

## Supplementary Material

# Synthesis of 2,6-Diamino-substituted Purine Derivatives and Evaluation of Cell Cycle Arrest in Breast and Colorectal Cancer Cells

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**Table S1.** Data from docking calculation by Autodock Vina of reversine and the HN(7) and HN(9) tautomers of each molecule **1-3** with Aurora-B Kinase and Monopolar Spindle 1.

Compound <sup>a</sup>	<i>Aurora-B kinase</i> (PDB ID: 2VGO)			<i>Monopolar spindle 1</i> (PDB ID: 3H9F)		
	$\Delta E^b$	H-bond <sup>c,d</sup>	Aminoacidic hydrophobic interactions	$\Delta E^b$	H-bond <sup>c,d</sup>	Aminoacidic hydrophobic interactions
<b>Reversine<sup>c</sup></b>	-35.56	C(2)-N/L99 (3.15)	V107, E171, F172, A173, R175, G176, E177, K180, L223	-39.75	N(9)/E603 (2.87) C(2)-N/G605 (3.34)	K529, I531, V539, A551, I586, M602, C604, N606, I607, D608, L654, I663, D664, M671, Q672, P673, I531, V539, A551, I586, M602, E603, G605, N606, I607, D608, L654, I663, D664, M671, Q672, P673
<b>1a</b>	-35.98	C(2)-N/L99 (3.16)	V107, E171, F172, A173, R175, G176, E177, K180, L223, A233	-36.40	-	I531, V539, A551, I586, M602, C604, G605, N606, I607, D608, L654, I663, D664, Q672, P673
<b>1b</b>	-37.24	C(2)-N/L99 (3.20)	V107, E171, F172, A173, R175, G176, E177, K180, L223, A233	-38.49	N(9)/E603 (2.87)	I531, V539, A551, I586, M602, C604, G605, N606, I607, D608, S611, L654, I663, D664, Q672, P673
<b>2a</b>	-32.64	C(6)-N/E177(3.14)	L99, K101, V107, F172, A173, R175, G176, K180, L223	-35.56	N(9)/D664 (3.13) C(2)-N/D608 (3.12)	K528, I531, V539, A551, I586, E603, N606, I607, L654, I663, M671, Q672, P673
