

long-wavelength region compared to the corresponding spectrum in DMF. The presence of RNA/DNA practically does not change the spectrum's shape and the maximum's location, that points to only weak interaction of Y3 with these biopolymers. On the other hand, in the presence of BSA or BSA-SDS, there is a short-wavelength shift of the absorption maximum towards that for DMF. This shift points to the strong binding of the dye Y3 to the native or denatured serum albumin with a high increase in fluorescence emission.

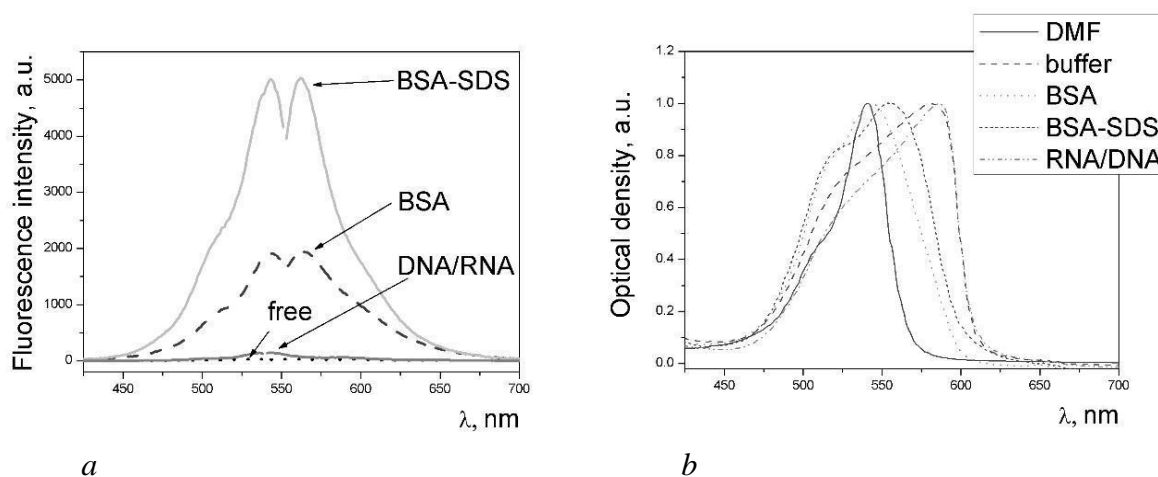


Fig. 2 (a) Fluorescence emission (right) and excitation (left) spectra of cyanine dye Y3 in an unbound state and the presence of serum albumin, BSA-SDS system, DNA/RNA in 50 mM Tris–HCl (pH 7.9) buffer. (b) The Vis absorption spectra of the cyanine dye Y3 in DMF, buffer in an unbound state and in the presence of BSA, BSA-SDS, RNA/DNA. The optical density of the dye was normalized to unity at corresponding maximum wavelengths of the dye spectra. Dye concentration 5 μ M.

Due to the specificity of studied trimethine cyanine dyes to serum albumin and albumin-SDS system, they could be considered promising fluorescent dyes for applications demanding noncovalent labeling of proteins, proteins detection, and quantification in solution, gel electrophoresis, or for protein analysis.

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2-OXOIMIDAZOLIDIN-4-YLIDENEPYPERIDINESULFONILAMIDES AS POTENTIAL ANTIBACTERIALS AGAINST MULTIDRUG-RESISTANT MICROBIAL PATHOGENS

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With the emergence of multidrug-resistant bacterial strains, there is an urgent need to find antibacterial agents directed at alternative molecular targets. It is known that imidazolones are important scaffolds and biologically active compounds. Functionalized derivatives of imidazolones were recognized due to their significant antibacterial and antifungal properties, including antituberculosis activity, anticancer, anti-inflammatory, antihistamine, antihypertensive, antiparkinsonian and anthelmintic activities [1,2]. It was found that 2-thioxo-4-imidazolidinone derivatives which involved various substituents exhibited moderate antibacterial activity against *Staphylococcus aureus* and *Pseudomonas aeruginosa* and significant antifungal activities toward *Candida albicans* and *Aspergillus niger* [3].

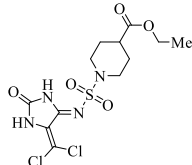
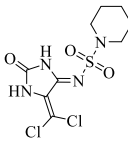
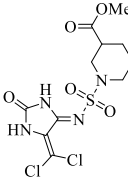
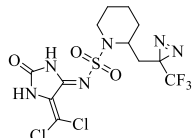
The aim of the current study was to evaluate the antibacterial activity of a series of 2-oxoimidazolidin-4-ylidenepiperidinesulfonamides against multidrug-resistant strains using *in silico* and *in vitro* study.

The antibacterial activity of compounds was evaluated by disc diffusion method in Mueller-Hinton agar [4] against standard (ATCC) and multi-resistant (MDR) strains of Gram-negative *Escherichia coli* and Gram-positive *Staphylococcus aureus*. Bacterial cultures were obtained from the Museum of Microbial Culture Collection of the Shupyk National Healthcare University of Ukraine. The bacterial inoculum contained 1×10^5 colony forming units per mL. Studied compounds applied on standard paper disks (6 mm) in a volume of 0.02 ml. All tested compounds were dissolved in 0.1% dimethyl sulfoxide solution. The compound content on the disk was 3.0 μ M. The activity of tested compounds was evaluated by zone diameter of the growth inhibition. The tests were repeated three times.

In vitro antibacterial activity results of studied 2-oxoimidazolidin-4-ylidenepiperidinesulfonamides against Gram-negative ATCC and MDR *E. coli* and Gram-positive *S. aureus* strains are shown in Table 1.

