

One hydrogen bond doesn't make a separation or does it? Resolution of amines by diacetoneketogulonic acid

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1. Experimental section

Materials. All compounds were purchased from Aldrich and of ACS ($\geq 99\%$) quality.

Preparation of diastereomeric salts. 100 mg of (-)-2,3:4,6-Di-O-isopropylidene-2-keto-L-gulonic acid, (diacetoneketogulonic acid, DAG) was dissolved in excess amount of the related amines and the crystals were harvested immediately after appearance. Many attempts were made to crystallize DAG with S-MeBUAM (rate of evaporation was varied, as well as the crystallisation temperature) but all experiments yielded gels.

Single Crystal X-Ray Diffraction. **Diffraction** data for all compounds were collected on a Bruker DUO APEX II diffractometer¹ with graphite monochromated Mo K α 1 radiation ($\lambda = 0.71073 \text{ \AA}$) at 173 K using an Oxford Cryostream 700. Data reduction and cell refinement were performed using SAINT-Plus² and the space groups were determined from systematic absences by XPREP³ and further justified by the refinement results. In all cases, the structures were solved in the aid of X-Seed⁴ by direct methods using SHELXS-97⁵ and refined using full-matrix least-squares/difference Fourier techniques using SHELXL-97.⁵ The hydrogen atoms bound to carbon atoms were placed at idealized positions and refined as riding atoms with $U_{\text{iso}}(\text{H}) = 1.2 U_{\text{eq}}(\text{Ar-H, CH}_2)$ or $1.5 U_{\text{eq}}(\text{CH}_3)$. Diagrams and publication material were generated using PLATON⁶ and X-Seed. Experimental details of the X-ray analyses are provided in Table S1. CIFs for each structure have been deposited with the Cambridge Structural Database (CCDC 950602-950607).

¹ Bruker **2005**. *APEX2*. Version 1.0-27. Bruker AXS Inc., Madison, Wisconsin, USA.

² Bruker **2004**. *SAINTE-Plus* (including *XPREP*). Version 7.12. Bruker AXS Inc., Madison, Wisconsin, USA.

³ Bruker **2003**, *XPREP2*. Version 6.14. Bruker AXS Inc., Madison, Wisconsin, USA.

⁴ L. J. Barbour, *J. Supramol. Chem.*, **2001**, *1*, 189-191.

⁵ G. M. Sheldrick, *SHELXS-97 and SHELXL-97 Programs for crystal structure determination and refinement*. University of Göttingen, 1997.

⁶ A. L. Spek, *J. Appl. Crystallogr.* **2003**, *36*, 7-13.

