Insight into amoxicillin sodium heterosolvates and non-solvated form: crystal structures, phase transformation behaviors and desolvation mechanism

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Computational Analysis

The interaction energy ($\Delta E_{\rm C}({\rm A-B})$) between methanol and amoxicillin sodium of S_{M-M} could be calculated by the following equation¹⁻³,

$\Delta E_{\rm C}({\rm A-B}) = \Delta E({\rm A-BC}) - \Delta E({\rm A-C})$	(1)
$\Delta E(\text{A-BC}) = E(\text{ABC}) - E(\text{A}) - E(\text{BC})$	(2)
$\Delta E(A-C) = \Delta E(AC) - \Delta E(A) - \Delta E(C)$	(3)

Therefore,

$$\Delta E_{\rm C}({\rm A-B}) = E({\rm ABC}) - E({\rm BC}) - E({\rm AC}) + E({\rm C})$$
(4)

The interaction energy ($\Delta E_A(B-C)$) between methanol and methyl acetate of S_{M-M} could be calculated as follows

$$\Delta E_{A}(B-C) = E(ABC) - E(AB) - E(AC) + E(A)$$
(5)

where molecule A, B, and C represent amoxicillin sodium, methanol and methyl acetate, respectively.



Figure S1. Different structures of S_{M-M} in the computational analysis.



Figure S2. The PXRD patterns of $S_{M\text{-}M}$ before and after drying.



Figure S3. The PXRD patterns of S_{M-E} before and after drying.





Figure S5. The FTIR spectra of Amoxicillin sodium form I and three heterosolvates.



Figure S6. Polarizing microscopy images of three heterosolvates.



Figure S7. Experimental and simulated PXRD patterns of form I and S_{M-M} .



Figure S8. Coordinate bonds in crystal structure (a. S_{M-M} , b. Form I).



Figure S9. Detailed distribution of different interactions in form I.



Figure S10. Detailed distribution of different interactions in S_{M-M} .



Figure S11. TGA curves of three solvates using different heating rates: (a) S_{M-M} (b) S_{E-M} (c) S_{M-E}



Figure S12. DSC curves of these three solvates using different heating rates: (a) S_{M-M}
(b) S_{E-M} (c) S_{M-E} (d) S_{M-M} and S_{E-M} with 2 K/min (wide endothermic peaks are marked with dotted line)



Figure S13. HSM images of S_{E-M} during the heating process.



Figure S14. HSM images of S_{M-E} during the heating process.

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	D-H···A	d(D-H), Å	d(H…A), Å	d(D-A), Å	∠(DHA), °
Form I	O₅-H…O₂	0.942	1.817	2.565	133.580
	C_{15A} -H···O ₄	0.93	1.992	2.875	157.818
S_{M-M}	O_{MT} -H···O _{MAC}	0.848	2.337	2.863	174.366
	N_2 -H···O ₁	0.880	2.063	2.941	175.080
	O ₅ -H…O ₂	0.840	1.808	2.610	159.150

Table S1 Relevant hydrogen bond data of form I and $S_{M\mbox{-}M}$

Table S2 The relevant data in the calculation of the packing coefficient C_k

	$V_{\rm mol}$	V_{cell}	$C_{ m k}$
Form I	337.84	1852.9	0.7293
Structure 2	372.71	2388.6	0.6322
S_{M-M}	442.05	2388.6	0.7403

Notes and references

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