Supporting information: Trans vs Cis: A Computational Study of Enasidenib Resistance due to IDH2 Mutations

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Abstract
This file includes supplementary methods and a section on data availability.

Keywords
PCMEDA, drug resistance, targeted therapy, resistance mutations

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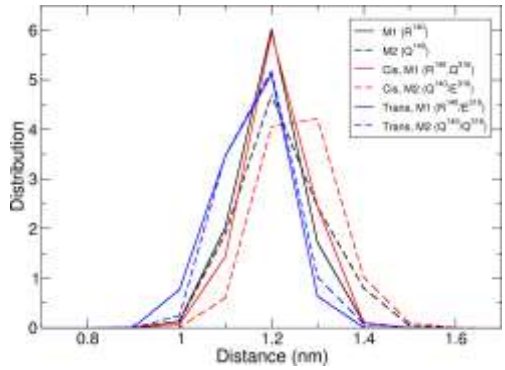
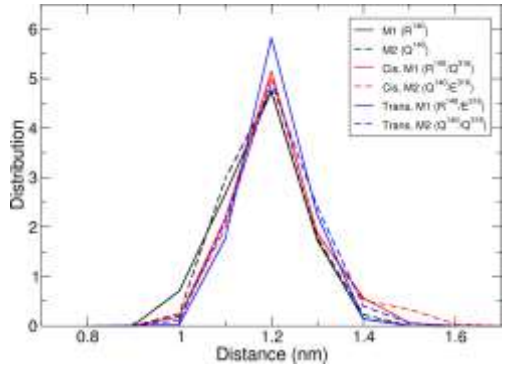


(a) Apo IDH2



(b) Drug-bound IDH2

Figure 1. Distance distribution for the opening of the back cleft in IDH2, as calculated from the distance between the Cα atoms of residues Tyr^{238} and His^{381}. M1 is monomer 1 and M2 is monomer 2.

2. Supplementary Tables

Table 1. Median and maximal Cα RMSD values calculated from four 100 ns simulations. All values in nm.

Protein	Median RMSD	Max RMSD
R140Q apo	0.24	0.36
Cis apo	0.27	0.42
Trans apo	0.23	0.34
R140Q holo	0.25	0.46
Cis holo	0.24	0.39
Trans holo	0.24	0.35

3. Data availability

Input files for energy calculations, EDA and NCI are freely available at:

`https://dx.doi.org/10.6084/m9.figshare.25205792`