Supplementary Information

Insights into the stereoselectivity of human SETD7

methyltransferase

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Figure S1. The best docked pose (cyan) and original crystal struture (yellow) were supeimposed very well. The RMSD value referred to crystal pose was 0.337 Å.



Figure S2. The initial structure for MD simulations. (A). The (R)-PFI-2/SETD7/SAM system was colored in cyan. (B). The (S)-PFI-2/SETD7/SAM system was colored in green. SAM and antipodes were presented with sticks and sphere.



Figure S3. The RMSD of enantiomers and the C α from residues of SETD7. The average value of RMSD from both inhibitors were under 2.0 Å



Figure S4. The conformation ensembles. Resides 190-200, 340-350 were in cyan and magenta color, respectively. The skeleton of protein was in white cartoon. SAM and inhibitors were displayed in orange and pink color sticks.



Figure S5. The average distance between the methyl group of SAM and the pyrrolidine moiety of inhibitor. (A). The (R)-PFI-2/SETD7/SAM system. (B). The (S)-PFI-2/SETD7/SAM system.



Figure S6. The atom labels of (R)-PFI-2 is same to (S)-PFI-2.



Figure S7. Residues are within 5 Å of the enantiomers. Both (R)-PFI-2 and (S)-PFI-2 are presented by ocean blue sticks. Co-factor SAM are displayed with sticks in different color in the ternary complex structure. Residues are showed in thin sticks with cyan and green color. (A). The (R)-PFI-2/SETD7/SAM system. (B). The (S)-PFI-2/SETD7/SAM system.



Figure S8. The hydrophobic channel mainly constructed by residues TYR245, LEU267, TYR305 and TYR335, which filled with the pyrrolidine moiety from enantiomers and the methyl of SAM. Both (R)-PFI-2 and (S)-PFI-2 are presented by ocean blue sticks. Co-factor SAM are displayed with sticks in different color in the ternary complex structure. Residues are showed in thin sticks with cyan and green color. (A). The (R)-PFI-2/SETD7/SAM system. (B). The (S)-PFI-2/SETD7/SAM system.