Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (BioA), a PLP-dependent transaminase of *M. tuberculosis* (MtB), catalyzes the reversible transfer of the α-amino group from SAM to KAPA to form DAPA.

BioA has recently gained much importance as anti-TB drug target for its specificity in MtB and absence of the enzyme in higher eukaryotic organisms such as plants and mammals. Hence, there has been considerable effort in identifying novel lead molecule as BioA inhibitors.

**KAPA was taken as the reference molecule, XED force field was used to generate field points of KAPA.**

Cresset’s Spark program was used to grow new ligand by bioisosteric substitution.

Final structures of 3D molecules were selected based on field and shape similarity relative to the reference template molecule KAPA. 4CXQ active site was used as the excluded volume to penalize the steric clashes. Alignment scores ranged from 0.54-0.62.

2D-Diagram showing interaction of lead molecules in the active site of MtB BioA predicted by Glide docking program (Schrödinger, Inc., New York, NY, 2012)

The Crystal structure bound to KAPA (PDB ID: 4CXQ) showing H-bond interactions residues Tyr25, Trp64, Arg400, Tyr157, Gly316 and covalent interaction with co-factor PLP.

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1. Spark and Forge program (Cresset Bio Discovery Ltd., Cambridge, UK, 2015) were used for linking chemistry, scaffold replacement and field-based alignment.
2. Final structures of 3D molecules were selected based on field and shape similarity relative to the reference template molecule KAPA.
3. Protein active site was used as the excluded volume to penalize the steric clashes.
4. A series of 300 molecules were designed and QikProp program (Schrödinger, Inc., New York, NY, 2012) was used to screen the molecules according to ADME parameters.
5. Compounds with ADMET parameters in permissible ranges were docked in the active site of MtB BioA using Glide program (Schrödinger, Inc., New York, NY, 2012).
6. Compounds molecular ABA series and SSIM-7, having lowest Glide energy (-59.70 kcal mol-1 to -42.35 kcal mol-1) and high GlideXP score (-11.32 kcal mol-1 and -9.38 kcal mol-1) showed good interactions with the active site of MtB BioA.
7. These novel lead molecules designed by in silico approach could be viewed as potential MtB BioA inhibitors.

**Conclusion**

Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (BioA), a PLP-dependent transaminase of *M. tuberculosis* (MtB), catalyzes the reversible transfer of the α-amino group from SAM to KAPA to form DAPA.

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