Table S1 Crystal data for amine salts of DAG

Compound	(DAG ⁻)(BUAM ⁺)	(DAG ⁻)(R-MeBUAM ⁺)	(DAG ⁻)(R-PEA ⁺)	(DAG ⁻)(S-PEA ⁺)	(DAG ⁻)(S-NEA ⁺)	(DAG ⁻)(R-NEA ⁺)
CCDC no.	950602	950603	950605	950607	950606	950604
Chemical formula	(C ₁₂ H ₁₇ O ₇)(C ₄ H ₁₂ N ⁺)	(C ₁₂ H ₁₇ O ₇)(C ₅ H ₁₄ N ⁺)	(C ₁₂ H ₁₇ O ₇)(C ₈ H ₁₂ N ⁺)	(C ₁₂ H ₁₇ O ₇)(C ₈ H ₁₂ N ⁺)	(C ₁₂ H ₁₇ O ₇)(C ₁₂ H ₁₄ N ⁺)	(C ₁₂ H ₁₇ O ₇)(C ₁₂ H ₁₄ N ⁺)
<i>M_r</i>	347.40	361.43	395.44	395.44	445.50	445.50
Cell setting, space group	Orthorhombic, <i>P</i> 2 ₁ 2 ₁ 2 ₁	Orthorhombic, <i>P</i> 2 ₁ 2 ₁ 2 ₁	Monoclinic, <i>P</i> 2 ₁	Monoclinic, <i>P</i> 2 ₁	Monoclinic, <i>P</i> 2 ₁	Orthorhombic, <i>P</i> 2 ₁ 2 ₁ 2 ₁
Temperature (K)	173(2)	173(2)	173(2)	173(2)	173(2)	173(2)
<i>a</i> , <i>b</i> , <i>c</i> (Å)	6.1806(13), 14.641(3), 20.360(4)	6.3376(5), 15.4586(12), 20.0153(17)	14.4045(11), 6.2322(5), 23.4872(18)	14.634(3), 6.2305(12), 11.855(2)	13.740(5), 6.188(3), 15.056(6)	7.6206(4), 11.4755(9), 26.5274(16)
α , β , γ (°)	90.00, 90.00, 90.00	90.00, 90.00, 90.00	90.00, 103.762(2), 90.00	90.00, 102.86(3), 90.00	90.00, 113.998(8), 90.00	90.00, 90.00, 90.00
<i>V</i> (Å ³)	1842.3(7)	1960.9(3)	2048.0(3)	1053.8(4)	1169.4(8)	2319.8(3)
<i>Z</i>	4	4	4	2	2	4
<i>D_x</i> (Mg m ⁻³)	1.252	1.224	1.283	1.246	1.265	1.276
Radiation type	MoK α (λ = 0.71073)	MoK α (λ = 0.71073)				
μ (mm ⁻¹)	0.098	0.094	0.097	0.094	0.093	0.094
Crystal form, colour	rod, colourless	rod, colourless				
Crystal size (mm)	0.41 x 0.35 x 0.35	0.35 x 0.19 x 0.18	0.2 x 0.2 x 0.2	0.20 x 0.18 x 0.15	0.18 x 0.16 x 0.16	0.42 x 0.33 x 0.24
No. of measured, independent and observed reflections	9142, 4552, 3677	11503, 4035, 3545	10530, 7077, 5714	8188, 4682, 4129	6011, 4368, 3950	8259, 4679, 4396
<i>h</i> , <i>k</i> , <i>l</i> (min, max)	-8, 8; -10, 19; -27, 27	-7, 7; -17, 19; -25, 25	-17, 17; -5, 7; -28, 28	-19, 15, -8, 8, -15, 15	-16, 17; -7, 7; -17, 18	-9, 5; -4, -14; -33, 33
Θ (min, max.)	1.71, 28.40	1.66, 26.49	1.46, 25.84	2.01, 28.37	2.60, 26.51	2.35, 26.31
<i>R</i> [<i>F</i> ² > 2 σ (<i>F</i> ²)], <i>wR</i> (<i>F</i> ²), <i>S</i>	0.0374, 0.0953, 0.982	0.0323, 0.0812, 0.921	0.0382, 0.0872, 1.007	0.0351, 0.0888, 1.016	0.0429, 0.1191, 1.052	0.0365, 0.0968, 1.023
No. of parameters/restraints	274/6	236/3	516/7	262/4	298/4	298/3
$\Delta\rho_{\max}$, $\Delta\rho_{\min}$ (e Å ⁻³)	0.231, -0.168	0.192, -0.146	0.160, -0.151	0.239, -0.158	0.250, -0.214	0.285, -0.320

