Supplementary Material

A Comparison Study of Roseolumiflavin Solvates: Structural and Energetic Perspective on Their Stability

Takin Haj Hassani Sohi, Felix Maass, Constantin Czekelius, Vera Vasylyeva*

IR analysis

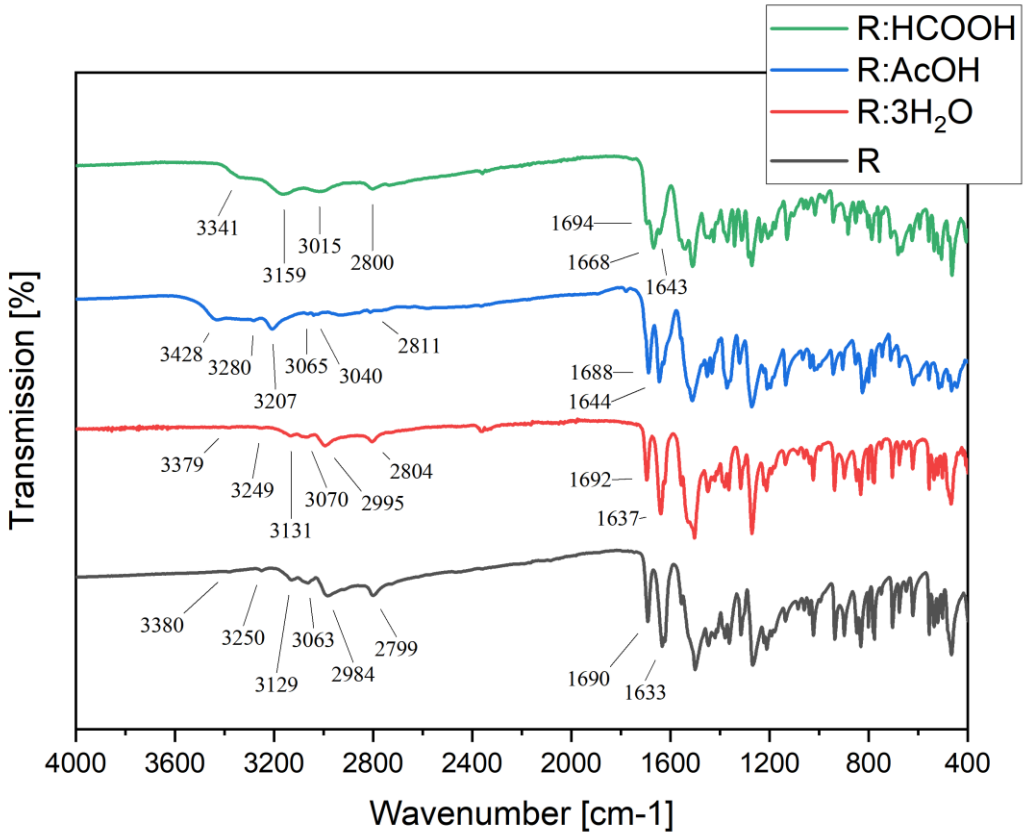

*Figure S1: Comparison of IR spectra of **R:HCOOH**, **R:AcOH**, **R:3H$_2$O** with **R**. Characteristic bands are highlighted.*

In comparison to **R**, for **R:AcOH** a new broad band at 3428 cm^{-1} appears which likely originates from O−H stretching vibration and overlaps the high N-H stretching band of pure **R** at 3380 cm^{-1}. Likewise, the band at 3207 cm^{-1} may be caused by intermolecular bonded O−H group. The amide C=O vibration at 1644 cm^{-1} is blue-shifted by +11 cm^{-1} while the band at 1689 cm^{-1} remains unmodified. Strong blue-shifts for the C−H vibrations at 2811 cm^{-1} by +12 cm^{-1} and the NC−H vibration at *ca.* 3030 cm^{-1} by *ca.* +36 cm^{-1} evince noticeable effects on the methyl group bonds.

R:3H$_2$O contains slightly blue-shifted C=O vibrational bands by 4 to 5 cm^{-1}, the N−H stretching bands are unaltered. The NC−H hydrogen stretching band at 2804 cm^{-1} is blue-shifted by +5 cm^{-1}, so are the bands for C−H vibrations at 3070 cm^{-1} by +7 cm^{-1} and 2995 cm^{-1} by +11 cm^{-1}, indicating substantial increase in bond strength in the new packing environment.