Table 1

In vitro antibacterial activity of 2-oxoimidazolidin-4-ylidenepiperidinesulfonamides

N	Compound	Zone diameter of growth inhibition, mm			
		<i>E. coli</i> ATCC ^a	<i>E. coli</i> MDR ^b	<i>S. aureus</i> ATCC ^a	<i>S. aureus</i> MDR ^b
1		23	15	32	20
2		36	23	32	21
3		30	21	28	17
4		30	20	28	18

^a American Type Culture Collection 25922 / 25923 strains of *E. coli* / *S. aureus*

^b *E. coli* and *S. aureus* clinical isolates resistant to Ampicillin, Carbenicillin, Ceftazidime, Oxacillin, Tetracycline.

The data presented in Table 1 show that studied compounds exhibited high activity against both Gram-negative *E. coli* and Gram-positive *S. aureus* strains. 2-Oxoimidazolidin-4-ylidenepiperidinesulfonamides demonstrated significant activity against ATCC *S. aureus* and *E.*

coli strains with a range of inhibition zone diameters 23-36 mm. At the same time tested compounds were active against *S. aureus* and *E. coli* MDR strains with an inhibition zone diameters of 15-21 mm and showed moderate effect (35-40% lower than the activity against ATCC strains).

The 2-oxoimidazolidin-4-ylidenepiperidinesulfonamides were studied *in silico* using molecular docking calculation as possible inhibitors of UDP-N-acetylenolpyruvylglucosamine reductase (MurB) of bacterial wall. Molecular docking studies revealed that the 2-oxoimidazolidin-4-ylidenepiperidinesulfonamides exhibits the affinity to MurB. The corresponding *E. coli* and *S. aureus* crystal structure of MurB (5MMO [5] and 3U2D [6] respectively) downloaded from Protein Data Bank [7]. The structures of 2-oxoimidazolidin-4-ylidenepiperidinesulfonamides were drawn by Marvin Sketch software [8] and optimized using MMFF94s force field in the Avogadro program [9]. The ligands and enzymes pdbqt files were prepared using a program AutoDock Tools version 1.5.6 [10]. Molecular docking was performed by Autodock Vina software [11].

Thus, the potential antibacterial mechanism of the tested compounds realized through inhibition of bacterial wall synthesis. The complexation of the one of the studied 2-oxoimidazolidin-4-ylidenepiperidinesulfonamides **4** into the active site of *E. coli* MurB is stabilized by hydrogen bonds of 2-oxoimidazolidin-4-ylidenepiperidinesulfonamide scaffold with amino acid residues Ser116 and Arg327. The amino acid residue Arg327 also has halogen bonds with trifluoromethyl group of 2-((3-(trifluoromethyl)-3*H*-diazirin-3-yl)methyl)piperidinyl substituent. Estimated binding energies of formatted complexes *E. coli* and *S. aureus* MurB with ligand **4** were -8.9 and -10.4 kcal/mol respectively.

Studied 2-oxoimidazolidin-4-ylidenepiperidinesulfonamides as potential MurB inhibitors appear to be effective antibacterials against multidrug-resistant *E. coli* and *S. aureus* bacterial pathogens.

1. Ammar, Y.A., El-Sharief, M. A. M. Sh., Ghorab, M.M. et al. New Imidazolidineiminothione, Imidazolidin-2-one and Imidazoquinoxaline Derivatives: Synthesis and Evaluation of Antibacterial and Antifungal Activities // 2016. – 13(3). - P. 466-475. DOI: 10.2174/1570179412666150817221755.

2. Siwach, A., Verma, P.K. Synthesis and therapeutic potential of imidazole containing compounds // BMC Chemistry. - 2021. – 15(12). <https://doi.org/10.1186/s13065-020-00730-1>.

3. Jabara, L.A.A., Mutlaq, D. Z., Al-Shawi A. A. A. Synthesis of novel 2-thioxo-4-imidazolidinone derivatives and evaluation of their antibacterial, and antifungal activities // Egyptian Journal of Chemistry. - 2021. - 64(6). - P. 3059-3067. DOI: 10.21608/EJCHEM.2021.66960.3442.

4. Bauer, A.W., Kirby, W.M., Sherris, J.C. et al. Antibiotic Susceptibility Testing by a Standardized Single Disk Method // Am. J. Clin. Pathol. – 1966. - 45(4). - P. 493–496.

5. Zeleke, D., Eswaramoorthy, R., Belay, Z. et al. Synthesis and Antibacterial, Antioxidant, and Molecular Docking Analysis of Some Novel Quinoline Derivatives // Journal of Chemistry. – 2020. - 2020. – P. 1-16. doi.org/10.1155/2020/1324096.

6. Eakin, A.E., Green, O., Hales, N. et al. Pyrrolamide DNA gyrase inhibitors: fragment-based nuclear magnetic resonance screening to identify antibacterial agents. Antimicrob Agents Chemother // 2012. - 56(3). - P.1240-1246. doi: 10.1128/AAC.05485-11.

7. www.rcsb.org.

8. Marvin n. n. n. (5.2.4.), 201n (2009), ChemAxon (<http://www.Chemaxon.com>).

9. Alonso H., Bliznyuk A.A., Gready J.E. Combining docking and molecular dynamic simulations in drug design // Med. Res. Rev. – 2006 – 26. - P. 531-568.

10. Michel F.Sanner. A Component-Based Software Environment for Visualizing Large Macromolecular Assemblies. Structure. 2005. Volume 13, Issue 3, , P. 447-462 doi.org/10.1016/j.str.2005.01.010.

11. Trott O., Olson A. J. AutoDock Vina: improving the speed and accuracy of docking with a new scoring function, efficient optimization and multithreading // J. Comput. Chem. – 2010. – 31. - P. 455-461.