<b>2b</b>	-33.05	-	L99, V107, F172, A173, G176, E177, K180, L223	-36.82	C(2)-N/G605 (3.32)	I531, V539, A551, I586, M602, E603, C604, N606, I607, D608, L654, I663, D664, M671, Q672, P673
<b>3a</b>	-34.31	C(2)-N/L99 (2.87)	V107, F172, A173, G176, E177, K180, L223	-33.47	-	I531, G605, N606, I607, D608, S611, D664, P673, D674, T675
<b>3b</b>	-35.56	C(2)-N/L99 (2.97) N(9)/A173 (3.15)	V107, F172, G176, E177, K180, L223, A233	-35.98	N(9)/E603 (3.08)	I531, A551, I586, C604, G605, I607, D608, L654, I663, D664, M671, Q672, P673

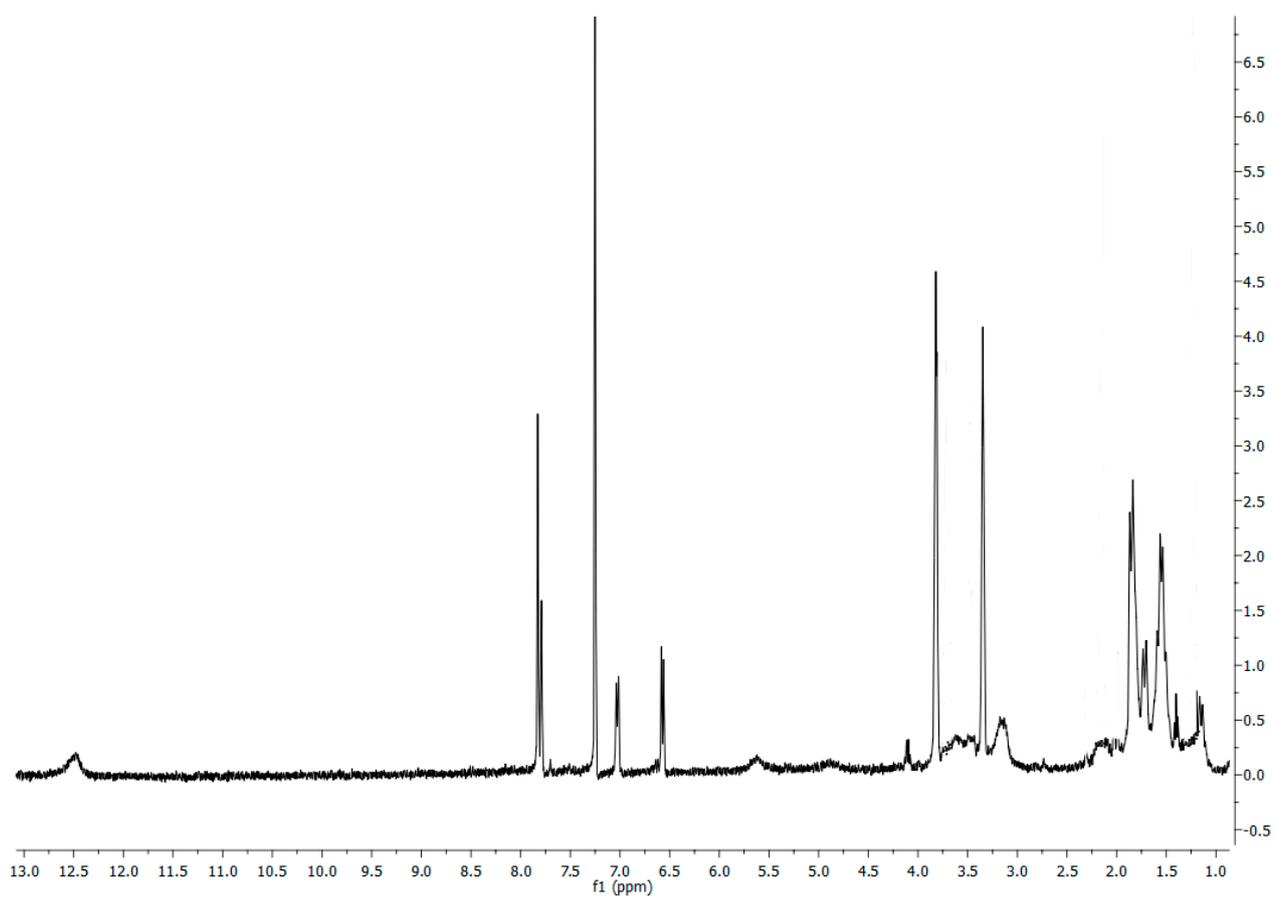
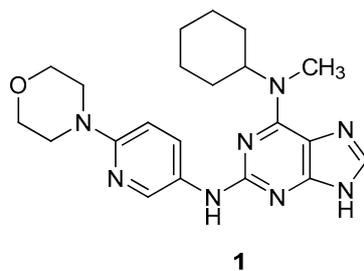
<sup>a</sup> **a**=HN(7) tautomer; **b**= HN(9) tautomer

<sup>b</sup> Calculated docking energy in kJ/mol

