

Atomistic Graph Analysis in Estrogen Receptor Alpha

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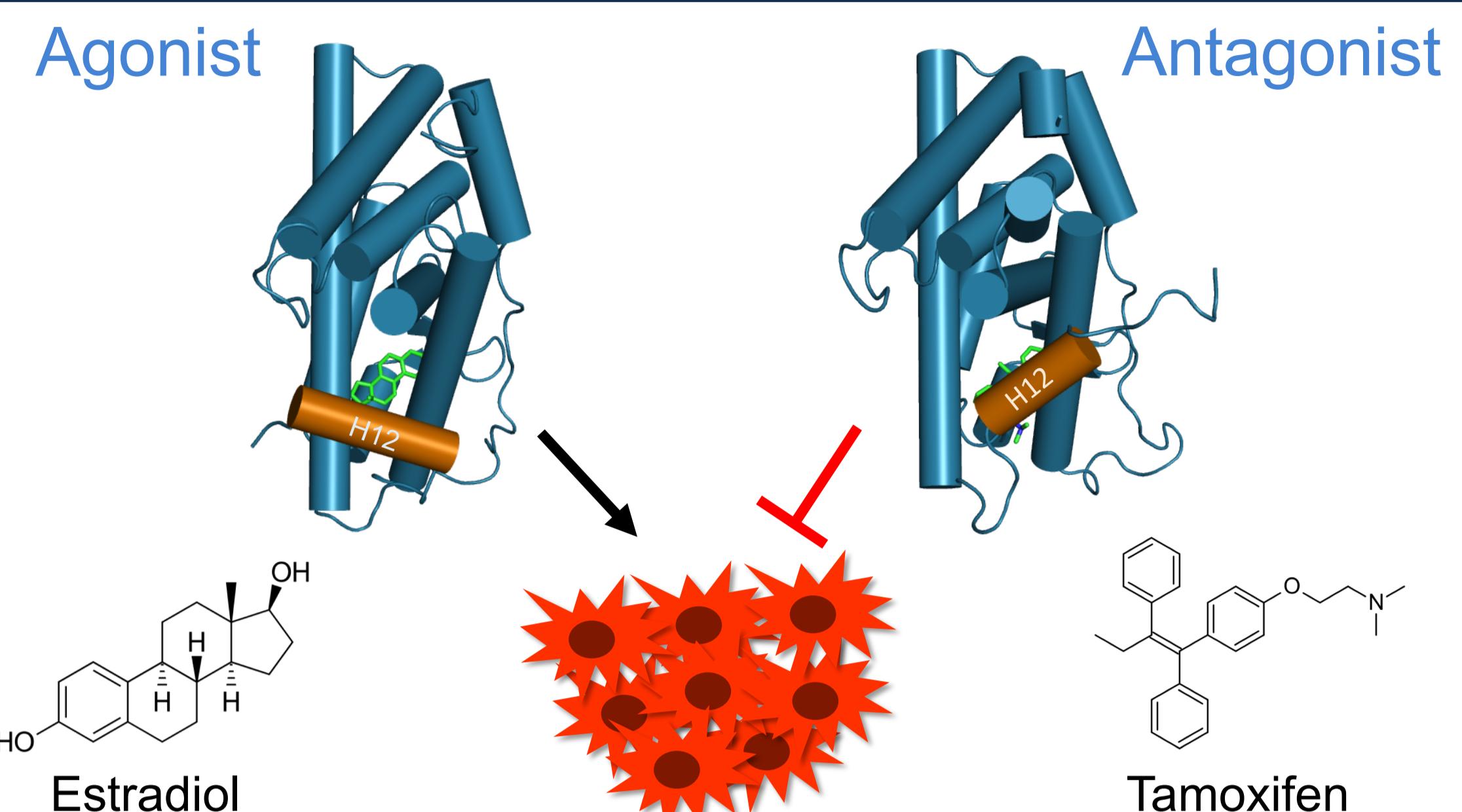
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1. Estrogen receptor alpha is a key player in breast cancer

Estrogen receptor alpha (ER α) is the main driver in breast cancer (BC) development and progression, and drugs inhibiting ER α are the main focus of treatment in BC. Current chemotherapies based on inhibiting ER α become ineffective when recurrent tumours develop resistance against anti-estrogens.

We here present the application of novel diffusion-based approaches to identify potential new target sites in ER α and explore underlying resistance mechanisms.