The spectrum for **R:HCOOH** displays a broad band at 3341 cm^{-1} representing the O-H vibration band of the solvent molecule. Here, the N-H stretching vibrational mode of the imide group at 3159 cm^{-1} is overlapped by it. The broad band at 3015 cm^{-1} is likely caused by C-H stretching vibrations of the **R** methyl groups, blue-shifted by +26 cm^{-1}. Also, the C=O stretching bands of the imide group at 1694 cm^{-1} and 1643 cm^{-1} are blue-shifted by +5 cm^{-1} and +10 cm^{-1}, respectively. At 1668 cm^{-1} a new band arises, which is to be identified as the C=O stretching mode of the acid unit.

Simulated PXRD patterns

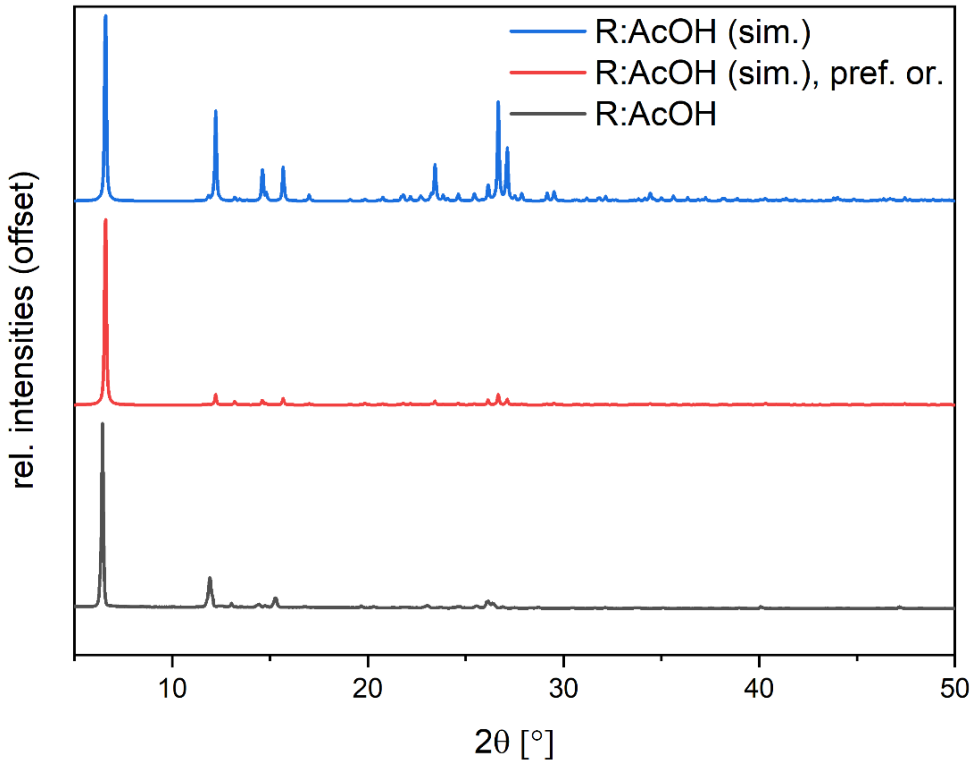

*Figure S2: Experimental powder pattern of **R:AcOH** compared to simulated patterns of **R:AcOH** and adjusted simulated pattern for consideration of preferred orientation from single crystal data.*