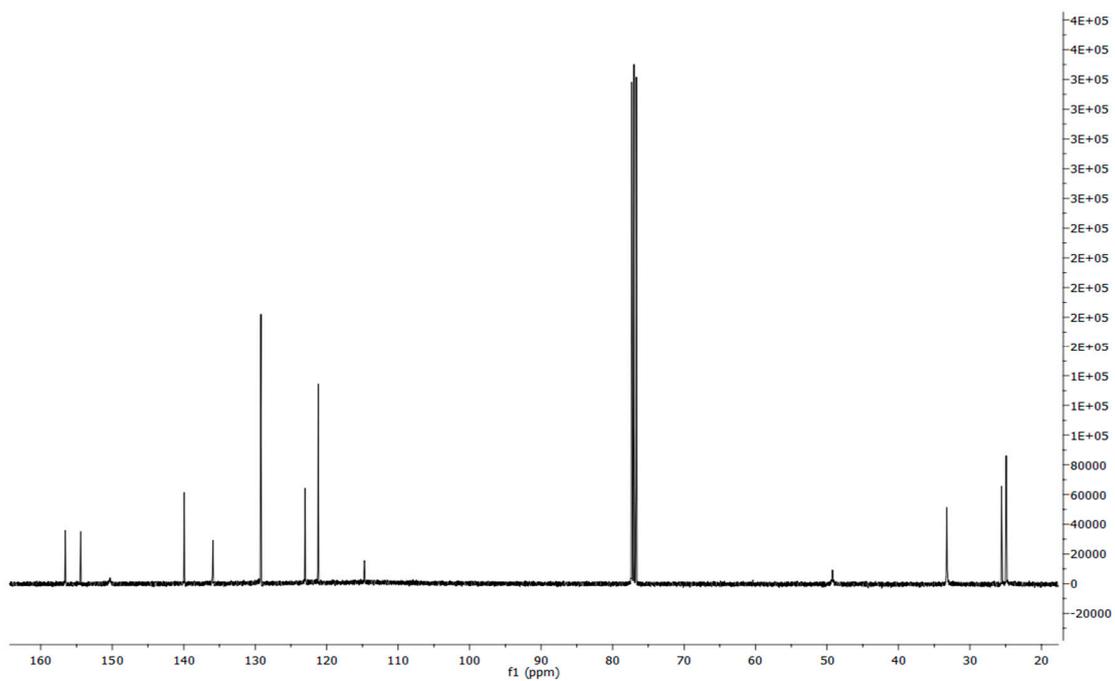
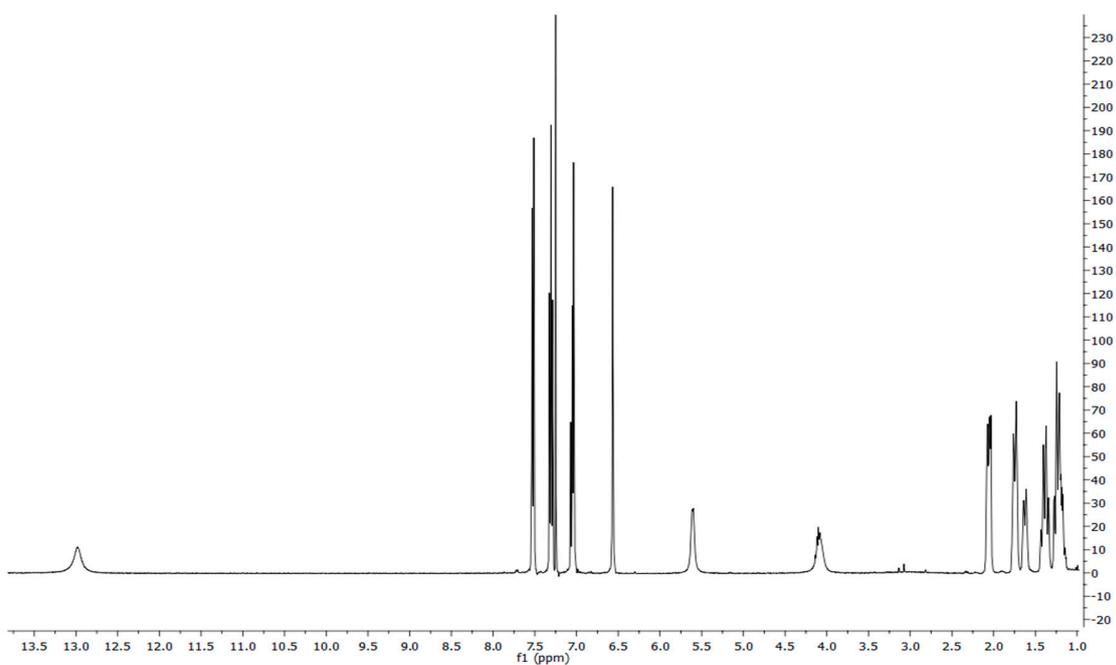
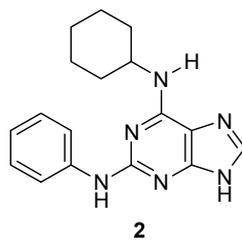
<sup>c</sup> Position on the molecular structures in according to the numbering reported in Figure 1

<sup>d</sup> H-bond distance in Å reported in brackets

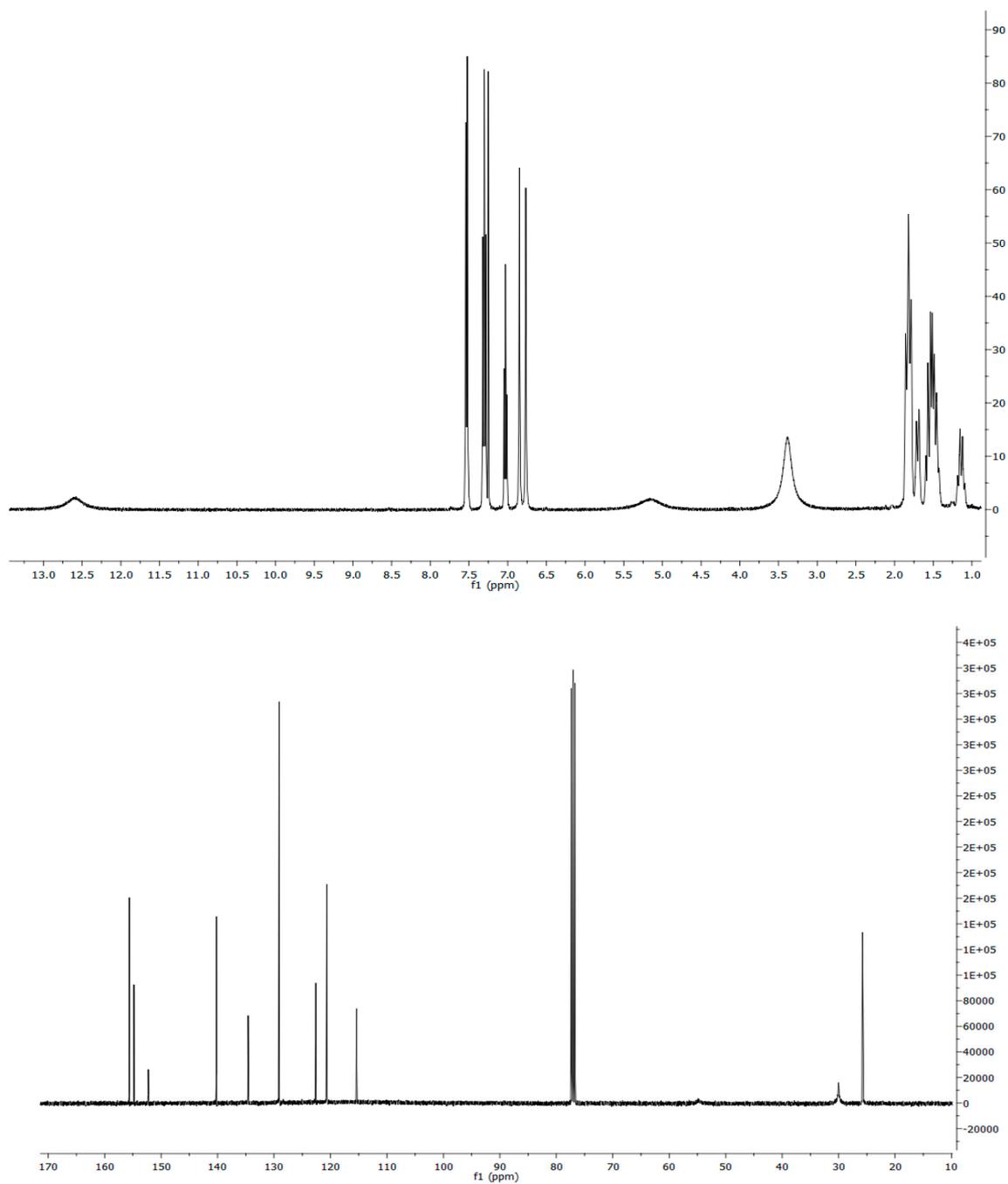
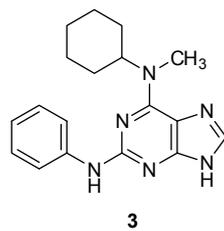
<sup>e</sup> HN(9) tautomer according to the crystal structure of reversine-Aurora B kinase complex (D'Alise, A.M. *et al.*, *Mol.Cancer Ther.* **2008**, 7, 1140-1149. doi:10.1158/1535-7163.MCT-07-2051) cited in file 2VGO.pdb.



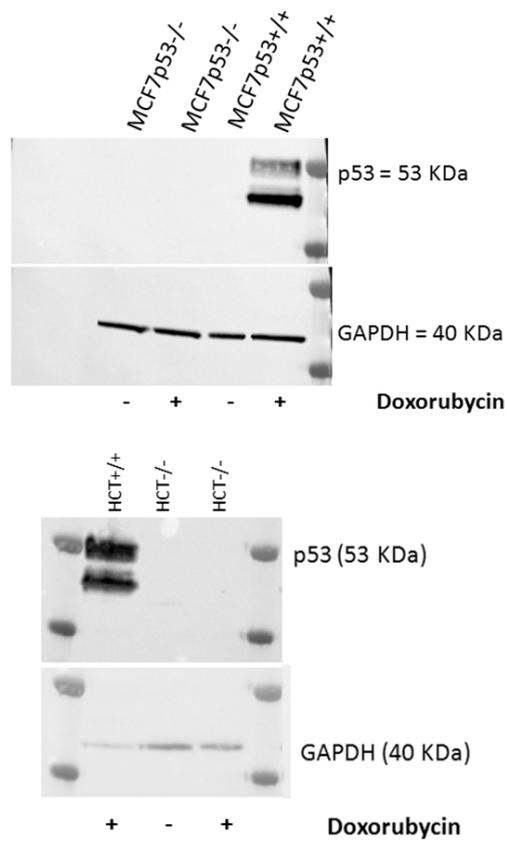
**Fig. S1.** <sup>1</sup>H NMR spectrum (400MHz, CDCl<sub>3</sub>) of reversine-like molecule **1**, isolated as trifluoroacetate salt.