Table S2 Hydrogen bond metrics for the amine salts of DAG

<i>D-H...A</i>	<i>D-H</i> (Å)	<i>H...A</i> (Å)	<i>D...A</i> (Å)	<i>D-H...A</i> (°)	<i>Symmetry descriptor</i>
(DAG⁻)(BUAM⁺)*					
N24-H24A...O15*	0.91	1.85	2.7520(6)	171	x-1/2,1/2-y,-z
N24-H24B...O14*	0.91	1.92	2.8115(6)	167	x-1,y,z
N24-H24C...O15	0.91	1.93	2.8009(6)	160	
(DAG⁻)(R-MeBUAM⁺)					
N25-H25A...O15	0.91	1.93	2.8360(2)	169	
N25-H25B...O14*	0.91	1.94	2.8087(2)	159	x-1,y,z
N25-H25C...O15*	0.91	1.86	2.7735(2)	175	x-1/2,1/2-y,-z
(DAG⁻)(R-PEA⁺)					
N28-H28A...O14*	0.94	1.89	2.8210(2)	174	x,y-1,z
N28-H28B...O15	0.93	1.95	2.8500(2)	161	
N28-H28B...O1	0.93	2.52	3.0806(2)	119	
N28-H28C...O43*	0.88	2.03	2.8907(2)	166	x,y-1,z
N56-H56A...O15	0.94	1.93	2.8640(2)	172	
N56-H56B...O42*	0.92	1.83	2.7468(2)	177	x,y-1,z
N56-H56C...O43	0.85	2.04	2.8471(2)	158	
N56-H56C...O31	0.85	2.60	3.079(2)	116	
N56-H56C...O29	0.85	2.717	3.311(2)	128	
(DAG⁻)(S-PEA⁺)					
N28-H28A...O15	0.91	1.90	2.7688(6)	161	
N28-H28A...O3	0.91	2.56	3.1319(6)	121	
N28-H28B...O15*	0.91	1.96	2.8464(6)	165	1-x,y-1/2,-z
N28-H28C...O14*	0.91	1.88	2.7898(6)	174	x,y-1,z
C23-H23...O6*	0.95	2.55	3.5011(7)	177	x,y,z-1
C27-H27B...O3*	0.98	2.44	3.3967(7)	165	1-x,y-1/2,-z
(DAG⁻)(S-NEA⁺)					
N32-H32A...O15	0.91	1.82	2.7334(11)	175	
N32-H32B...O15*	0.91	2.00	2.8899(12)	165	1-x,1/2+y,-z
N32-H32C...O14*	0.91	1.92	2.8352(11)	177	x,1+y,z
C30-H30...O6	1.00	2.68	3.671(1)	169	
(DAG⁻)(R-NEA⁺)					
N32-H32A...O15	0.92	1.81	2.7203(2)	168	
N32-H32B...O14*	0.92	1.80	2.7237(2)	175	1-x,-1/2+y,1/2-z
N32-H32C...O6	0.92	1.98	2.8753(2)	162	
C5-H5A...O15*	0.99	2.40	3.3777(3)	170	1-x,-1/2+y,1/2-z

* For (DAG⁻)(BUAM⁺) only one of the disorder is included. The hydrogen bonding of the other disorder is virtually the same.