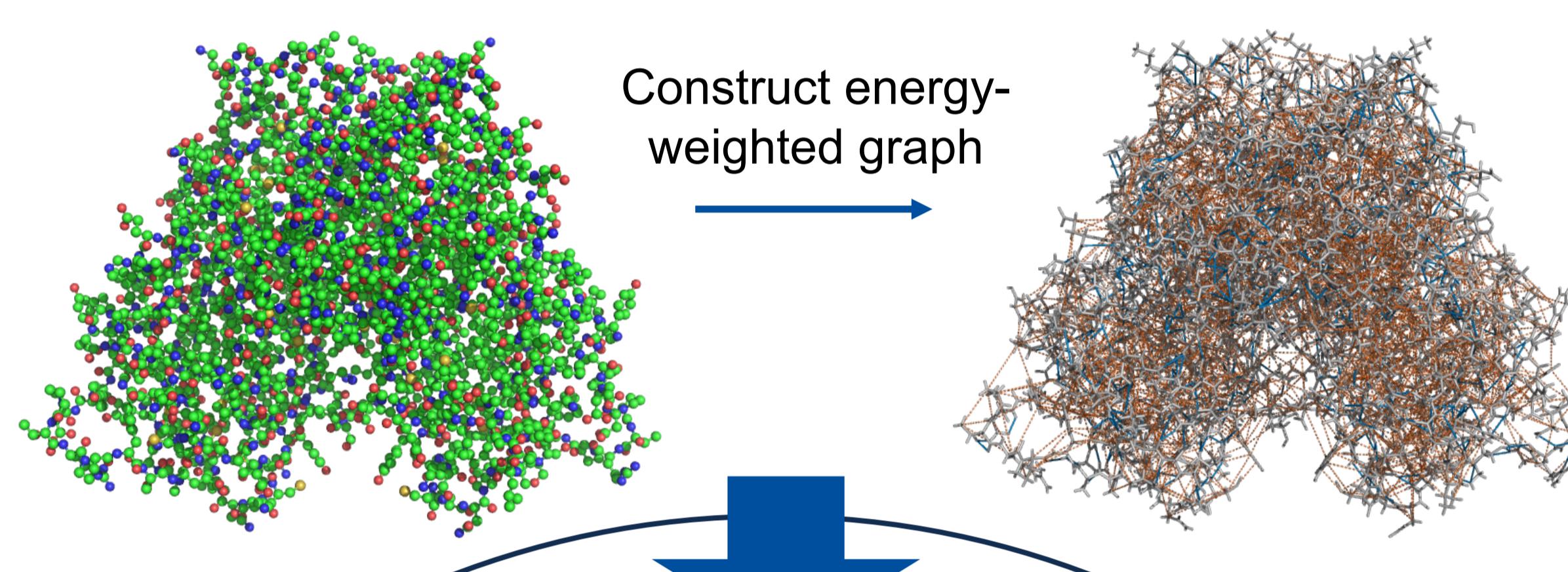
This presents an alternative approach to investigate a well studied protein by providing an atomistic resolution of the molecular mechanism of ER α .



Atomistic graph models reveal molecular mechanism of ER α and allow investigation of cancer mutations with high efficiency.

2. Atomistic, energy-weighted graph construction based on biological structure

Each atom in a biological structure is represented as a node in a graph. This allows us to preserve atomistic detail and distinguishes our methodology from coarse-graining approaches^{1,2}.