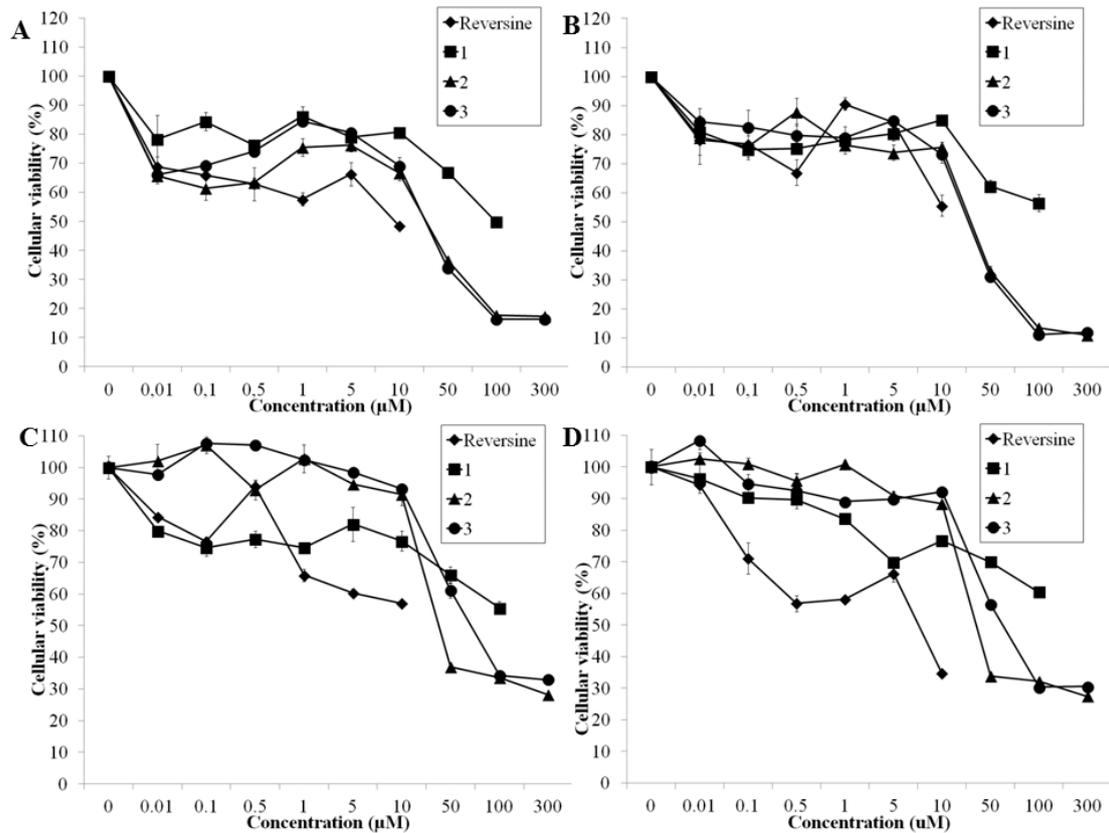
**Fig. S2.** <sup>1</sup>H- and <sup>13</sup>CNMR spectra (CDCl<sub>3</sub>) of compound **2**.



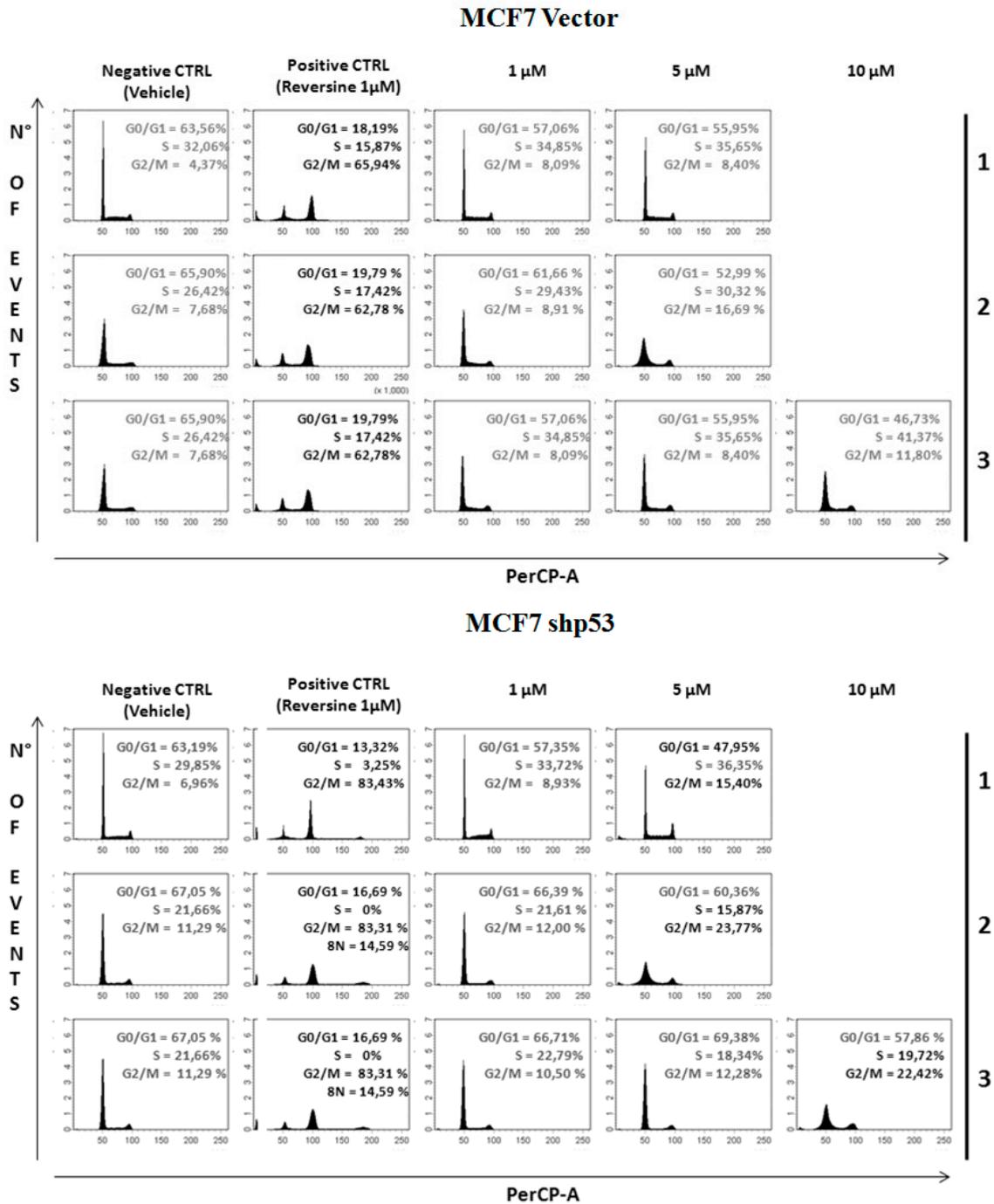