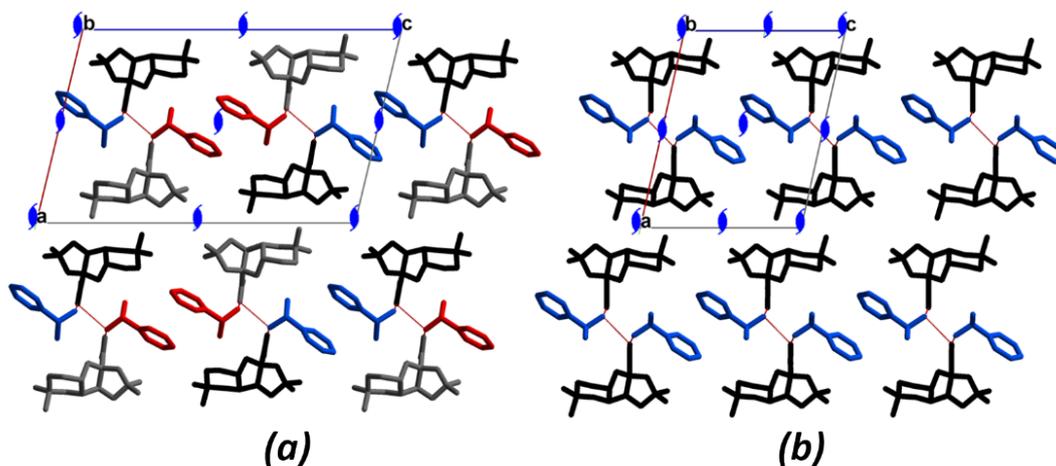


Figure S1 Packing diagrams of (DAG⁻)(R-PEA⁺) (DAG⁻)(S-PEA⁺), *a* and *b* respectively. The symmetry equivalent molecules are coloured accordingly and the unit cells are presented with the positions of the 2 fold screw axes.

Table S3 Torsion angles of the -COO⁻ moiety of DAG in the different structures

	<i>C10-C2-C13-O14</i> (°)
(DAG ⁻)(BUAM ⁺)	0.1
(DAG ⁻)(R-MeBUAM ⁺)	-5.9
(DAG ⁻)(R-PEA ⁺) mol A	-0.5
mol B	-2.7*
(DAG ⁻)(S-PEA ⁺)	-12.1
(DAG ⁻)(S-NEA ⁺)	-10.8
(DAG ⁻)(R-NEA ⁺)	-50.6

