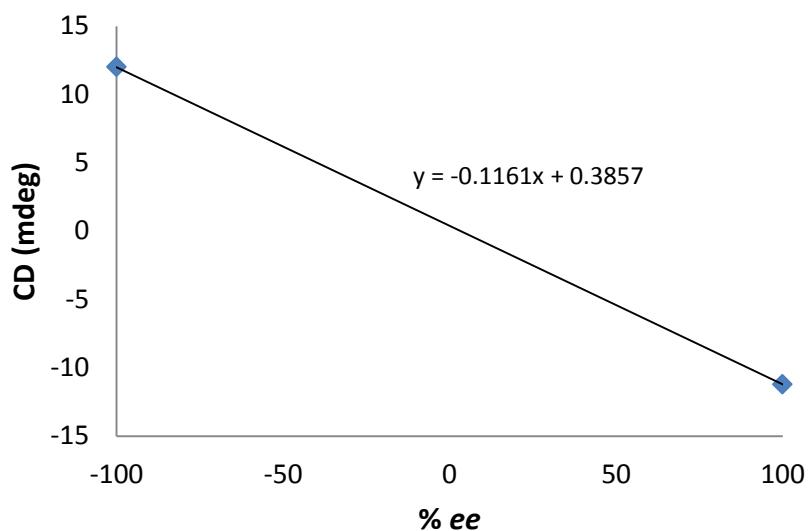


Figure S14. Calibration curve for **AMH** (2 mM) and **HCA** (2 mM) in acetonitrile at 25°C, measured by the stand alone CD spectrophotometer.

Unknown	CD _{317nm} (mdeg)	% ee _{calc}	% ee _{actual}	% Error
1	-11.9	106.2	100.0	6.2
2	0.7	-2.5	0.0	2.5
3	-4.9	45.2	45.0	0.2
4	-8.1	73.1	70.0	3.1
5	6.9	-56.4	-60.0	3.6
6	5.1	-40.2	-35.0	5.2
7	-9.0	80.8	80.0	0.8
8	-1.0	12.0	10.0	2.0

Table S3. Results of the stand alone CD spectrophotometer analysis of the eight unknown samples of **AMH**. The average error was determined to be 2.9%.

e) Unknown ee Calculations: HPLC-CD Detector

MBA:

The same eight test samples prepared for the stand alone spectrophotometer were used for the HPLC-CD detector, independently comprised of **MBA** guest (2 mM total amine content per vial) with **HCA** (2 mM) in acetonitrile. A 5 uL sample was injected onto the HPLC column, and the UV and CD were measured at 317 nm. The same two pure (*R*)-**MBA** and (*S*)-**MBA** (2 mM) enantiomeric standards were used. From these standards a 2-point calibration curve was created,¹³ which is pictured below. The best-fit trendline of this plot was used to relate the measured CD signal at 317 nm of the unknown guest to the *ee* of the sample. The results of this analysis, along with the errors, are also shown below in **Figure S15** and **Table S4**.

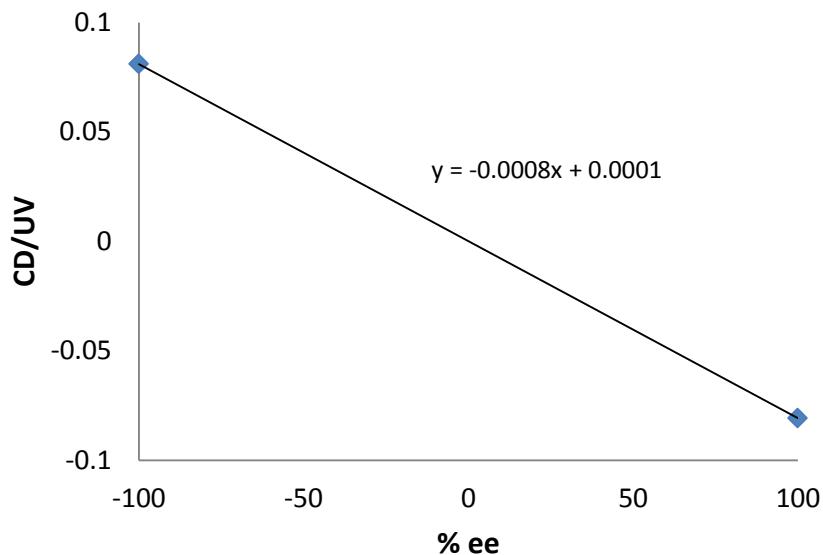


Figure S15. Calibration curve for **MBA** (2 mM) and **HCA** (2 mM) in acetonitrile at 25°C, with the CD and UV signals measured at 317 using the HPLC-CD.