**Fig. S3.** <sup>1</sup>H- and <sup>13</sup>CNMR spectra (CDCl<sub>3</sub>) of compound **3**.



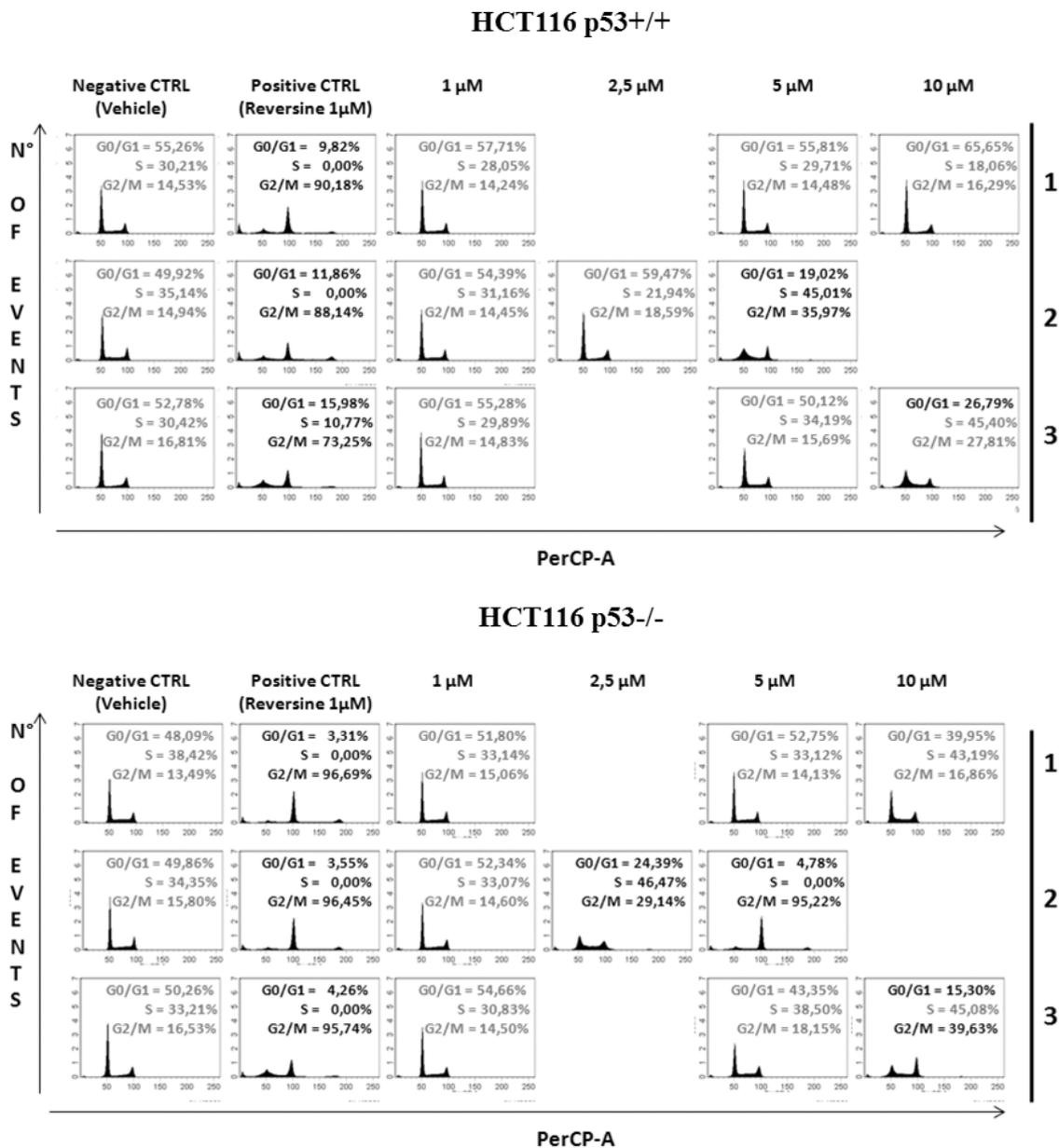