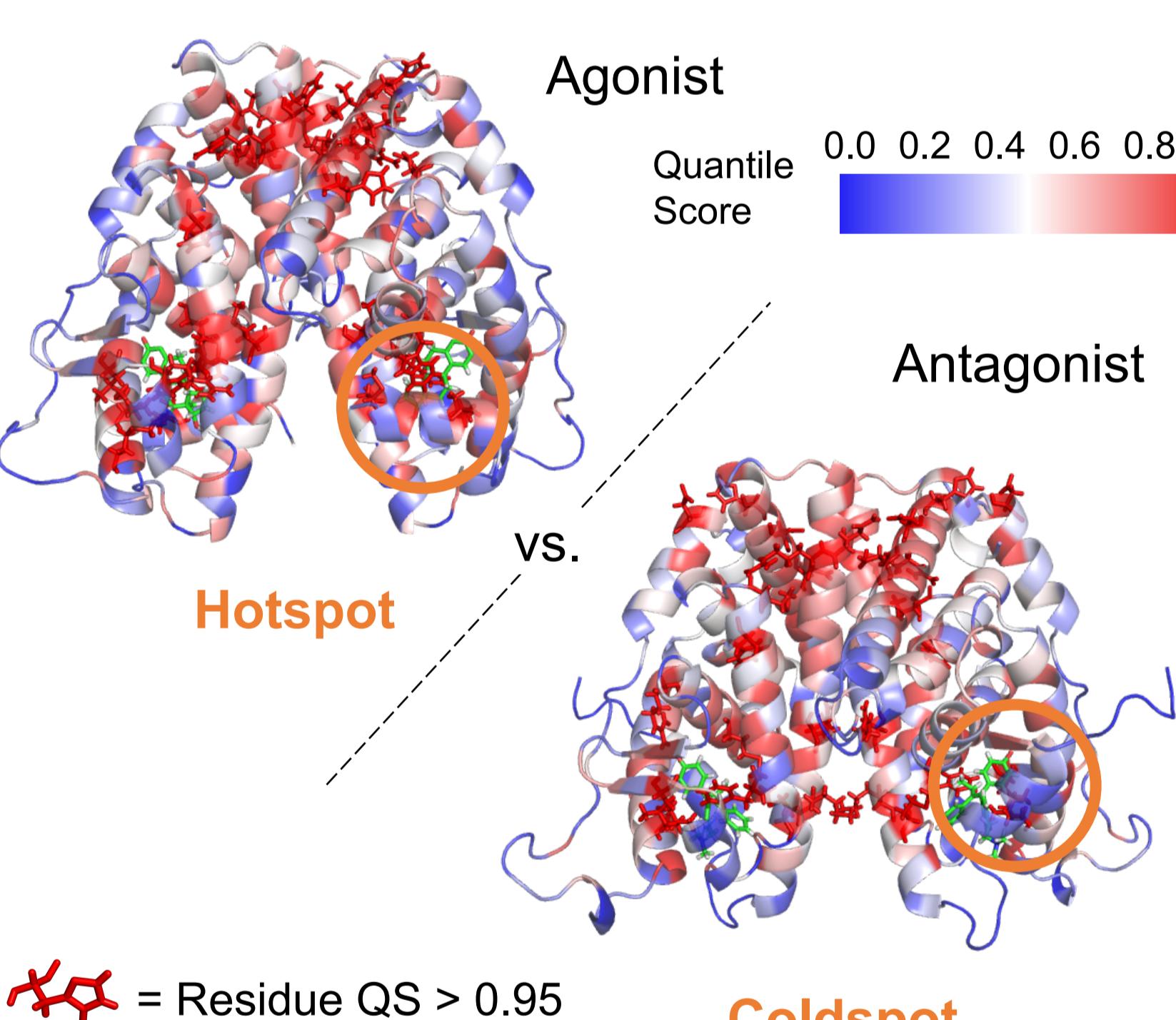


Assigning edge weight according to bond type captures physico-chemical properties of the structure.

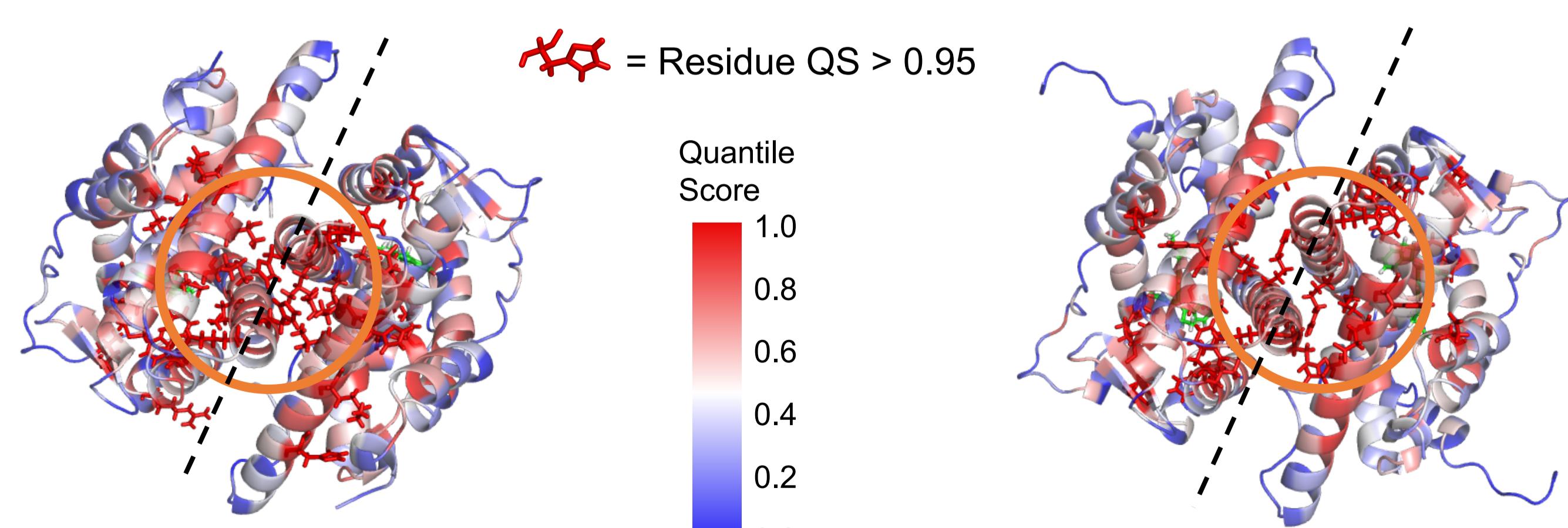
The following bond types are encoded:

1. Covalent bonds
2. Hydrogen bonds
3. Hydrophobic interactions
4. Electrostatic interactions

4. Bond-to-bond propensities reveal communication within ER α



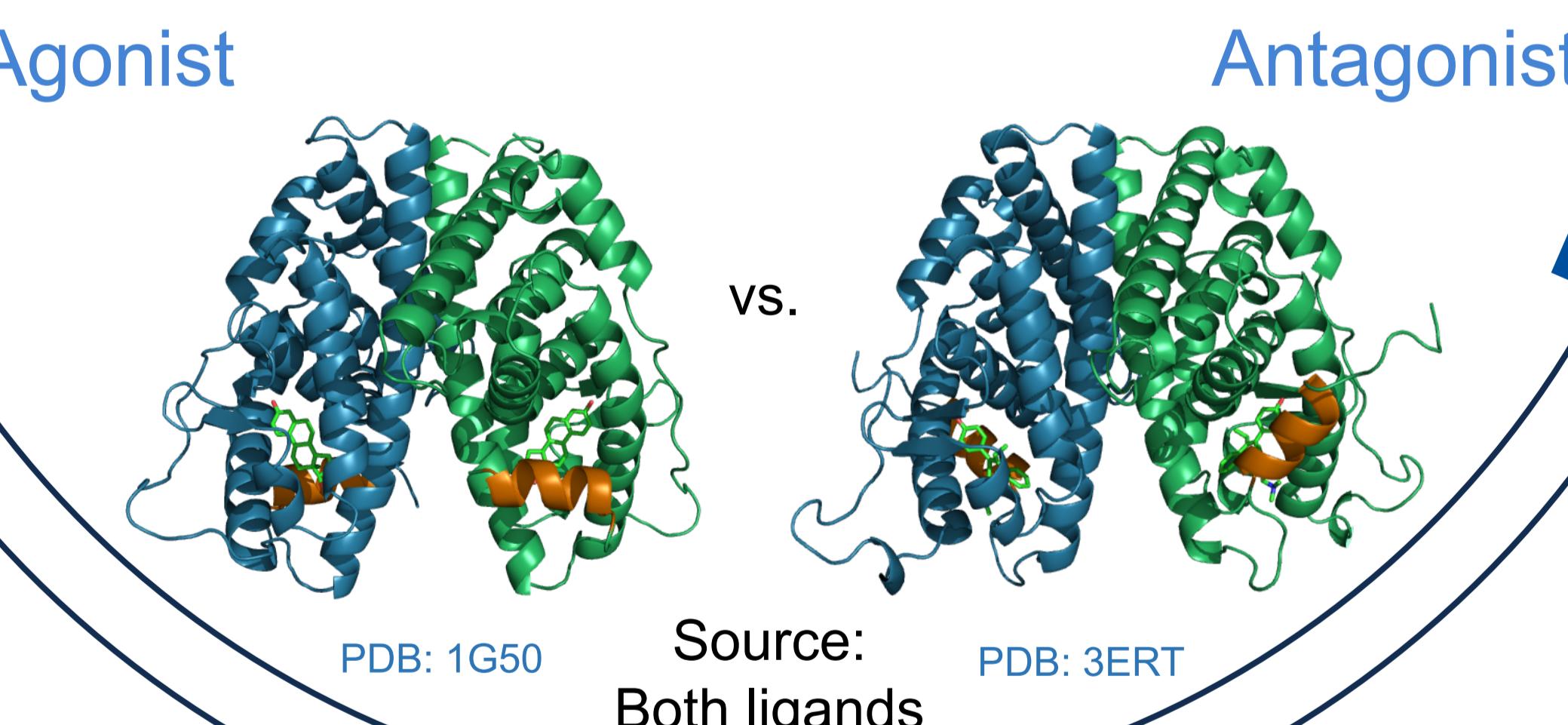
We confirm the molecular mechanism of ER α by calculating the connectivity for each residue respective to the active site. We find a high connectivity between estradiol and helix 12 which is not present in the inhibited protein. This also provided evidence for the necessity of dimer formation that is observed *in vivo*⁴.