Unknown	$\text{CD}_{317\text{nm}}/\text{UV}_{317\text{nm}}$	% ee calc	% ee actual	% Error
1	-0.074	91.3	90.0	1.3
2	0.032	-40.5	-40.0	0.5
3	-0.017	20.5	20.0	0.5
4	0.060	-75.9	-75.0	0.9
5	0.007	-9.8	-10.0	0.2
6	0.069	-86.8	-85.0	1.8
7	-0.031	37.7	35.0	2.7
8	-0.001	1.2	0.0	1.2

Table S4. Results of the HPLC-CD analysis of the eight unknown samples of **MBA**. The average error was determined to be 1.1%

MPP:

The same eight unknown samples prepared for the stand alone spectrophotometer were used for the HPLC-CD detector, independently comprised of **MPP** guest (2 mM total amine content per vial) with **HCA** (2 mM) in acetonitrile. A 5 uL sample was injected onto the HPLC column, and the UV and CD were measured at 317 nm. The same two pure (*R*)-**MPP** and (*S*)-**MPP** (2 mM) enantiomeric standards were used. From these standards a 2-point calibration curve was created,¹³ which is pictured below. The best-fit trendline of this plot was used to relate the measured CD signal at 317 nm of the unknown guest to the ee of the sample. The results of this analysis, along with the errors, are also shown in **Figure S16** and **Table S5**.

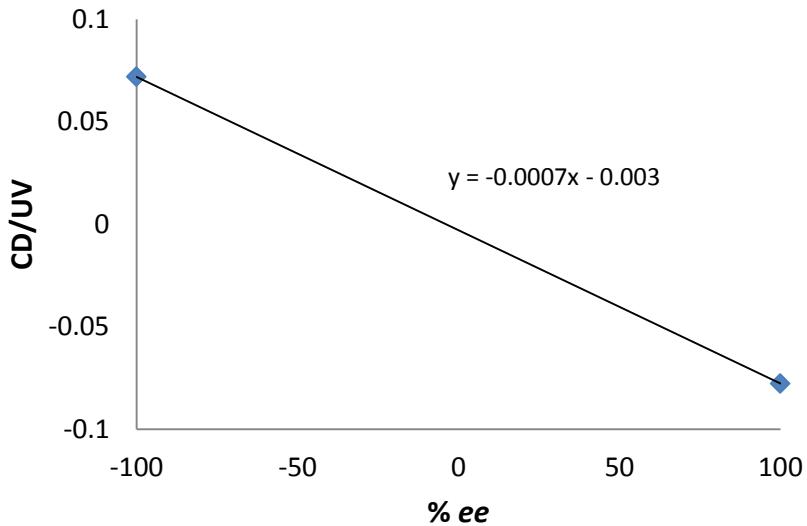


Figure S16. Calibration curve for **MPP** (2 mM) and **HCA** (2 mM) in acetonitrile at 25°C, with the CD and UV signals measured at 317 using the HPLC-CD.

Unknown	CD _{317nm} /UV _{317nm}	% ee _{calc}	% ee _{actual}	% Error
1	-0.062	84.3	80.0	4.3
2	-0.030	38.5	38.5	0.0
3	0.065	-96.9	-90.0	6.9
4	-0.0006	-3.4	0.0	3.4
5	-0.019	23.2	25.0	1.8
6	-0.012	12.6	15.0	2.4
7	0.036	-55.0	-50.0	5.0
8	0.033	-51.5	-45.0	6.5

Table S5. Results of the HPLC-CD analysis of the eight unknown samples of **MPP**. The average error was determined to be 3.8%

AMH:

The same eight unknown samples prepared for the stand alone spectrophotometer were used for the HPLC-CD detector, independently comprised of **AMH** guest (2 mM total amine content per vial) with **HCA** (2 mM) in acetonitrile. A 5 uL sample was injected onto the HPLC column, and the UV and CD were measured at 317 nm. The same two pure (*R*)-**AMH** and (*S*)-**AMH** (2 mM) enantiomeric standards were used. From these standards a 2-point calibration curve was created,¹³ which is pictured below. The best-fit trendline of this plot was used to relate the measured CD signal at 317 nm of the unknown guest to the *ee* of the sample. The results of this analysis, along with the errors, are also shown below in **Figure S17** and **Table S6**.

