5,6,7,8-Tetrahydro-[1,2,4]triazolo[5,1-b]quinazolin-9(4H)-one

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The triazole ring in the title molecule, C9H10N4O, is not quite coplanar with the six-membered ring to which it is fused, the dihedral angle between the two least-squares planes being 2.52 (6)°. In the crystal, a layered structure is formed by N—H···N and C—H···O hydrogen bonds plus slipped π-stacking interactions, with the fused cyclohexene rings projecting to either side.

Structure description

Compounds containing nitrogen heterocycles make up a significant portion (approximately 60%) of small drug molecules that have been approved by the FDA (Ramli & Essassi, 2015; Martins et al., 2015). Quinazoline is a frequently occurring structural feature in natural products and pharmaceutically active molecules, which possess a range of useful biological properties, including anti-SARS-CoV-2 (e.g. Karan et al., 2021), anticancer (e.g. Zhao et al., 2021), antiviral (e.g. El-Shershaby et al., 2021), antimicrobial, anti-inflammatory (e.g. Zhang et al., 2020), and antifungal activities (e.g. Ibrahim et al., 2021).

A puckering analysis of the C2–C7 ring of the title compound (Fig. 1) gave the parameters Q = 0.4922 (12) Å, θ = 129.71 (14)° and ϕ = 326.36 (18)°. This conformation is quite similar to a half-chair form. The C8/N2/C9/N3/N4 ring is closer to planarity than is the C1/C2/C7/N1/C8/N4 ring (r.m.s. deviations of the fitted atoms are 0.0128 and 0.0042 Å, respectively) and the dihedral angle between their mean planes is 2.52 (6)°. In
the crystal, N1—H1⋯N3 hydrogen bonds (Table 1) form chains of molecules extending along the c-axis direction, which are linked into layers parallel to the bc plane by weak C—H⋯O hydrogen bonds (Table 1 and Fig. 2). The layer formation is assisted by slipped π-stacking interactions between inversion-related C1/C2/C7/N1/C8/N4 rings [centroid–centroid distance = 3.4033 (6) Å, slippage = 0.96 Å]. The layers pack along the a-axis direction with van der Waals contacts between them (Fig. 3).

Synthesis and crystallization

1H-1,2,4-Triazol-5-amine (0.5 g, 5.95 mmol) and ethyl 2-oxocyclohexanecarboxylate (0.951 ml, 5.95 mmol) were combined and heated under reflux in 10 ml of acetic acid for 1 h. The solid product obtained was recrystallized from ethanol solution to afford colorless crystals.

Refinement

Crystal data, data collection and structure refinement details are summarized in Table 2.
Acknowledgements

The support of NSF-MRI Grant #1228232 for the purchase of the diffractometer and Tulane University for support of the Tulane Crystallography Laboratory are gratefully acknowledged. Author contributions are as follows. Conceptualization, MT and AB; methodology, WE and AB; investigation, WE, AD; writing (original draft), JTM and YR; writing (review and editing of the manuscript), YR; formal analysis, YR; supervision, YR and MT; crystal-structure determination and validation, JTM.

References

Bruker (2021). APEX4 and SAINT. Bruker AXS LLC, Madison, Wisconsin, USA.

full crystallographic data

*IUCrData* (2023). 8, x230409  [https://doi.org/10.1107/S2414314623004091]

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Crystal data

C₉H₁₀N₄O  
Mr = 190.21  
Monoclinic, *P*2₁/c  
*α* = 9.7925 (3) Å  
*β* = 7.9648 (3) Å  
*γ* = 11.8039 (4) Å  
*β* = 113.553 (1)°  
*V* = 843.95 (5) Å³  
*Z* = 4  

*F*(000) = 400  
*D*ₐ = 1.497 Mg m⁻³  
Cu *Kα* radiation, *λ* = 1.54178 Å  
Cell parameters from 9958 reflections  
θ = 4.1–72.3°  
*µ* = 0.86 mm⁻¹  
*T* = 150 K  
Column, colourless  
0.36 × 0.15 × 0.12 mm

