

Molecular model of tyrosyl-DNA phosphodiesterase 1 for a structure-based screening for its inhibitors

Gushchina, I.V.

Faculty of Bioengineering and Bioinformatics, Lomonosov Moscow State University, Leninskie Gory 1, bldg. 73, 119991 Moscow, Russia, irinafb@gmail.com

Nilov, D.K.

Belozersky Institute of Physicochemical Biology, Lomonosov Moscow State University, Leninskie Gory 1, bldg. 40, 119991 Moscow, Russia, nilov@belozersky.msu.ru

Zakharenko, A.L.

Institute of Chemical Biology and Fundamental Medicine, Russian Academy of Sciences, Siberian Branch, Lavrentiev avenue 8, 630090 Novosibirsk, Russia, sashaz@niboch.nsc.ru

Lavrik, O.I.

Institute of Chemical Biology and Fundamental Medicine, Russian Academy of Sciences, Siberian Branch, Lavrentiev avenue 8, 630090 Novosibirsk, Russia, lavrik@niboch.nsc.ru

Švedas, V.K.

Belozersky Institute of Physicochemical Biology, Lomonosov Moscow State University, Leninskie Gory 1, bldg. 40, 119991 Moscow, Russia, vytas@belozersky.msu.ru

Cancer cells often become resistant to radiation and chemotherapy due to their ability to eliminate induced damage of DNA [1]. Therefore, the inhibition of DNA repair enzymes is considered to be a way to increase the efficiency of cancer therapy. One of such enzymes, tyrosyl-DNA phosphodiesterase 1 (Tdp1), cleaves irreversible covalent complexes of DNA with topoisomerase which accumulate under the influence of various exogenous factors (e.g. irinotecan drug) [2].

We present the original full-atomic model of Tdp1 built with the consideration of ionization states of active site residues and aimed for virtual screening for novel inhibitors (Fig. 1). The interactions of the His263 and His493 catalytic residues with phosphate group of the substrate were described by hybrid quantum mechanics/molecular mechanics method with the use of RM1 Hamiltonian [3]. Residues which are important for substrate and potential inhibitors binding were identified (His263, His493, Lys265, Lys495, Asn283,

Asn516). Structure-based virtual screening for Tdp1 inhibitors was performed in a commercial library of low-molecular-weight compounds containing the sulphonate group (this functional group is structurally similar to the substrate's phosphate). We selected several compounds which form hydrogen bonds with important active site residues (Fig. 2). Experimental investigation by enzyme assay demonstrated the inhibitory effect of these compounds in the micromolar concentration range which confirms the applicability of the obtained Tdp1 model for computer-aided screening.

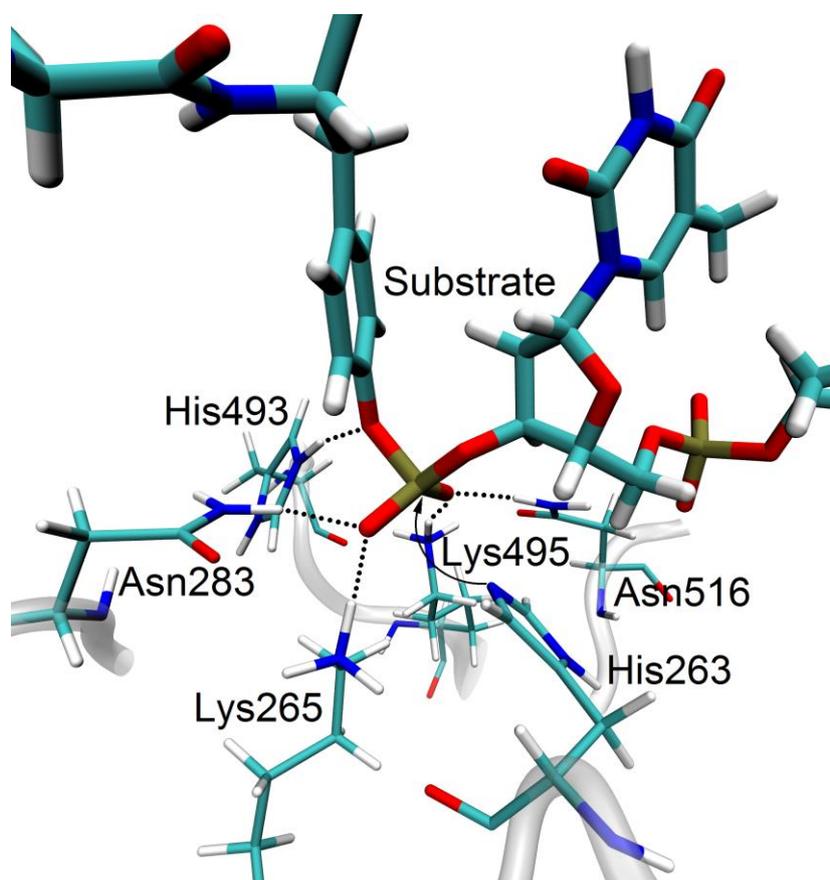


Fig. 1. The active site of the full-atomic Tdp1 model with residues important for substrate and potential inhibitors binding. Dotted lines indicate hydrogen bonds. The arrow shows the nucleophilic attack of His263 on 3'-phosphate of the substrate during the catalysis.

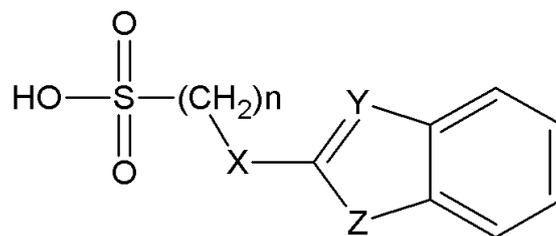


Fig. 2. Chemical structure of potential Tdp1 inhibitors selected by virtual screening.

This work was supported by the Ministry of Education and Science of the Russian Federation (State agreement № 14.604.21.0018, ID RFMEFI60414X0018).

1. L.Gatti, F.Zunino (2005) Overview of tumor cell chemoresistance mechanisms, *Methods in Molecular Medicine*, **111**:127–148.
2. T.S.Dexheimer, S.Antony, C.Marchand, Y.Pommier (2008) Tyrosyl-DNA Phosphodiesterase as a Target for Anticancer Therapy, *Anti-cancer Agents in Medicinal Chemistry*, **8**:381–389.
3. R.C.Walker, M.F.Crowley, D.A.Case (2008) The implementation of a fast and efficient hybrid QM/MM potential method within the Amber 9.0 sander module, *Journal of Computational Chemistry*, **29**:1019-1031.