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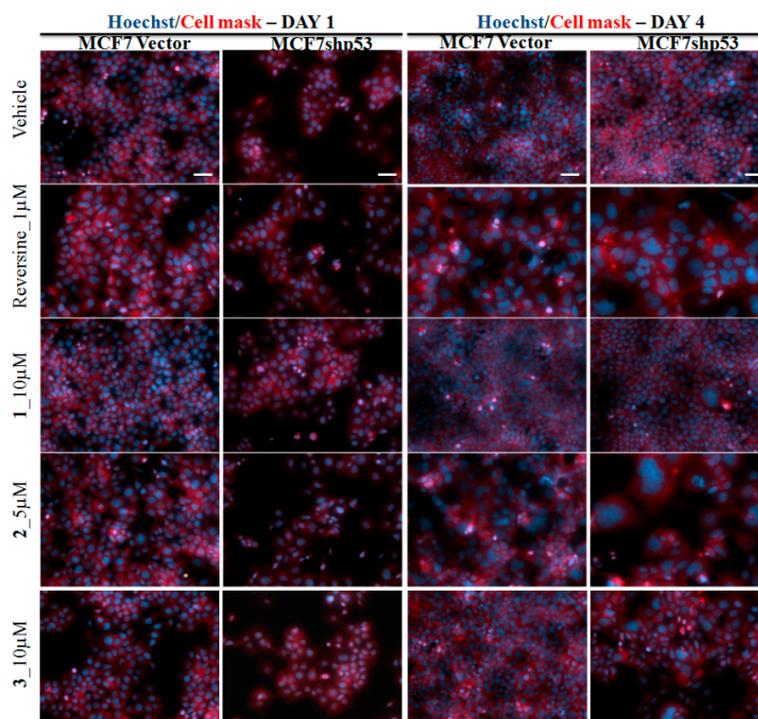
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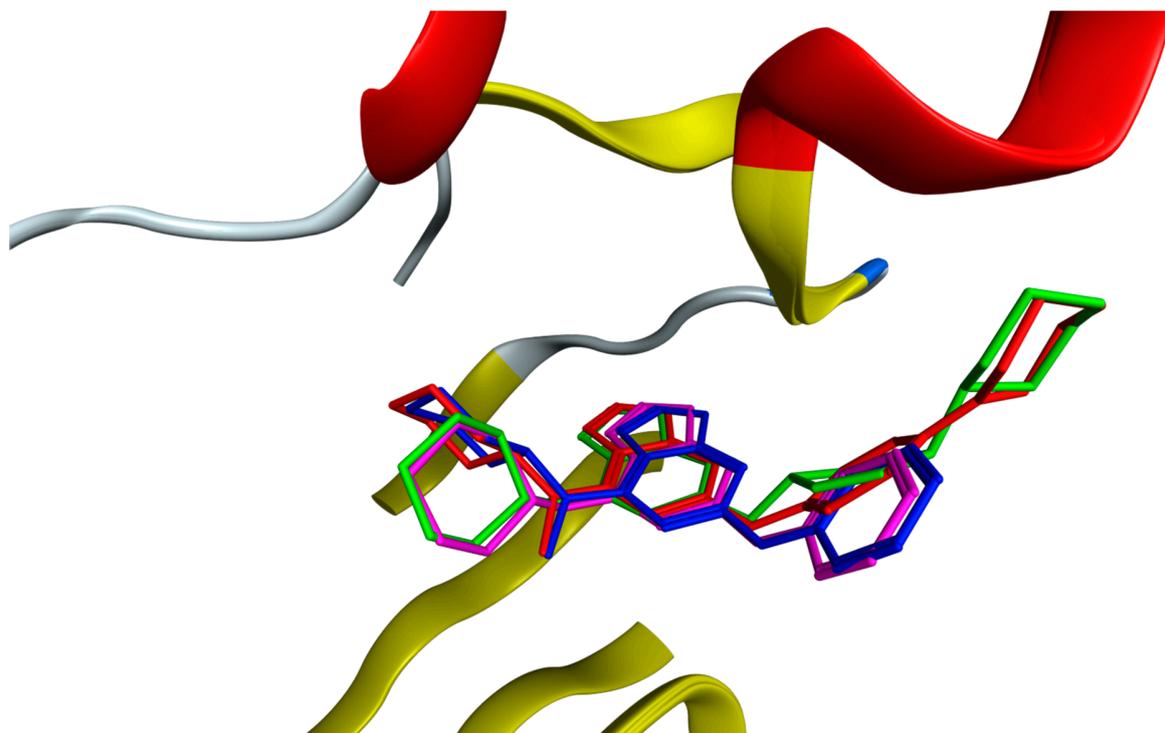