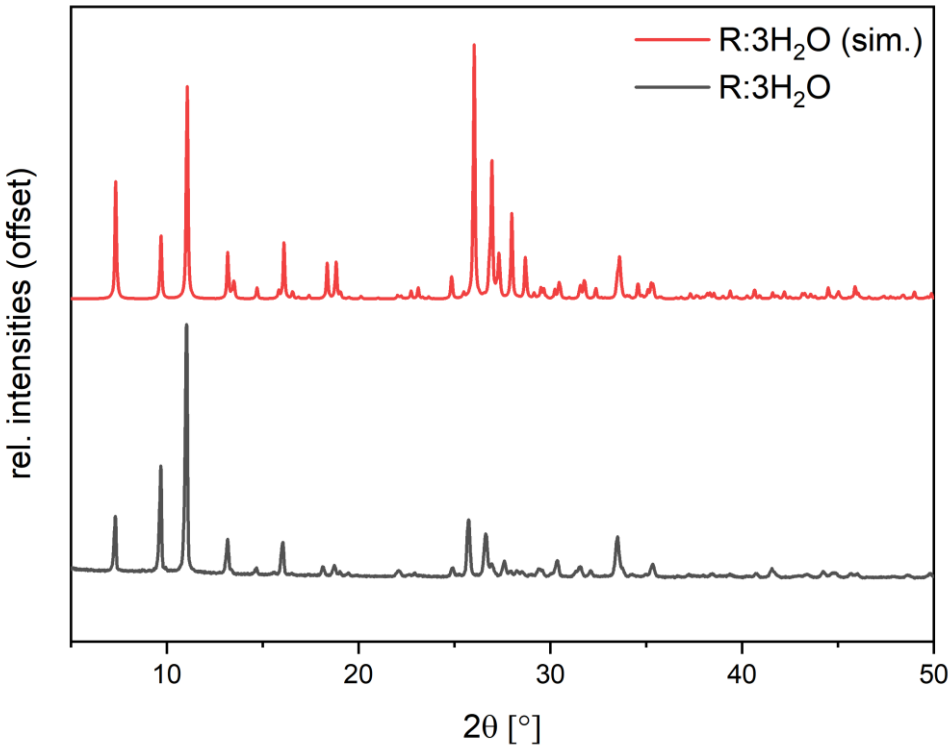

*Figure S3: Experimental powder pattern of **R:3H₂O** compared to simulated pattern from single crystal data.*

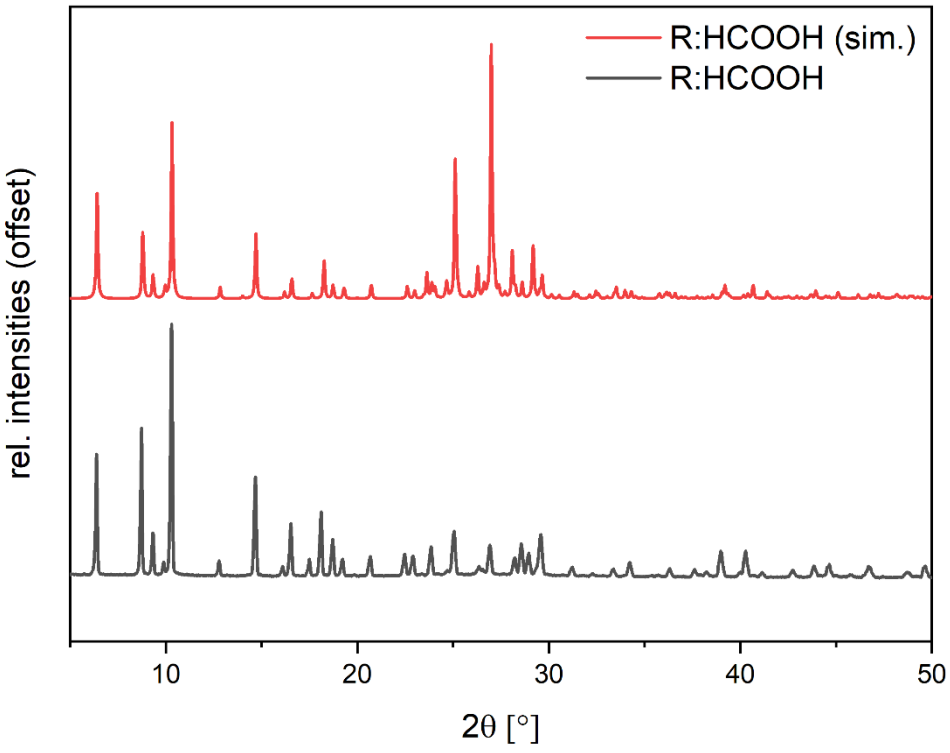

*Figure S4: Experimental powder pattern of **R:HCOOH** compared to simulated pattern from single crystal data.*

