

NMR-AIDED DESIGN OF CLINICAL STAGE PROTEIN-PROTEIN-INTERACTION INHIBITORS: THE MCL-1 SUCCESS STORY

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The structure-based design of small-molecule inhibitors targeting protein-protein interactions (PPIs) remains a huge challenge as the drug must bind typically wide and shallow protein sites. A PPI target of high interest for hematological cancer therapy is Myeloid cell leukaemia 1 (Mcl-1), a pro-survival guardian protein from the Bcl-2 family. Despite previously considered undruggable, six small molecule Mcl-1 inhibitors have recently entered clinical trials.

Here we report the free in solution NMR conformational analysis of the clinical stage Mcl-1 inhibitors AZD5991, AMG-176 and S64315, and compare the free 3D conformers with the protein-bound conformers determined by crystallography.^[1] Our data reveal high plasticity of the Mcl-1 protein and a marked ligand-induced pocket deepening. NMR-based free ligand conformer analysis demonstrates that such unprecedented induced-fit is uniquely achieved by designing highly rigid inhibitors, preorganized in their bioactive conformation. By elucidating key chemistry design principles, this work provides a roadmap for targeting the largely untapped PPI class more successfully.

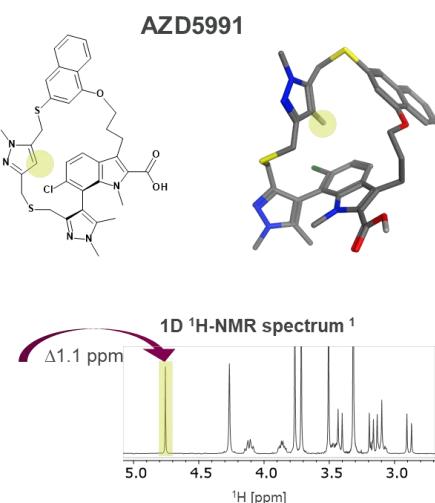


Figure 1. The free in solution conformer of Mcl-1 inhibitor AZD5991 shows a characteristic ^1H -NMR fingerprint signal (green background), indicating aromatic ring packing and pre-structuring in the bioactive, protein-bound conformation. The arrow highlights the upfield shifted ^1H signal compared with the 2D-HOSE predicted value.

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REFERENCES

[1] A. E. Tron, et al., *Nat. Commun.* **2018**, *9*, 5341.