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# *In silico* analysis of biological activity of 9'-methoxy substituted 6'*H*-spiro[cycloalkyl-1,5'-tetrazolo[1,5-*c*]quinazolines]

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**Introduction.** The search for novel biologically active compounds remains a key direction in modern medicinal chemistry. Quinazoline derivatives are of particular interest due to their diverse pharmacological properties, including anticancer, antimicrobial, and anti-inflammatory activities. The introduction of methoxy substituents into the molecular structure can significantly influence their physicochemical and biological characteristics. *In silico* methods, such as molecular docking and ADMET prediction, provide an effective tool for the preliminary evaluation of potential biological activity and pharmacokinetic properties of these compounds, accelerating the process of drug discovery.

**Materials and methods.** The study employed SwissTargetPrediction to identify potential biological targets of the proposed compounds. Molecular docking was conducted to evaluate binding affinities to the predicted targets. ADME analysis was performed to assess pharmacokinetic parameters and drug-likeness profiles of the investigated molecules[1].

**Results and discussion.** ADME and target prediction analyses were carried out for a range of 9′-methoxy-6′*H*-spiro[cycloalkyl-1,5′-tetrazolo[1,5-*c*]quinazolines]. According to SwissTargetPrediction results, the investigated compounds demonstrated a high probability of interaction with several biologically relevant proteins, including nicotinamide phosphoribosyltransferase (NAMPT), cytochromes P450 (CYP11B1, CYP11B2), glycogen synthase kinase-3 beta (GSK3B), TRPM8 ion channel, and melatonin receptors MTNR1A/MTNR1B. Among these, GSK3B showed predicted to be the most promising therapeutic target for further docking studies[2].

The predicted toxicity class for all compounds was $LD_{50} \approx 2500$ mg/kg, indicating low acute toxicity[3]. ADME analysis revealed that all molecules comply with Lipinski's rule of five and have optimal physicochemical characteristics molecular weight 229–327, TPSA ≈ 65 Å², log P 2.2–3.2, supporting their potential as drug-like compounds. Solubility assessment (log S ≈ −2.5 to −4.7) indicated moderate to good aqueous solubility, suggesting both oral and parenteral usability.

Pharmacokinetic profiling predicted satisfactory permeability and acceptable interaction with CYP isoenzymes, confirming favorable biopharmaceutical parameters. Overall, the studied molecules, exhibit promising pharmacological potential as GSK3B inhibitors, which may be relevant for the treatment of neurodegenerative and metabolic disorders.

**Conclusions.** The conducted *in silico* study revealed that 9′-methoxy substituted 6′*H*-spiro[cycloalkyl-1,5′-tetrazolo[1,5-*c*]quinazolines] possess favorable ADME properties and low predicted toxicity. SwissTargetPrediction and docking results indicate potential GSK3B inhibitory activity, highlighting these compounds as promising candidates for further biological evaluation.

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