Crystal structures of R:AcOH, R:AcOH:H_2O, R:3H_2O and R:HCOOH

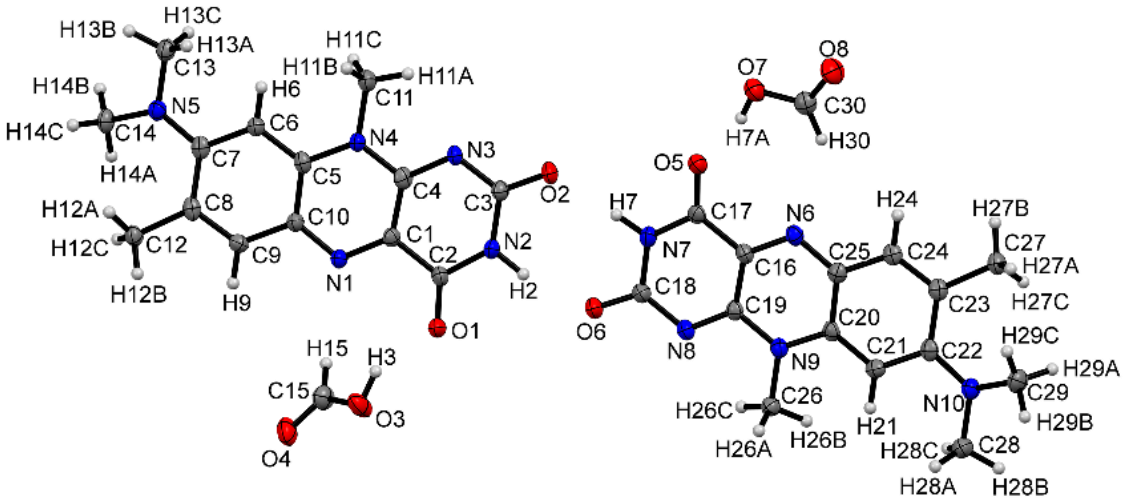

*Figure S5: Asymmetric unit of **R:HCOOH**. View along the crystallographic a-axis.*

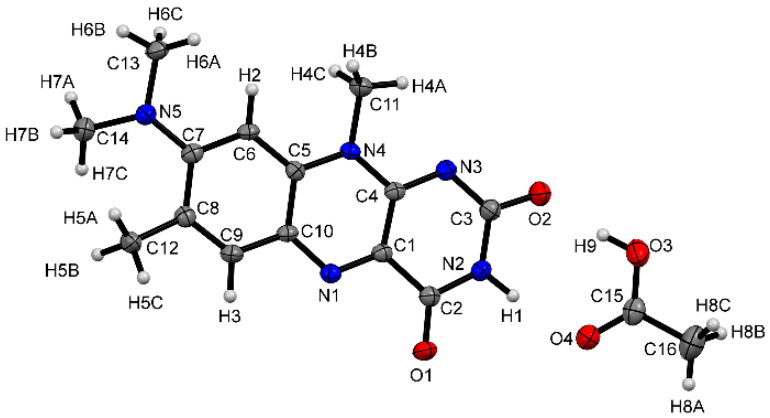

*Figure S6: Asymmetric unit of **R:AcOH**. View along the crystallographic a-axis.*

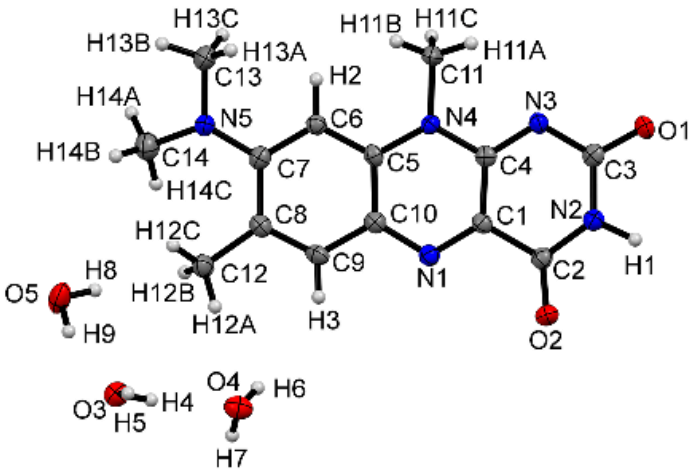

*Figure S7: Asymmetric unit of **R:3H_2O**. View along the crystallographic a-axis.*

