

Structure-based drug discovery in bromodomains

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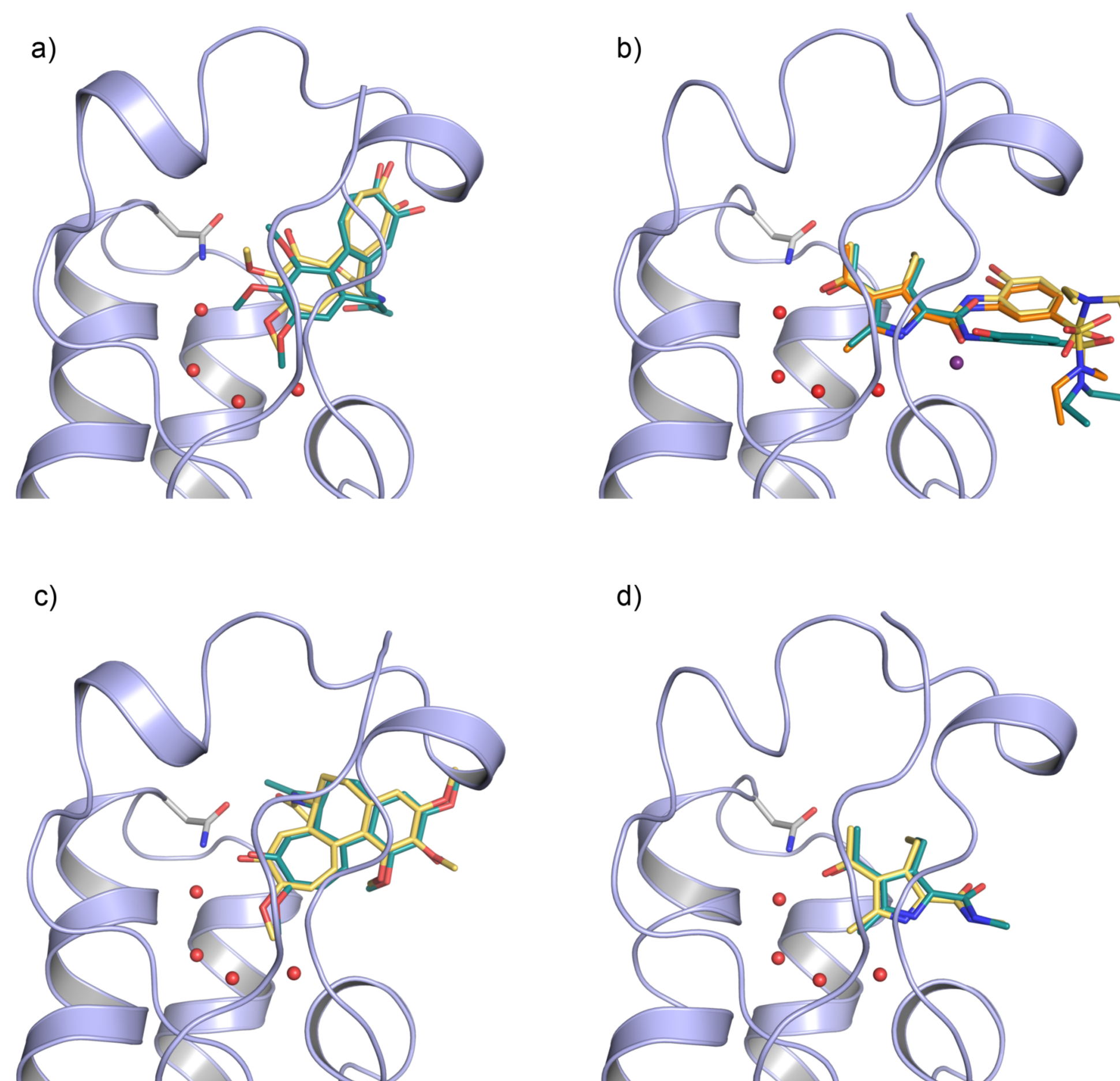
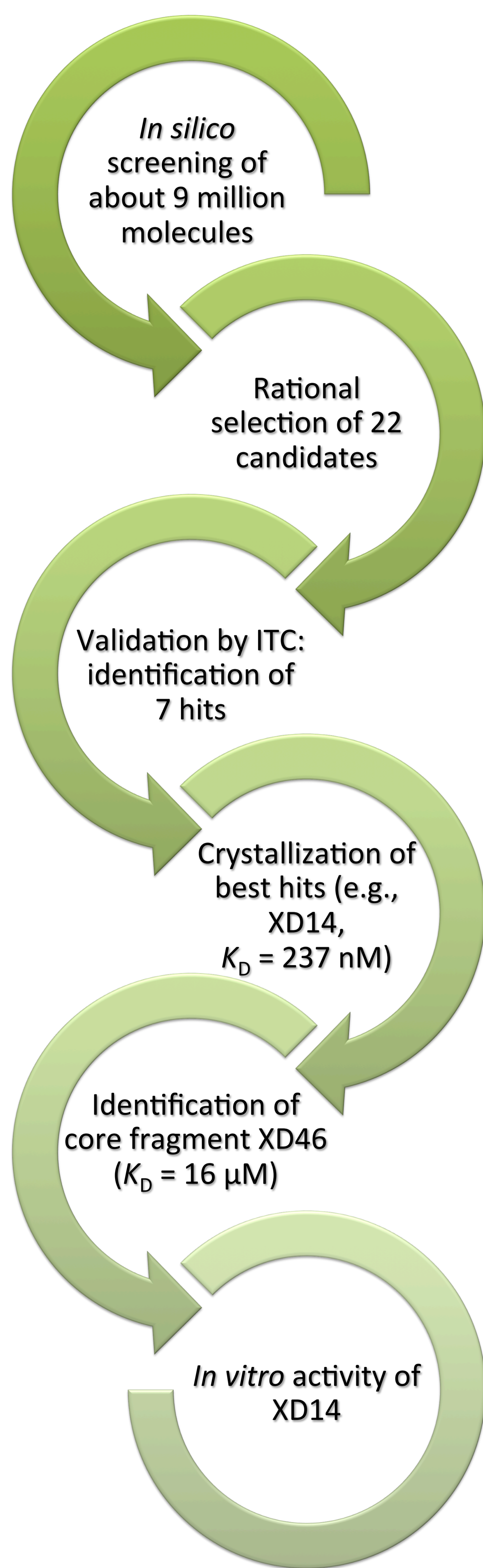
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