Data collection

Bruker D8 VENTURE PHOTON 3 CPAD  
Radiation source: INCOATEC *µ*S micro-focus source  
Detector resolution: 7.3910 pixels mm⁻¹  
φ and *ω* scans  
(SADABS; Krause *et al.*, 2015)

| *h* = −12→12  
| *k* = −9→9  
| *l* = −14→14

Refinement

| Refinement on *F*²  
| Least-squares matrix: full  
| *R*(*F*² > 2σ(*F*²)) = 0.030  
| *wR*(*F*²) = 0.080  
| *S* = 1.07  
| 1657 reflections  
| 131 parameters  
| 0 restraints  
| Primary atom site location: dual

| Secondary atom site location: difference Fourier map  
| Hydrogen site location: mixed  
| H atoms treated by a mixture of independent and constrained refinement  
| *w* = 1/[σ²(*F*₂) + (0.0413*P*)² + 0.2836*P*]  
| where *P* = (*F*₂ + 2*F*₁)/3

| (∆/σ)max = 0.001  
| ∆ρmax = 0.24 e Å⁻³  
| ∆ρmin = −0.19 e Å⁻³

Special details

**Experimental.** The diffraction data were obtained from 18 sets of frames, each of width 0.5° in *ω* or *φ*, collected with scan parameters determined by the "strategy" routine in *APEX*. The scan time was *θ*-dependent and ranged from 4 to 15 sec/frame.
Geometry. All esds (except the esd in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles and torsion angles; correlations between esds in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell esds is used for estimating esds involving l.s. planes.

Refinement. Refinement of $F^2$ against ALL reflections. The weighted $R$-factor $wR$ and goodness of fit $S$ are based on $F^2$, conventional $R$-factors $R$ are based on $F$, with $F$ set to zero for negative $F^2$. The threshold expression of $F^2 > 2\sigma(F^2)$ is used only for calculating $R$-factors(gt) etc. and is not relevant to the choice of reflections for refinement. $R$-factors based on $F^2$ are statistically about twice as large as those based on $F$, and $R$-factors based on ALL data will be even larger. H-atoms attached to carbon were placed in calculated positions (C—H = 0.95 - 0.98 Å) and included as riding contributions with isotropic displacement parameters 1.2 - 1.5 times those of the attached atoms. That attached to nitrogen was placed in a location derived from a difference map and was refined independently.

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### Geometric parameters (Å, °)

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C9—N3—N4—C1  177.90 (9)  C3—C2—C7—C6  0.39 (15)
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N3—N4—C1—O1  2.46 (15)  C8—N1—C7—C6  −176.34 (8)
C8—N4—C1—C2  1.78 (14)  C5—C6—C7—C2  13.45 (14)
N3—N4—C1—C2  −176.39 (8)  C5—C6—C7—N1  −168.67 (8)
O1—C1—C2—C7  178.33 (10)  C9—N2—C8—N1  −178.78 (10)
N4—C1—C2—C7  −2.93 (13)  C9—N2—C8—N4  0.72 (10)
O1—C1—C2—C3  −2.81 (15)  C7—N1—C8—N2  176.72 (9)
N4—C1—C2—C3  175.93 (8)  C7—N1—C8—N4  −2.74 (14)
C7—C2—C3—C4  16.83 (14)  N3—N4—C8—N2  −0.13 (11)
C1—C2—C3—C4  −162.02 (9)  C1—N4—C8—N2  −178.56 (8)
C2—C3—C4—C5  −47.48 (12)  N3—N4—C8—N1  179.43 (8)
C3—C4—C5—C6  62.20 (11)  C1—N4—C8—N1  1.00 (14)
C4—C5—C6—C7  −43.86 (11)  N4—N3—C9—N2  1.08 (11)
C1—C2—C7—N1  1.46 (15)  C8—N2—C9—N3  −1.16 (11)
C3—C2—C7—N1  −177.34 (9)

Hydrogen-bond geometry (Å, º)

\begin{tabular}{|c|c|c|c|c|}
\hline
D—H···A & D—H & H···A & D···A & D—H···A \\
\hline
N1—H1···N3\textsuperscript{i} & 0.919 (15) & 1.907 (15) & 2.8208 (12) & 173.1 (13) \\
C9—H9···O1\textsuperscript{ii} & 0.95 & 2.57 & 3.3282 (12) & 137 \\
\hline
\end{tabular}

Symmetry codes: (i) x, −y+1/2, z−1/2; (ii) −x+1, y−1/2, −z+3/2.