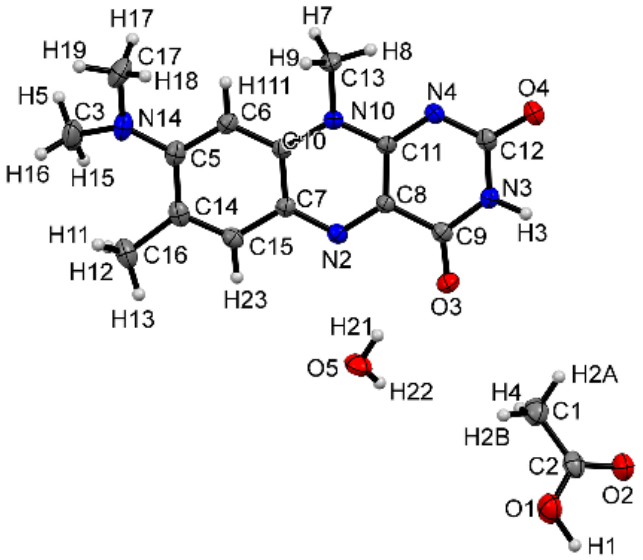

*Figure S8: Asymmetric unit of **R:AcOH:H₂O**. View along the crystallographic a-axis.*

Overview of the hydrogen bonds

D-H···A	D−H [Å]	H···A [Å]	D···A [Å]	D−H···A [°]
N1-H1···O4	0.94(3)	1.95(3)	2.879(2)	170(3)
O3-H9···O2	0.88(4)	1.72(4)	2.596(2)	173(4)
C6-H2···O1	0.95(2)	2.53(2)	3.472(3)	172(2)
(intra) C11-H4A···N3	0.96(2)	2.20(2)	2.725(3)	112.8(18)
C16-H8B···O2	0.95(3)	2.47(3)	3.420(3)	173(3)

*Table S1: Geometries of hydrogen bonded interactions of **R:AcOH**.*

D-H···A	D−H [Å]	H···A [Å]	D···A [Å]	D−H···A [°]	A−H···A [°]	Sum(XY,YZ)
N2-H1···O5	0.99(6)	1.78(6)	2.774(5)	174(6)		
O3-H4···O4	0.83(4)	2.06(4)	2.887(4)	176(4)		
O3-H5···O4	0.93(5)	1.91(5)	2.833(5)	172(4)		
O4-H6···N3	0.77(7)	2.29(7)	2.981(5)	151(7)		
O4-H7···O1	0.79(5)	2.00(5)	2.759(4)	160(5)		
O5-H8···O1	0.89(6)	1.87(6)	2.752(4)	168(5)		
O5-H9···O3	0.89(5)	1.95(5)	2.805(5)	161(4)		
C11-H11A···N3	0.98	2.52	3.429(6)	154		
(intra) C11-H11A···N3	0.98	2.33	2.698(5)	101'	99'	354

*Table S2: Geometries of hydrogen bonded interactions of **R:3H₂O**.*

D-H···A	D−H [Å]	H···A [Å]	D···A [Å]	D−H···A [°]
O1-H1···O5	1.02(3)	1.54(3)	2.5483(19)	170(3)
N3-H3···O2	0.91(2)	2.05(2)	2.952(2)	173.1(15)
O5-H21···O3	0.831(12)	2.066(14)	2.8608(17)	160(2)
O5-H22···O4	0.835(16)	1.881(16)	2.7077(18)	170.5(19)
C13-H7···O4				
(intra) C13-H8···N4	0.98	2.58	3.461(2)	150
C17-H18···O3	0.98	2.26	2.723(2)	108
C15-H23···O1	0.98	2.52	3.386(2)	147
C6-H111···O4	0.949(18)	2.406(18)	3.352(2)	175.4(13)

*Table S3: Geometries of hydrogen bonded interactions of **R:AcOH:H₂O**.*

D-H···A	D−H [Å]	H···A [Å]	D···A [Å]	D−H···A [°]
N2-H2···O6	0.95(8)	1.91(7)	2.828(6)	163(6)
O3-H3···O1	0.89(12)	1.78(12)	2.577(5)	148(9)
N7-H7···O2	0.92(7)	1.86(8)	2.768(6)	175(7)
O7-H7A···O5	0.82	1.8	2.598(6)	165
C11-H11A···N3	0.96	2.25	2.719(7)	109
C26-H26C···N8	0.96	2.32	2.694(7)	102