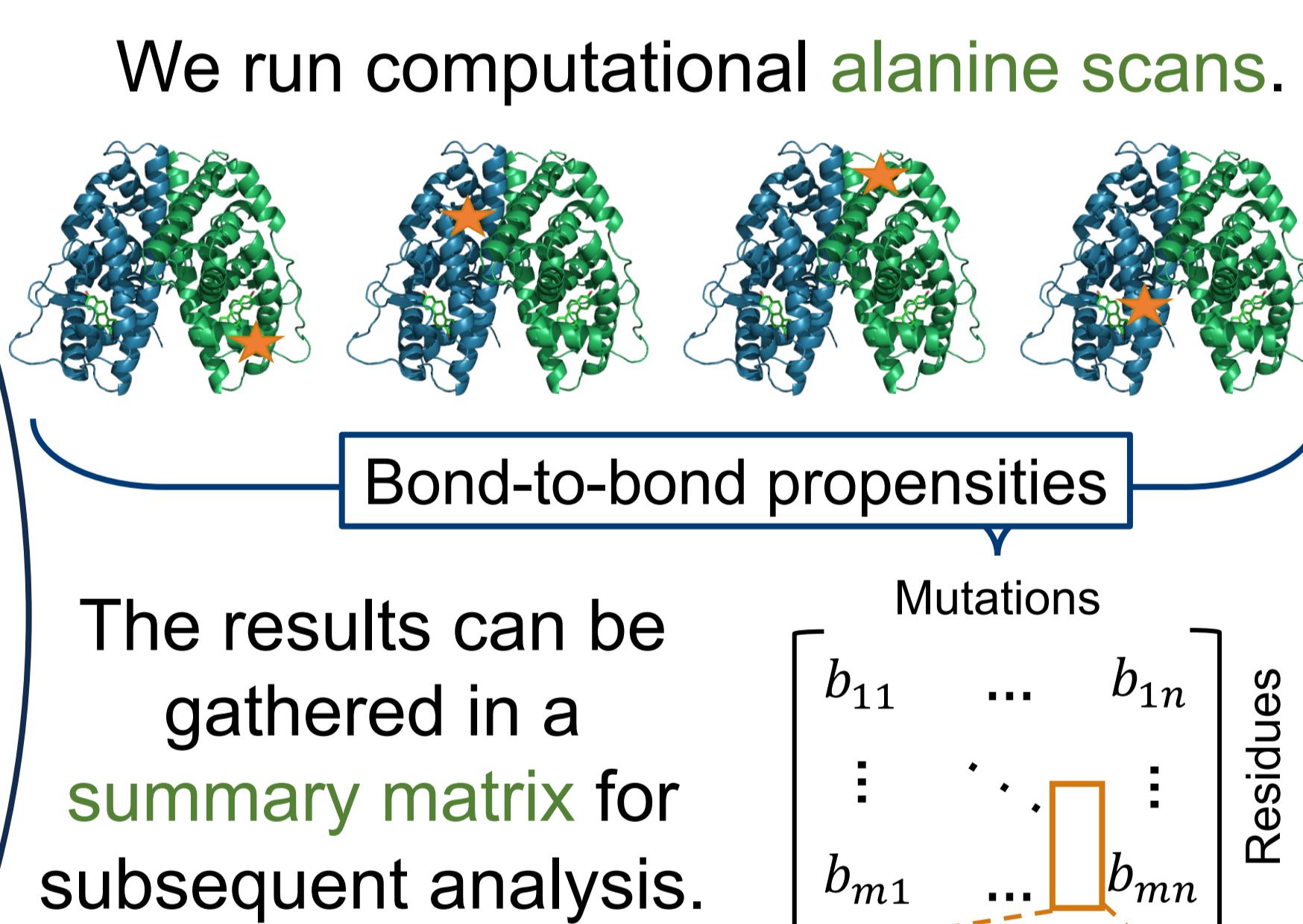
Our methods validate the basis of ER α functionality: positioning of helix 12 and necessity of dimerization.