* C38-C30-C41-O42

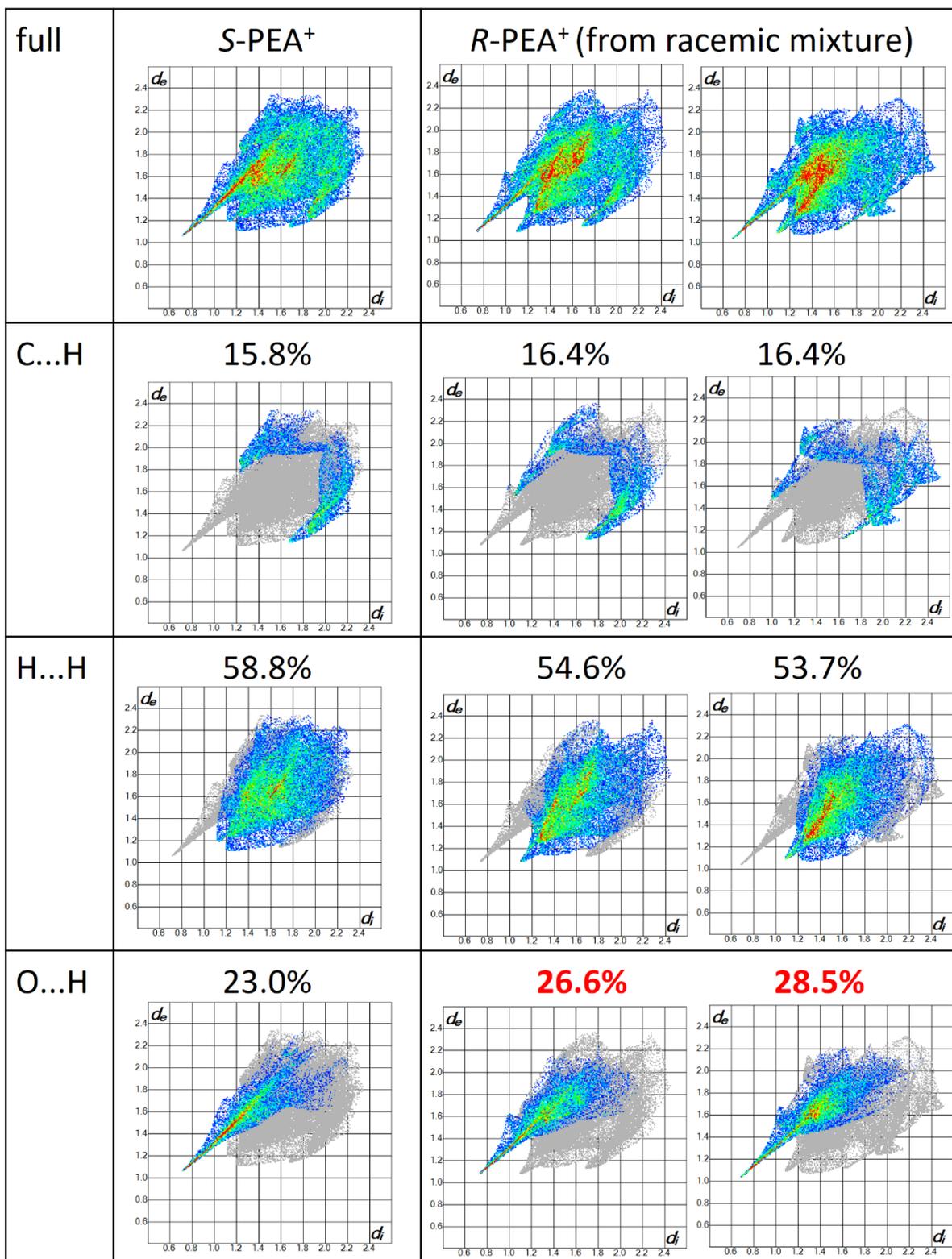


Figure S2 Fingerprint plots for the guest components *S*-PEA⁺ and *R*-PEA⁺ (full and highlighted sections of the relevant interactions, such as C...H, H...H and O...H) in structures (DAG⁻)(*S*-PEA⁺) and (DAG⁻)(*R*-PEA⁺), respectively. Note the higher amount of O...H contacts of the *R*-PEA⁺ cation (red) in the crystal obtained from the racemic mixture of the amine.