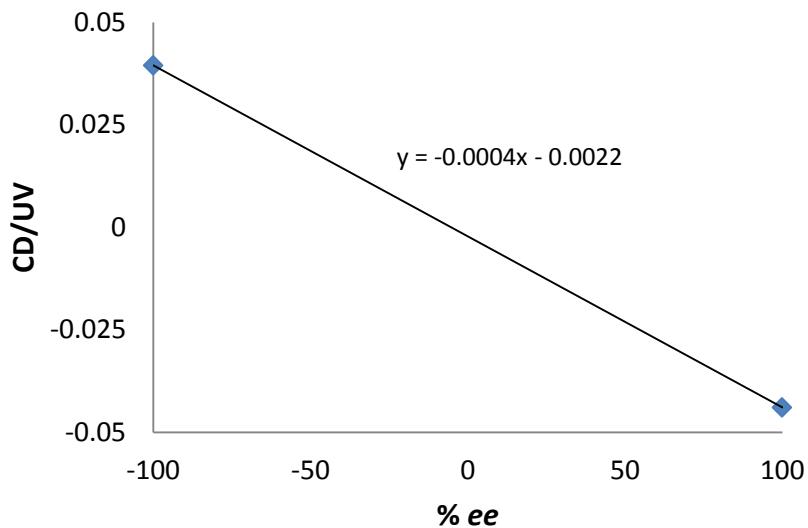


Figure S17. Calibration curve for **AMH** (2 mM) and **HCA** (2 mM) in acetonitrile at 25°C, with the CD and UV signals measured at 317 using the HPLC-CD.

Unknown	$\text{CD}_{317\text{nm}}/\text{UV}_{317\text{nm}}$	% ee calc	% ee actual	% Error
1	-0.044	103.2	100.0	3.2
2	-0.0007	-3.8	0.0	3.8
3	-0.019	43.1	45.0	1.9
4	-0.031	70.9	70.0	0.9
5	0.023	-64.2	-60.0	4.2
6	0.013	-39.0	-35.0	4.0
7	-0.035	81.5	80.0	1.5
8	-0.005	6.6	10.0	3.4

Table S6. Results of the HPLC-CD analysis of the eight unknown samples of AMH. The average error was determined to be 2.9%

f) *Synthetic Samples Reaction and Workup*

A stock solution was made by dissolving pyridoxal-5'-phosphate (PLP) (25 mg, 0.098 mmol) in 20 mL 0.2 M borate buffer at pH 10.5 that contained 1 M isopropylamine. A portion of this stock solution (600 uL) was added to each reaction vial, which contained a premeasured amount of transaminase (5 mg). The stock solution for the starting material ketone was made by dissolving the ketone (20 mg) in pure DMSO (1.6 mL). After the enzyme had dissolved, a portion of the ketone stock solution (150 uL) was added to the enzyme vial. The reaction vials were capped, and shaken with a constant temperature of 45°C at 350 rpm. After 24 hours the vials were removed from the heating incubator. They sat at room temperature for 10 minutes,

until the insoluble enzyme had settled to the bottom. The top 500 uL of the solution was removed by pipet, and transferred to a deep well 2 mL Adam block 96 well plate. A 1 mL portion of DCM was added to the plate, and the wells were covered and agitated to mix. The amine guest was partitioned to the organic layer, and this layer was removed by pipet (0.75 mL) and transferred to the next row of wells. The solvent was evaporated from the wells by blowing N₂ gas over the top, and redisolved in acetonitrile (350 uL). This was split into two 175 uL portions. To the first was added **HCA** (4 mM) at diluted to 1 mL, the **HCA** at a higher concentration to account for the excess isopropylamine present in solution. The second portion was used to determine yield and *ee* for each product. The LCAP at 210 nm was determined using an Agilent 1100 HPLC (Column: Waters X-Bridge C18 (150x4.6mm, 3.5 um), Gradient elution: A=2 mM NH₄HCO₂ pH 10.5 in water, B=2 mM NH₄HCO₂ pH 10.5 in 90% MeCN/10% water; 5-95% B (0-3 min), 95% (3-5 min), 5 min post time; 1.5 mL/min, room temperature. 1 uL sample injection).

g) Synthetic **MBA** *ee* Determination

The calibration curve for synthetic **MBA** was found by plotting the g-factor (area of the CD at 317 divided by area of the UV at 317) against *ee* for pure enantiomers of **MBA**. One equivalent of guest (2 mM) was used relative to **HCA** (200 uL, 2 mM). From these standards a 2-point calibration curve was created,¹³ which is pictured below. The best-fit trendline of this plot was used to relate the measured CD signal at 317 nm of the unknown guest to the *ee* of the sample. The *ee* values for the unknown

synthetic samples were found by imputing the g-factor for each sample as the y-value in the trendline. The results are found in **Figure S18** and **Table S7**.

