

1,2,3-Trihydroxybenzene–1,3,5-triazine (1/1)

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Key indicators

Single-crystal X-ray study

 $T = 100\text{ K}$ Mean $\sigma(\text{C}-\text{C}) = 0.003\text{ \AA}$ R factor = 0.050 wR factor = 0.107

Data-to-parameter ratio = 14.5

For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

In the title molecular co-crystal, $\text{C}_6\text{H}_6\text{O}_3 \cdot \text{C}_3\text{H}_3\text{N}_3$, two hydrogen-bonded $R_4^4(18)$ tetrameric arrangements of molecules involving symmetry-related $\text{O}-\text{H} \cdots \text{N}$ hydrogen bonds link molecules of 1,2,3-trihydroxybenzene and 1,3,5-triazine to form an infinite double-chain motif. The one-dimensional array associates with neighbouring strands, *via* $\text{C}-\text{H} \cdots \text{O}$ interactions, to form supramolecular sheets that are stacked together by $\pi-\pi$ interactions in a three-dimensional assembly.

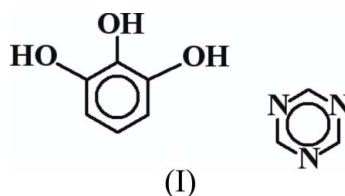
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Comment

Understanding the nature of non-covalent interactions is essential for the development of crystal engineering, in order to facilitate the rational design of supramolecular structures (Desiraju, 1989, 2005; Braga, 2003). As an extension of our studies of supramolecular synthons and crystal packing in molecular co-crystals formed by 'acidic' and 'basic' components, we now report the crystal structure of a (1/1) adduct, (I), of pyrogallol (1,2,3-trihydroxybenzene) and 1,3,5-triazine.



In the crystal structure of a (1/1) complex of pyrogallol and pyrimidine (Dobrzańska, 2005), two distinct synthons were identified, namely a heterosynthon formed *via* $\text{O}-\text{H} \cdots \text{N}$ hydrogen bonds and a homosynthon formed *via* weaker poorly directed $\text{O}-\text{H} \cdots \text{O}$ hydrogen bonds, coded as $R_4^4(18)$ and $R_2^2(10)$ graph sets, respectively. The crystal structure was stabilized by offset $\pi-\pi$ and $\text{C}-\text{H} \cdots \pi$ interactions, resulting in a herringbone packing mode. The same heterosynthon was also found in another co-crystal, of pyrogallol and hexamethylenetetramine, where a three-dimensional supramolecular framework was generated by $\text{C}-\text{H} \cdots \pi$ (arene) interactions (Tremayne & Glidewell, 2000).

The title co-crystal was prepared in order to investigate the effect on the hydrogen-bonding motif of introducing an additional N acceptor site in the heterocyclic ring. The asymmetric unit consists of one molecule of each of pyrogallol and 1,3,5-triazine (Fig. 1). The molecules are held together by hydrogen-bonded $\text{O1}-\text{H1} \cdots \text{N1}$, $\text{O2}-\text{H2} \cdots \text{N3}^i$ and $\text{O3}-\text{H3} \cdots \text{N2}^{ii}$ interactions (symmetry codes as in Table 1). This facilitates the formation of an infinite double-chain along [010] consisting of $R_4^4(18)$ tetrameric arrangements. The one-dimensional hydrogen-bonded chains of supramolecular

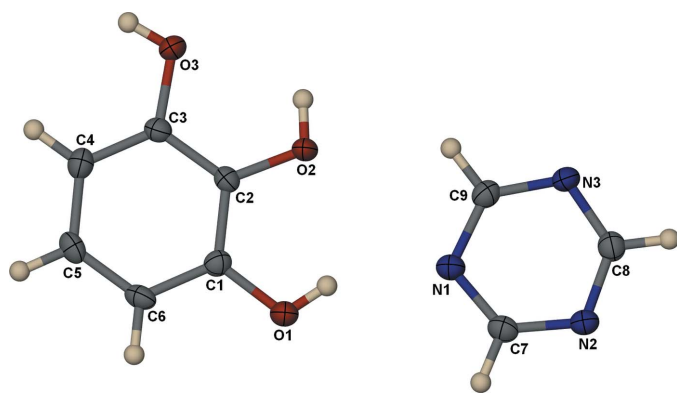


Figure 1
The asymmetric unit of (I), with atom labels and 50% probability displacement ellipsoids.

heterosynthons are further linked to one another *via* C5–H5···O1ⁱⁱⁱ [symmetry code: (iii) $\frac{3}{2} - x, \frac{1}{2} + y, \frac{3}{2} - z$] interactions [C···O = 3.448 (3) Å], to form supramolecular sheets (Fig. 2). Moreover, benzene and triazine rings from adjacent parallel sheets interact *via* offset π – π interactions (centroid···centroid distances 3.418 and 3.621 Å), to form a three-dimensional assembly (Fig. 3).

Only $R_4^4(18)$ heterosynthons formed *via* O–H···N hydrogen bonding are present in the structure of (I), and this motif seems to be favoured in supramolecular structures comprising pyrogallol and compounds containing two or more N acceptor sites.