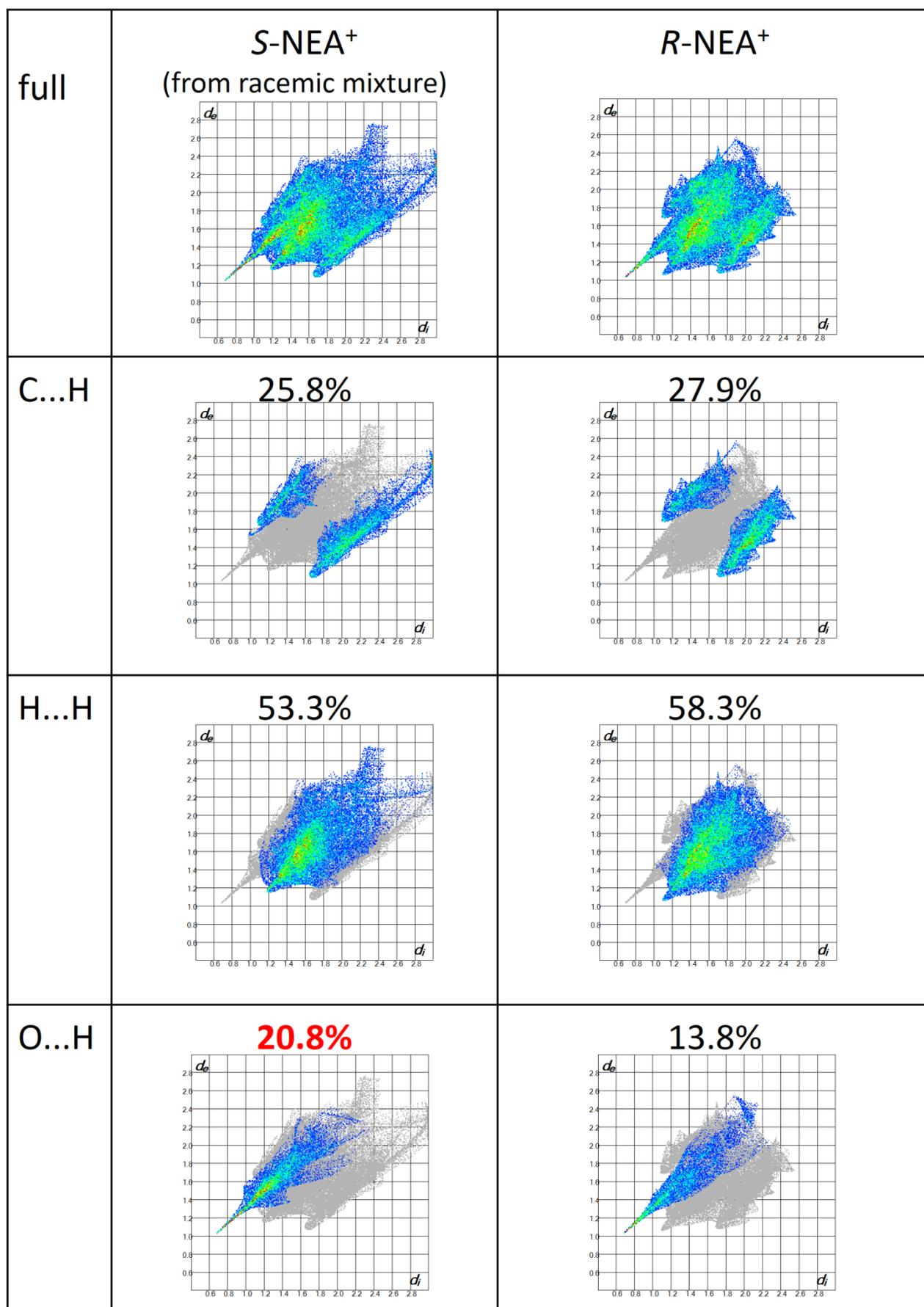


Figure S3 Fingerprint plots for the guest components *S*-NEA⁺ and *R*-NEA⁺ (full and highlighted sections of the relevant interactions, such as C...H, H...H and O...H) in structures (DAG⁻)(*S*-NEA⁺) and (DAG⁻)(*R*-NEA⁺), respectively. Note the higher amount of O...H contacts of the *S*-NEA⁺ cation (red) in the crystal obtained from the racemic mixture of the amine.

Lattice-energy calculations

The crystal structures were energy-minimised in full (including the unit-cell parameters) with the experimental space-group symmetry imposed. The energy-minimisations were carried out in *GRACE*¹, which in turn calls *VASP*²³⁴ for single-point pure density functional theory calculations. The Perdew-Burke-Ernzerhof (PBE) exchange-correlation functional⁵ was employed. *GRACE* adds a dispersion correction⁶ and an efficient energy-minimisation algorithm that takes full advantage of chemical information in the form of delocalized internal coordinates and approximate first and second derivatives. The energies are the total lattice enthalpies at $T = 0$ K and $P = 0$ GPa. This is the same method and these are the same energies that were used so successfully in the 2007 crystal structure prediction Blind Test⁷. The method was further validated on 225 molecular single crystal structures⁸. The calculation of lattice energies combining ionic interactions, hydrogen bonds, $\pi \cdots \pi$ interactions and Van der Waals interactions was validated by means of a successful crystal structure prediction on pyridinium chloride⁹. In addition to the lattice energies, the calculations also provide idealised positions for the hydrogen atoms.

The $-\text{COO}$ torsion angles in S-PEA, R-PEA ($Z'=2$), S-NEA and R-NEA are 12, 0, 3, 11 and 51°, respectively. The energy difference between the geometries of the DAG molecules in R-NEA and S-NEA is 0.83 kcal/mol in favour of R-NEA as determined from a dispersion-corrected PBE calculation.

2. Vapour sorption experiments

50 g of DAG was dried, sieved (30 μm), spread evenly in a Petri dish (\varnothing 70 mm) and placed in a vacuum desiccator which contained 100 ml of the racemic amine (PEA or NEA). The system was incubated for 30 mins on 50 °C to obtain an acceptable vapour pressure of the amine (ca. 4 mmHg for PEA and 0.02 mmHg for NEA).