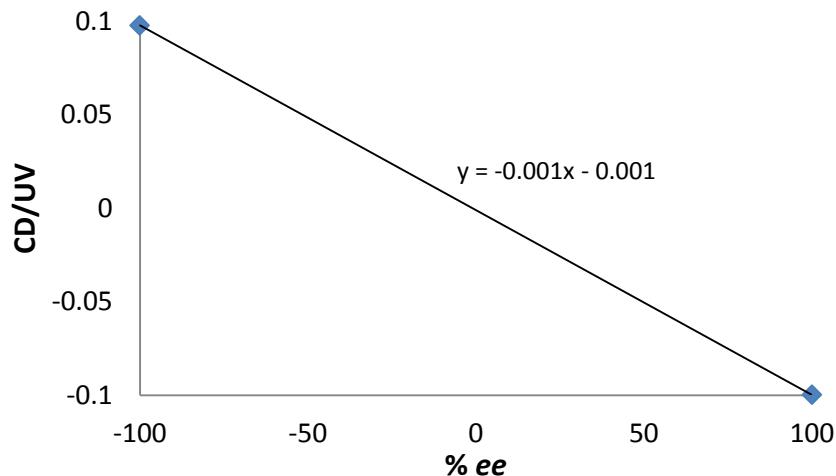


Figure S18. Calibration curve for synthetic **MBA** (2 mM) and **HCA** (4 mM) in acetonitrile at 25°C, with the CD and UV signals measured at 317 using the HPLC-CD.

Enzyme	LCAP _{210 nm} (HPLC)	% ee (Calc)	% ee (SFC) ¹⁴	% Error
TA PIG5	8.4%	-98.0	-100	2.0
ATA-234	32.7%	-96.9	-100	3.1
ATA-412	41.1%	99.2	100	0.8
ATA-303	28.2%	100.5	100	0.5
ATA-014	74.7%	99.0	100	1.0
CDX-010	91.7%	95.5	100	4.5
CDX-017	52.8%	97.3	100	2.6

Table S7. Results of the HPLC-CD analysis of the synthetic samples of **AMH**. The average error was determined to be 1.8%

h) Synthetic **CMA** *ee* Determination

The calibration curve for synthetic **CMA** was found by plotting the g-factor (area of the CD at 317 divided by area of the UV at 317) against *ee* for pure enantiomers of **CMA**. One equivalent of guest (2 mM) was used relative to **HCA** (200 uL, 2 mM). From these standards a 2-point calibration curve was created,¹³ which is pictured below. The best-fit trendline of this plot was used to relate the measured CD signal at 317 nm of the unknown guest to the *ee* of the sample. The *ee* values for the unknown synthetic samples were found by imputing the g-factor for each sample as the y-value in the trendline. The results are found in **Figure S19** and **Table S8**.

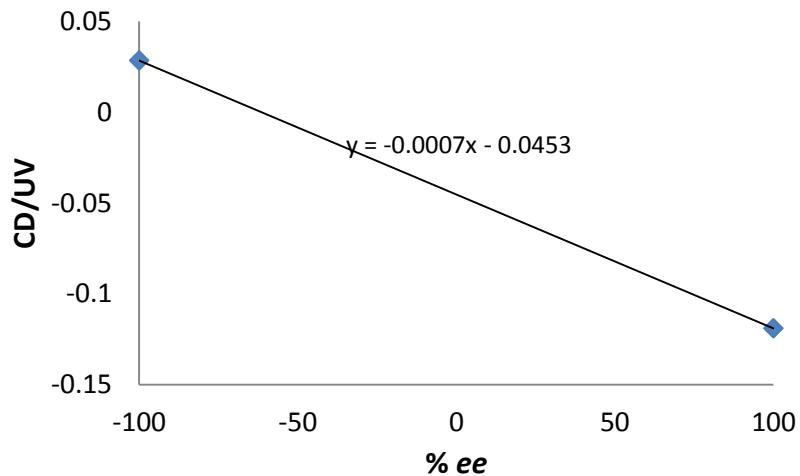


Figure S19. Calibration curve for synthetic **CMA** (2 mM) and **HCA** (4 mM) in acetonitrile at 25°C, with the CD and UV signals measured at 317 using the HPLC-CD.