*Table S4: Geometries of hydrogen bonded interactions of **R:HCOOH**.*

Lattice Energy and AIM calculations

The lattice Energy E_{lat} was calculated following the equation (1)

$$E_{lat} = \frac{E_{iss}}{Z} - \frac{\sum E_{isg,n}}{Z'} \quad (1)$$

where E_{lat} represents the lattice energy, E_{iss} the ideal static solid energy, E_{isg} the ideal static gas energy for each molecule, as well as Z and Z' the respective crystallographic parameters.

The binding energy (BE) in kcal/mol for neutral HBs based on the electron density at the BCPs can be estimated via following equation (2) provided by Emamian et al. [33]

$$BE \approx -223.08 \times \rho(r_{BCP}) + 0.7423 \quad (2)$$

With the electron density ρ in a.u. provided by the MultiWFN program package [22].

Crystal Explorer molecular interaction energies

Structure	Crystal Explorer model interaction energies calculations						
	N	Sym.op.	E_{ele}	E_{pol}	E_{dis}	E_{rep}	E_{tot}
R	2	x+1/2, -y+1/2, z+1/2	-23.7	-12.9	-21.9	25.8	-37.7
	1	-x, -y, -z	-45.6	-10.1	-116.9	71.5	-113.4
	1	-x, -y, -z	-56.1	-11.8	-122.3	76.8	-127.1
	1	-x, -y, -z	-70.8	-20.8	-14	95.5	-43.4
R:AcOH	1	x, y, z	-103.6	-24.4	-13.4	125.1	-62.0
	1	-x, -y, -z	-44.9	-11.7	-108.7	66.0	-110.0
	1	-x, -y, -z	-30.1	-7.6	-56.8	35.6	-64.9
	1	-x, -y, -z	-34.8	-11.8	-59.9	44.1	-70.5
	2	2-x, 1-y, 1-z	-21.6	-12.0	-21.9	26.0	-34.7
R:AcOH:H_2O	1	x, y, z	-41.0	-8.9	-8	35.6	-34.8
	1	1-x, 1-y, 2-z	-26.9	-5.4	-6.1	24.9	-22.4
	1	1-x, 0.5+y, 1.5-z	-48.8	-9.9	-5.4	57.2	-28.3
	1	-x, -y, -z	-27.6	-8.6	-66.4	37.1	-70.5
	1	-x, -y, -z	-53.4	-11.1	-113.6	76.6	-116.3
	2	x, -y+1/2, z+1/2	-20.0	-10.3	-14.0	16.1	-30.9
R:3H_2O	1	-x, -y, -z	-44.8	-9.2	-98.8	57.8	-104.6
	1	-x, -y, -z	-47.5	-9.8	-105.3	62.3	-110.7
	2	x, y, z	-18.3	-9.7	-16.4	13.2	-32.6
	1	x, y, -1+z	-45.2	-10.3	-5.5	44.9	-32.4
	1	x, 1+y, -1+z	-42.0	-9.7	-5.7	51.0	-25.1
	1	1-x, 1-y, -z	-42.1	-8.8	-4.1	45.7	-26.5
	1	1-x, 1-y, -z	-20.0	-8.3	-10.4	29.7	-18.0
R:HCOOH	1	x, y, z	-71.0	-20.7	-14.3	99.2	-41.6
	2	x, y, z	25.5	-9.8	-114.2	70.0	-36.5
	2	-x, y+1/2, -z	-25.8	-10.3	-15.7	24.9	-33.2
	1	x, y, z	-75.3	-19.1	-12.5	74.6	-58.5

Table S5: Crystal Explorer model interaction energies calculations, overview of strongest molecular interaction energy contributions in 3.8 Å cluster on central flavin unit with verbose parameters.

The scale factors used in Crystal Explorer molecular interaction energy calculations for CE-B3LYP (B3LYP/6-31G(d,p) electron densities are: k_{ele}=1.057, k_{pol}=0.74, k_{disp}=0.871 and k_{rep}=0.618.