3. Bond-to-bond Propensities

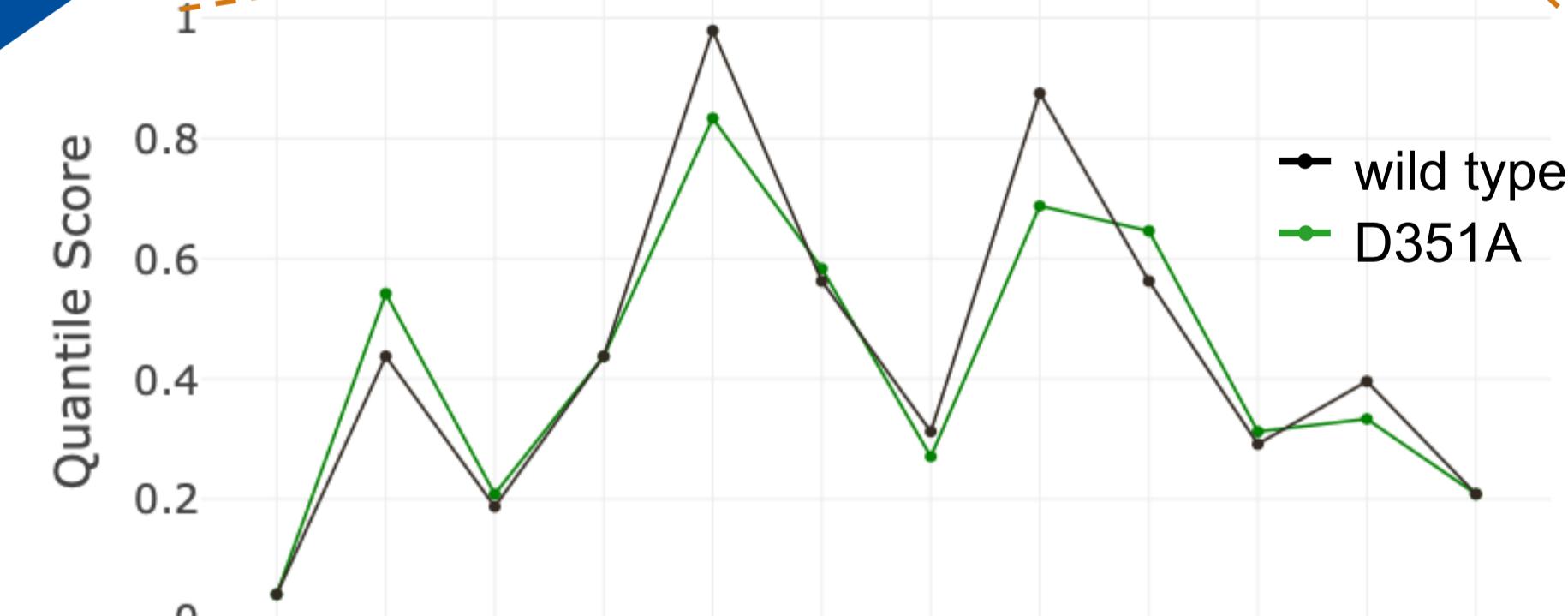
Measure the impact of energy fluctuations of source bonds on any other protein bond. Allows discovery of instantaneous communication between source and target bonds. Quantile regression allows a quantitative ranking of all bonds and subsequently residues. Detects allosteric pathways and sites in proteins and biological complexes³.



5. In-silico mutational studies identify path-disrupting mutations



The results can be gathered in a summary matrix for subsequent analysis.



Zooming into the data, we can gain insights on changes in communication towards helix 12: D351A is a mutation which decreases connectivity with H12 and might hint to a new drug target.

The computational efficiency of our methodology allows mutational studies to identify impactful residues.

Try it yourself!

Our methodologies will be available online in form of a user-friendly, interactive webserver: proteinlens.io

ProteinLens



Funding:

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