Experimental

Colourless crystals of (I) suitable for single-crystal X-ray diffraction were obtained by slow evaporation of an ethanolic solution of 1,2,3-trihydroxybenzene and 1,3,5-triazine (1:1 molar ratio) at room temperature.

Crystal data

$C_6H_6O_3 \cdot C_3H_3N_3$
 $M_r = 207.19$
 Monoclinic, $P2_1/n$
 $a = 8.7299$ (8) Å
 $b = 10.8999$ (10) Å
 $c = 9.7586$ (8) Å
 $\beta = 98.363$ (2)°
 $V = 918.71$ (14) Å³
 $Z = 4$

$D_x = 1.498$ Mg m⁻³
 Mo $K\alpha$ radiation
 Cell parameters from 2011 reflections
 $\theta = 2.8$ – 27.1 °
 $\mu = 0.12$ mm⁻¹
 $T = 100$ (2) K
 Block, colourless
 $0.27 \times 0.25 \times 0.20$ mm

Data collection

Bruker APEX CCD area-detector diffractometer
 ω scans
 Absorption correction: multi-scan (SADABS; Sheldrick, 1997)
 $T_{\min} = 0.666$, $T_{\max} = 0.977$
 5630 measured reflections

2011 independent reflections
 1049 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.062$
 $\theta_{\text{max}} = 27.1$ °
 $h = -8 \rightarrow 11$
 $k = -13 \rightarrow 11$
 $l = -11 \rightarrow 12$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.050$
 $wR(F^2) = 0.107$
 $S = 0.89$
 2011 reflections
 139 parameters

H-atom parameters constrained
 $w = 1/[\sigma^2(F_o^2) + (0.0395P)^2]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.20$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.20$ e Å⁻³

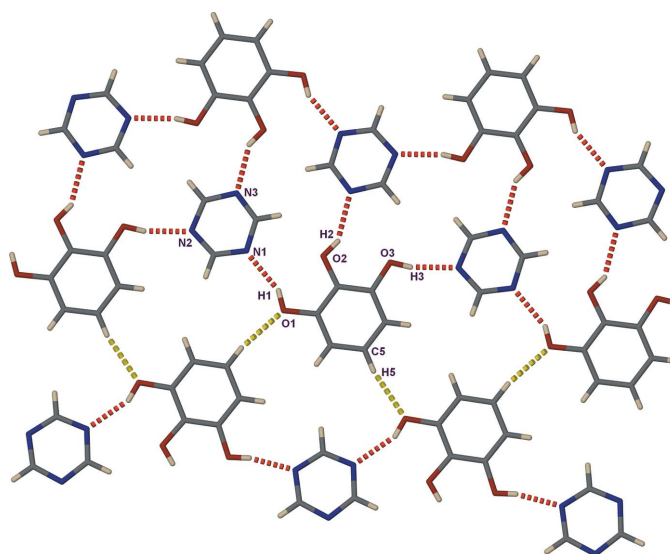


Figure 2
A perspective view of a two-dimensional supramolecular sheet in the structure of (I). Hydrogen bonds are shown as dashed lines (N–H···N indicated in red and C–H···O in yellow).

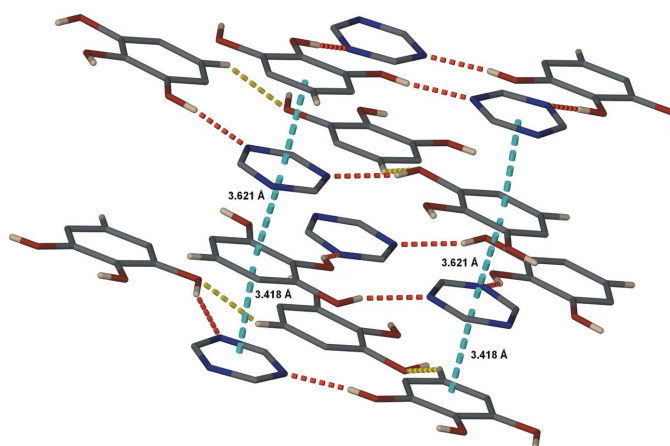


Figure 3
A capped-stick representation, showing the offset π – π interactions in the crystal packing of (I) (dashed blue lines). Dashed red and yellow lines represent N–H···N and C–H···O hydrogen bonds, respectively.

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
O1–H1···N1	0.84	2.08	2.863 (2)	155
O2–H2···N3 ⁱ	0.84	2.14	2.892 (2)	149
O3–H3···N2 ⁱⁱ	0.84	1.96	2.781 (2)	167

Symmetry codes: (i) $-x, -y + 1, -z + 1$; (ii) $x, y + 1, z$.

H atoms were positioned geometrically, with C–H = 0.95 Å and O–H = 0.84 Å, and were constrained to ride on their parent atoms, with $U_{\text{iso}}(\text{H}) = 1.2$ times $U_{\text{eq}}(\text{C}, \text{O})$.

Data collection: SMART (Bruker, 2001); cell refinement: SAINT (Bruker, 2002); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: X-SEED (Atwood & Barbour, 2003; Barbour, 2001); software used to prepare material for publication: X-SEED.

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