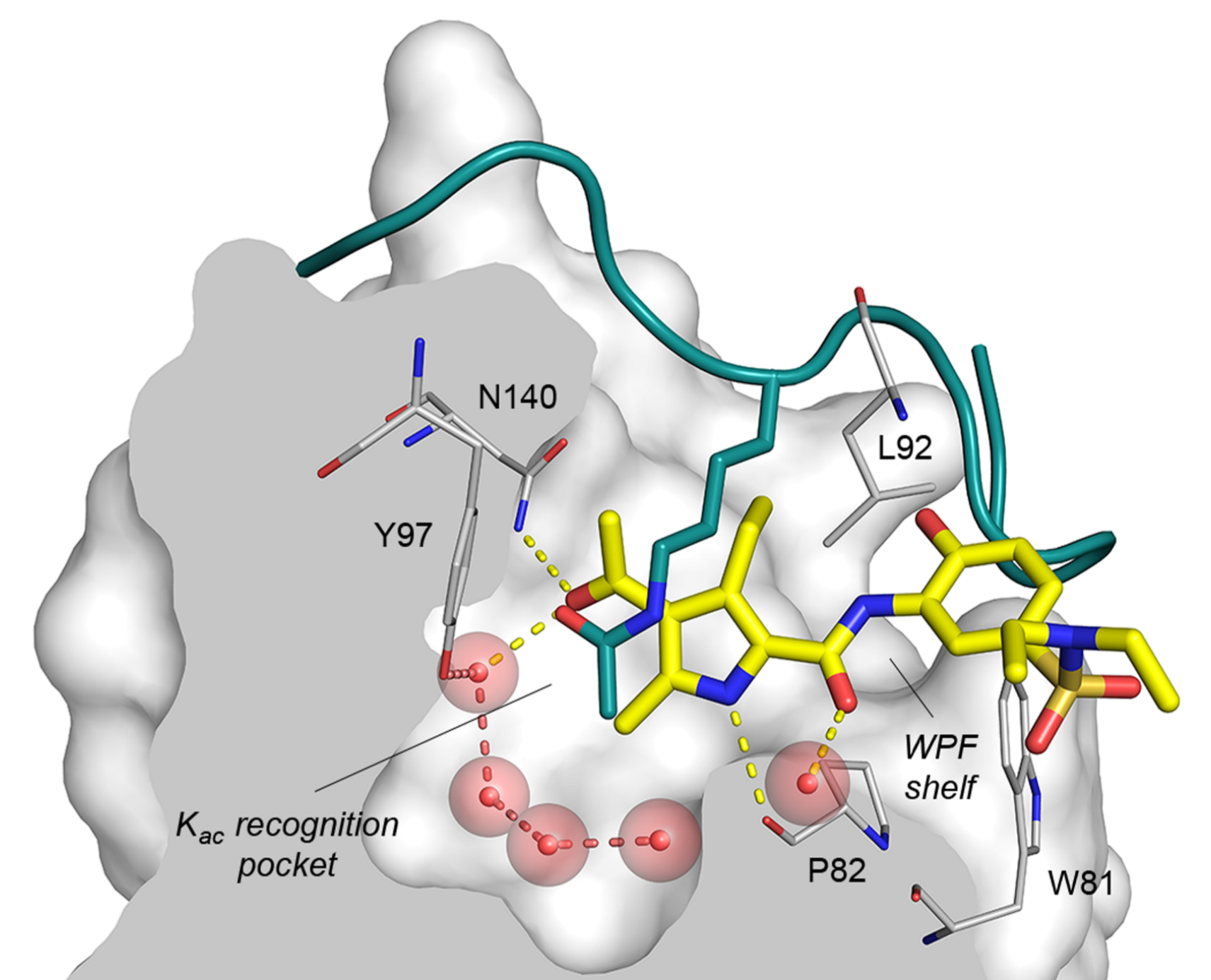
Bromodomains are epigenetic mark 'readers' that specifically recognize ϵ -N-acetylated lysine residues. Their potential as therapeutic targets has attracted much attention due to their implication as regulators of disease-relevant gene expression. We carried out a structure-based drug discovery project focusing on BRD4, a bromodomain of the BET subfamily that has been recently characterized as a key determinant in several types of cancer.