Powder X-ray diffraction experiments were carried out on a Bruker D8 diffractometer using Cu-K α radiation. The sample was ground to a fine powder and loaded into an aluminium tray. Where available these spectra were compared with those determined from the single crystal structures.

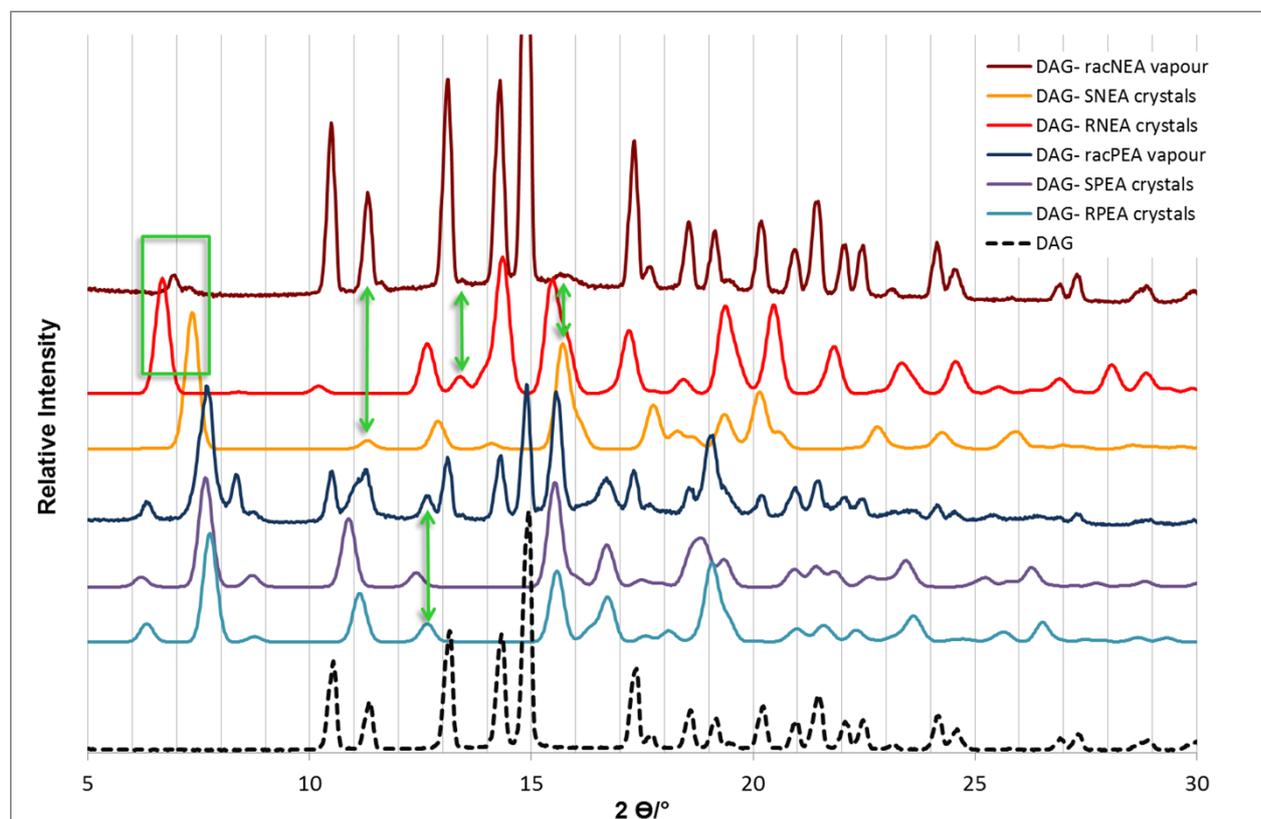


Figure S4 PXR D patterns obtained from DAG exposed to vapor of the different amines are compared to the single crystal structures obtained from crystallization experiments.

¹ M. A. Neumann, *GRACE*, Avant-garde Materials Simulation, Freiburg, Germany (<http://www.avmatsim.eu>).

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