## Supplementary file

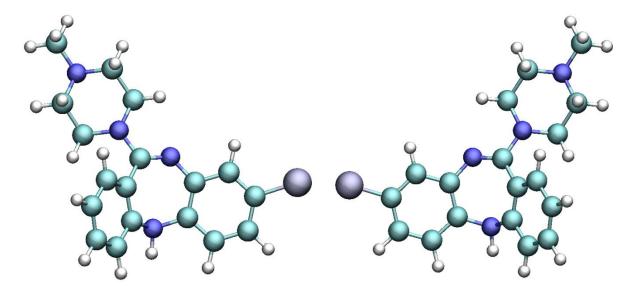
Antipsychotic clozapine binding to alpha-2-macroglobulin protects interacting partners against oxidation and preserves the anti-proteinase activity of the protein

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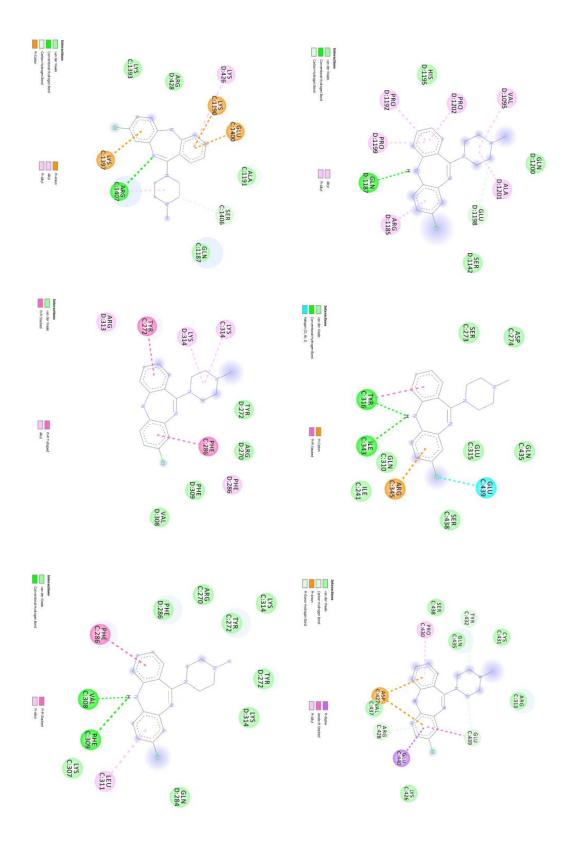
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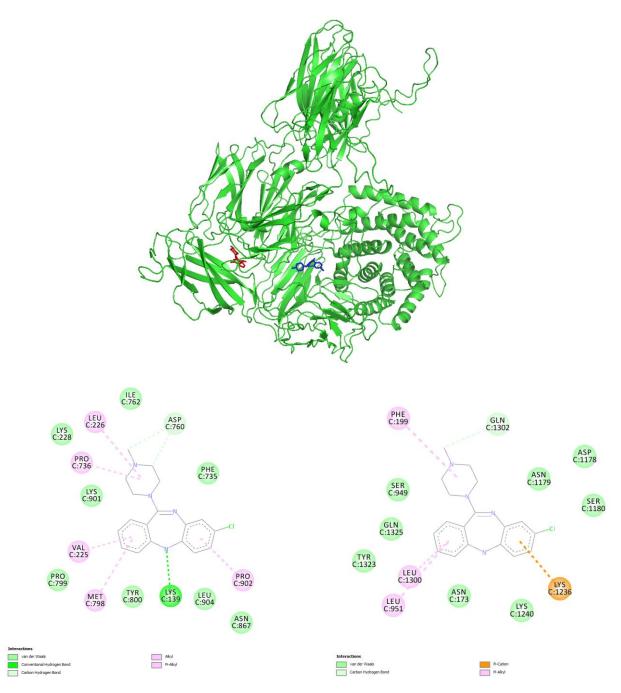
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**Figure S1**. Optimized structures of two atropisomers of the clozapine molecule. Left: P (plus) atropisomer. Right: M (minus) atropisomer. Two atropisomers are also enantiomers.



**Figure S2**. The 2D protein-ligand interaction diagram for the selected binding sites in clozapine binding pocket (Note: the residue numbers correspond to residue numbers in 4ACQ).



**Figure S3**. Two binding sites found in chain C by docking experiment. **Left and red**: binding site with binding energy 8.2 kcal/mol; **Right and blue**: binding site with binding energy 7.7 kcal/mol (Note: the residue numbers correspond to residue numbers in 4ACQ).

The two highest energy binding sites that can accommodate both atropisomers of clozapine found in a single chain docking simulation are presented in **Figure S2**. The first binding site (colored red in upper panel, left image in lower panel) has binding energy of 8.2 kcal/mol and is

located inside the protein. Ligand is interacting with amino acids from two beta sheets (867-875, 897-906) and surrounding loops. The dominant types of interactions are  $\pi$ -alkyl and alkyl-alkyl, and there is hydrogen bond between amino group from 1,4-diazepine ring and Lys139.

The second binding site is located between two beta sheets (945-951 and 1322-1332) and small  $\alpha$  helix (1225-1240). Binding energy in this site is 7.7 kcal/mol. Once again, hydrophobic  $\pi$ -alkyl and alkyl-alkyl interactions are the most abundant. Also, there is a cation- $\pi$  interaction between chlorobenzene ring and Lys1236.

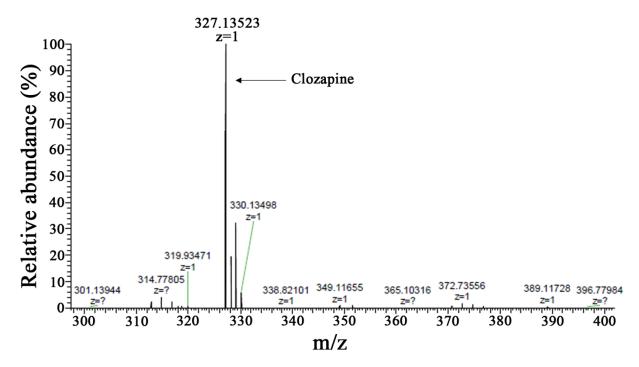


Figure S4. Mass spectrum of clozapine.