Hit identification



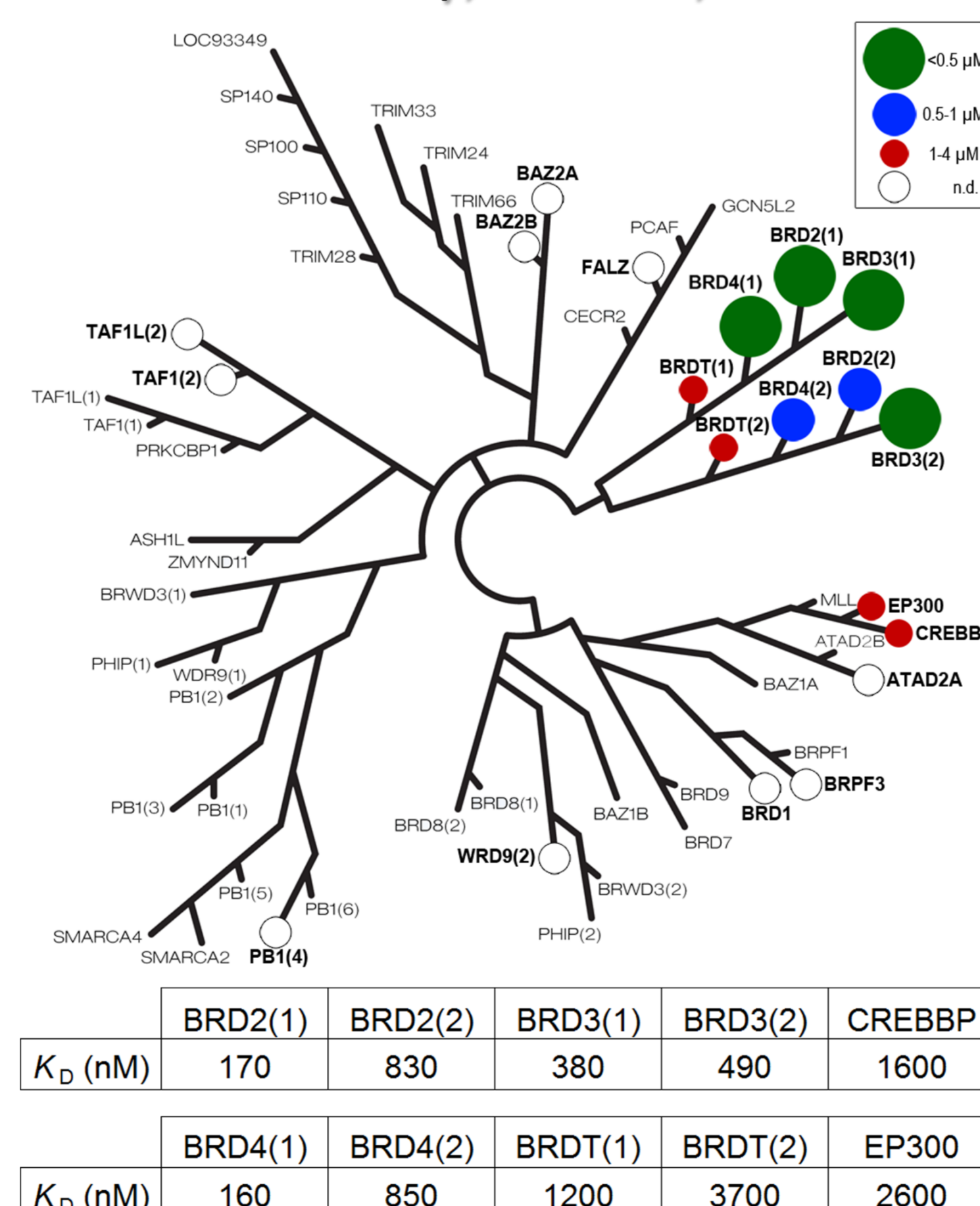
Docking models (turquoise) have accurately predicted the crystallographic binding mode (pale yellow) for identified hits: a) XD1, colchicine; b) XD14; c) XD25, colchicine; and d) XD46.

XD14 (yellow) mimics the recognition of an acetylated lysine peptide (green) by BRD4(1) exploiting key hydrogen-bond interactions. Five conserved water molecules surround the 4-acyl pyrrole core, and the aryl sulfonamide moiety engages in CH- π interactions with W81 and L92 ("WL trap").