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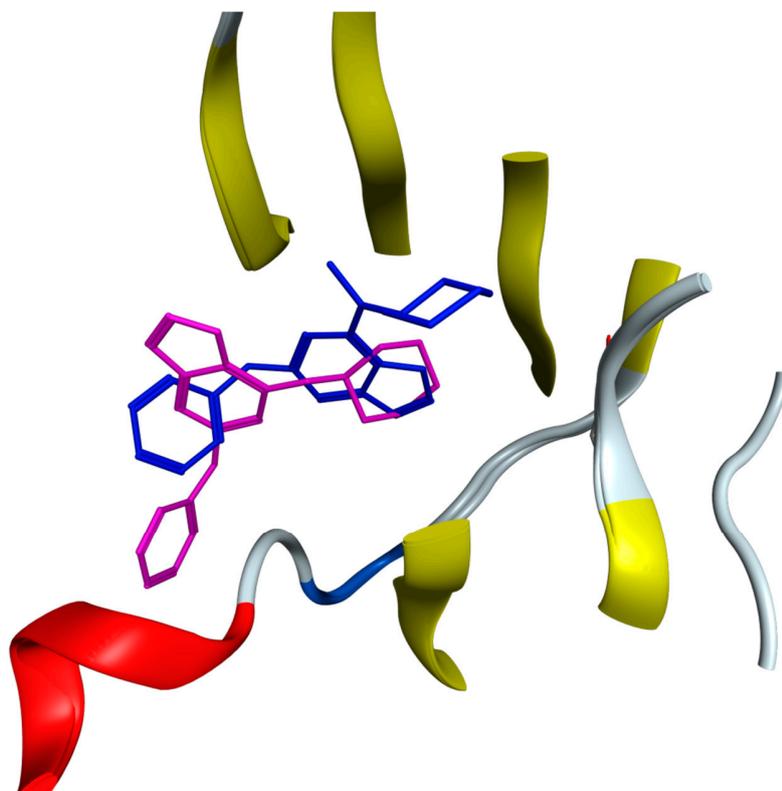
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