Enzyme	LCAP_{210 nm} (HPLC)	% ee (Calc)	% ee (SFC)¹⁵	% Error
TA PIG5	30.8%	-104.1	-97.9	6.2
ATA-234	77.2%	-97.6	-97.7	0.1
ATA-412	89.3%	96.1	100	3.9
ATA-303	55.1%	97.9	100	2.1
ATA-014	93.5%	90.5	100	9.5
CDX-010	94.6%	92.5	100	7.5
CDX-017	94.4%	91.4	99.8	8.4

Table S8. Results of the HPLC-CD analysis of the synthetic samples of **CMA**.
The average error was determined to be 4.7%

i) Synthetic **MPP** *ee* Determination

The calibration curve for synthetic **MPP** was found by plotting the g-factor (area of the CD at 317 divided by area of the UV at 317) against *ee* for pure enantiomers of **MPP**. One equivalent of guest (2 mM) was used relative to **HCA** (200 uL, 2 mM). From these standards a 2-point calibration curve was created,¹³ which is pictured below. The best-fit trendline of this plot was used to relate the measured CD signal at 317 nm of the unknown guest to the *ee* of the sample. The *ee* values for the unknown synthetic samples were found by imputing the g-factor for each sample as

the y-value in the trendline. The results of this analysis can be found in **Figure S20** and **Table S9**.

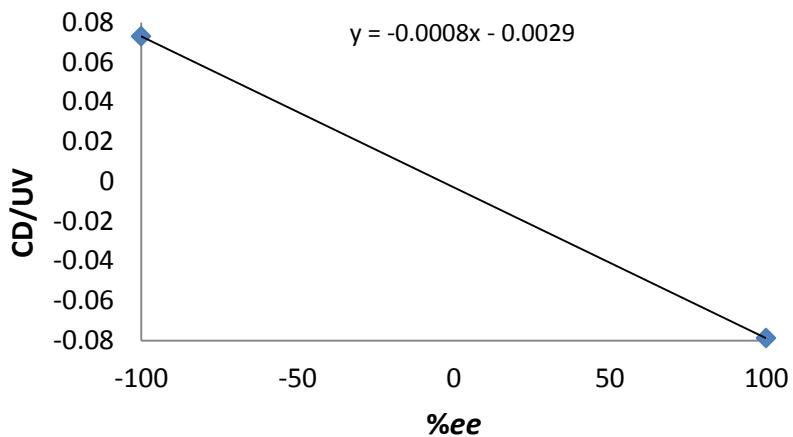


Figure S20. Calibration curve for synthetic **MPP** (2 mM) and **HCA** (4 mM) in acetonitrile at 25°C, with the CD and UV signals measured at 317 using the HPLC-CD.

Enzyme	LCAP _{210 nm} (HPLC)	% ee (Calc)	% ee (SFC) ¹⁶	% Error
TA PIG5	16.8%	-96.3	-93.9	2.4
ATA-234	81.3%	-96.0	-96.0	0.0
ATA-412	92.3%	92.7	95.7	2.9
ATA-303	71.9%	71.4	75.6	4.2
ATA-014	96.5%	48.1	49.8	1.7
CDX-010	99.5%	54.7	59.4	4.6
CDX-017	99.5%	69.9	72.6	2.7

Table S9. Results of the HPLC-CD analysis of the synthetic samples of **MPP**. The average error was determined to be 2.3%.

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 - 13) The use of 2-point calibration curves for these analyses can be justified because of the agreement found for MBA in the main text, as well as occasional spot checking to determine accuracy for the other analytes. The focus of this work is rapid *ee* determination, so more data points and repetitions would slow down the process.
 - 14) MBA *ee* determined using chiral SFC : IC-3 column (150x4.6mm, 3um); Isocratic mobile phase (6% MeOH with 25 mM IBA/94% CO₂); 3mL/min, 175 bar, 40°C; 11 min method, no post.

- 15) CMA *ee* determined using chiral SFC : OZ-3 column (150x4.6mm, 3um);
Isocratic mobile phase (6% MeOH with 25 mM IBA/94% CO2); 3mL/min, 200
bar, 40°C; 9 min method, no post.
- 16) MPP *ee* determined using chiral SFC : AD-3 column (150x4.6mm, 3um);
Isocratic mobile phase (6% IPA with 25 mM IBA/94% CO2); 3mL/min, 200 bar,
40°C; 10 min method, no post.