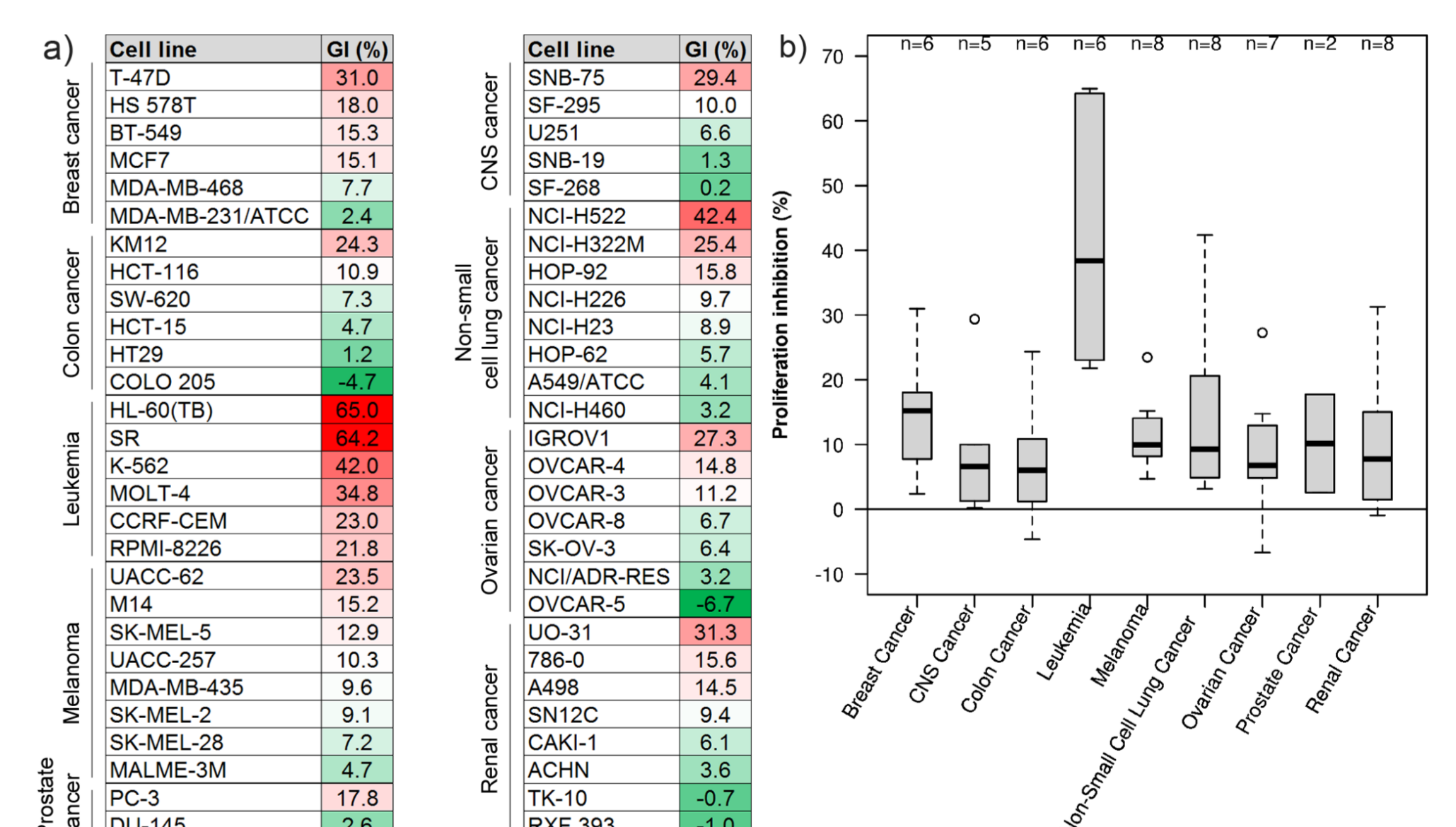
Bromodomain profiling

BROMOscan[®] shows that XD14 selectively inhibits the BET family, CREBBP, and EP300.



Cell proliferation assay

The NCI60 Human Tumor Cell line Anticancer Drug Screen indicates that XD14 selectively inhibits the growth of specific leukemia cell lines.



Conclusions

Structure-based virtual screening of about 9 million small molecules has yielded 7 novel scaffolds inhibiting the epigenetic target BRD4, including the potent 4-acyl pyrrole derivative XD14 ($K_D = 237$ nM). This promising hit compound inhibits the epigenetic target by mimicking the natural substrate, has selectivity for the BET bromodomain family, and inhibits cell proliferation of leukemia cell lines. Currently, *in vivo* activity of XD14 is being assessed and XD46 is being used as starting point for a fragment-based screening approach.



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SFB 992 Medical Epigenetics



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Prinjha RK, Witherington J, Lee K, Trends Pharmacol. Sci. (2012), 33(3): 146-53.

Lucas X, Wohlwend D, Hügler M, Schmidtunz K, Gerhardt S, Schüle R, Jung M, Einsle O, Günther S, Angew. Chem. Int. Ed. (2013), under review.

European Patent Office EP13164209.2.

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