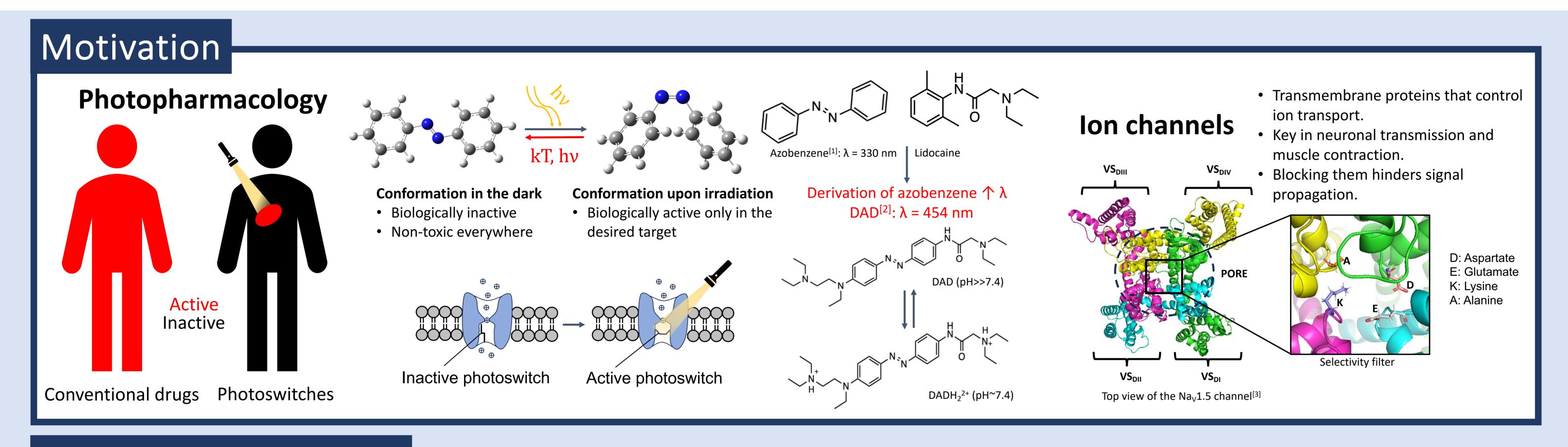
Photophysics and binding pockets of the DAD photoswitch in the $Na_{\rm V}1.5$ channel: a theoretical study.

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Computational details • Binding Pocket search (DADH 2+) Docking

• Binding Pocket search (DADH₂²⁺) Docking \longrightarrow GaMD \longrightarrow CMD \longrightarrow Normalization of pockets

More accurate pockets

• Absorption spectra

Static
vacuum (TDDFT, CASSCF, CASPT2)
and solvent (LR-PCM-TDDFT)

→ DAD, DADH₂²+, azobenzene

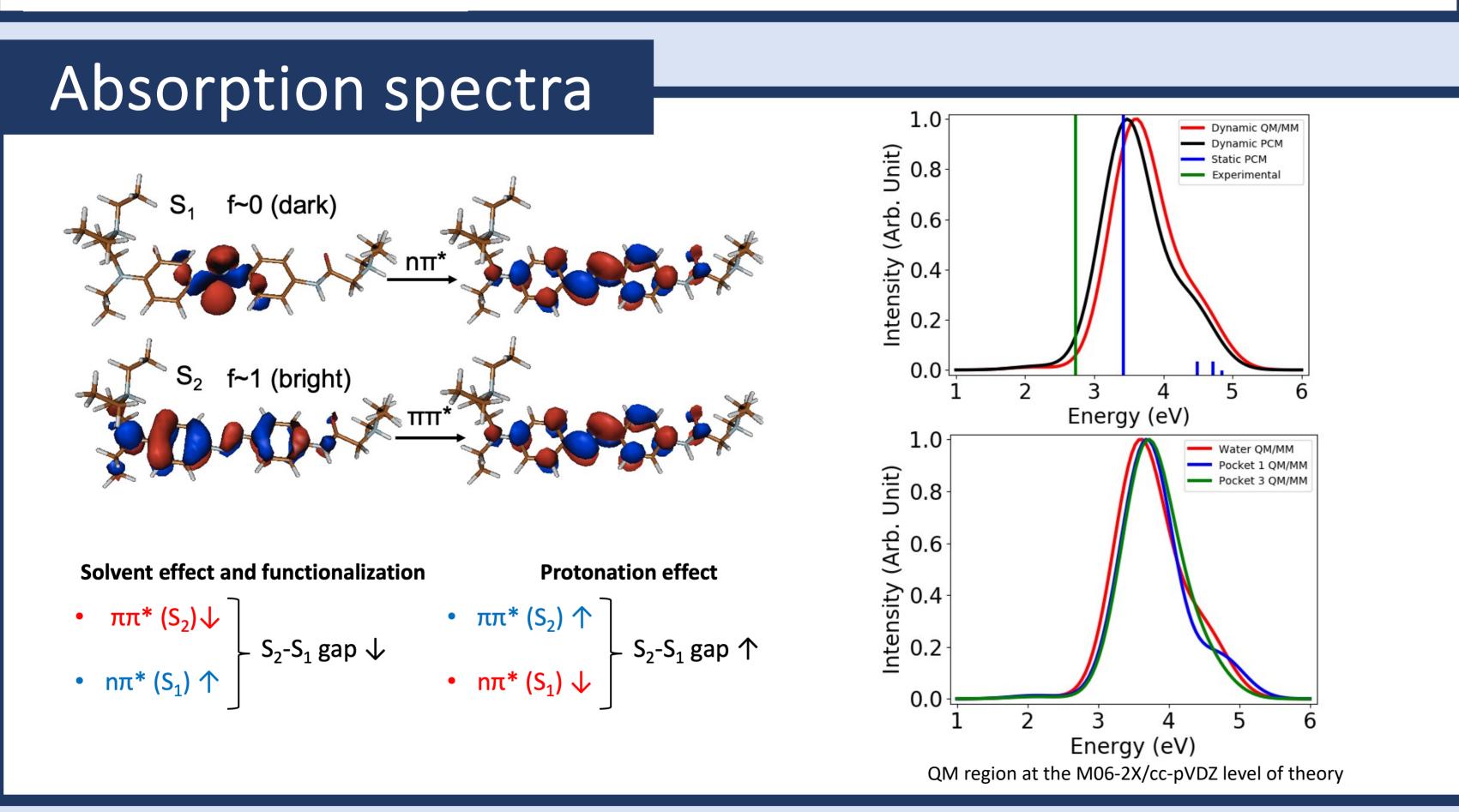
Dynamic
solvent (LR-PCM-TDDFT, QM/MM)
and pockets (QM/MM)

→ QM region = DADH₂²+

• Photoisomerization (DAD, DADH₂²⁺, azobenzene): vacuum (TDDFT) and solvent (LR-PCM-TDDFT)

Reweighting reaction coordinate Reweighting reaction coordinate | Ag of pockets | MMGBSA |

Binding pocket search **MMGBSA** Analysis **Reweighted PES** $\Delta G = -36.56 \text{ kcal/mc}$ 10.0 It may block the 17.5 channel $\Delta G = -56.95 \text{ kcal/mol}$ ₹ 12.5 ₽ 10.0 5.0 Pocket ' 4 6 8 10 Most important contribution to stabilisation: electrostatic RMSD (Å)



References

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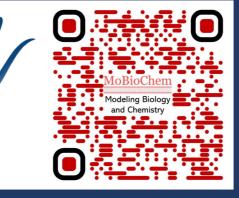
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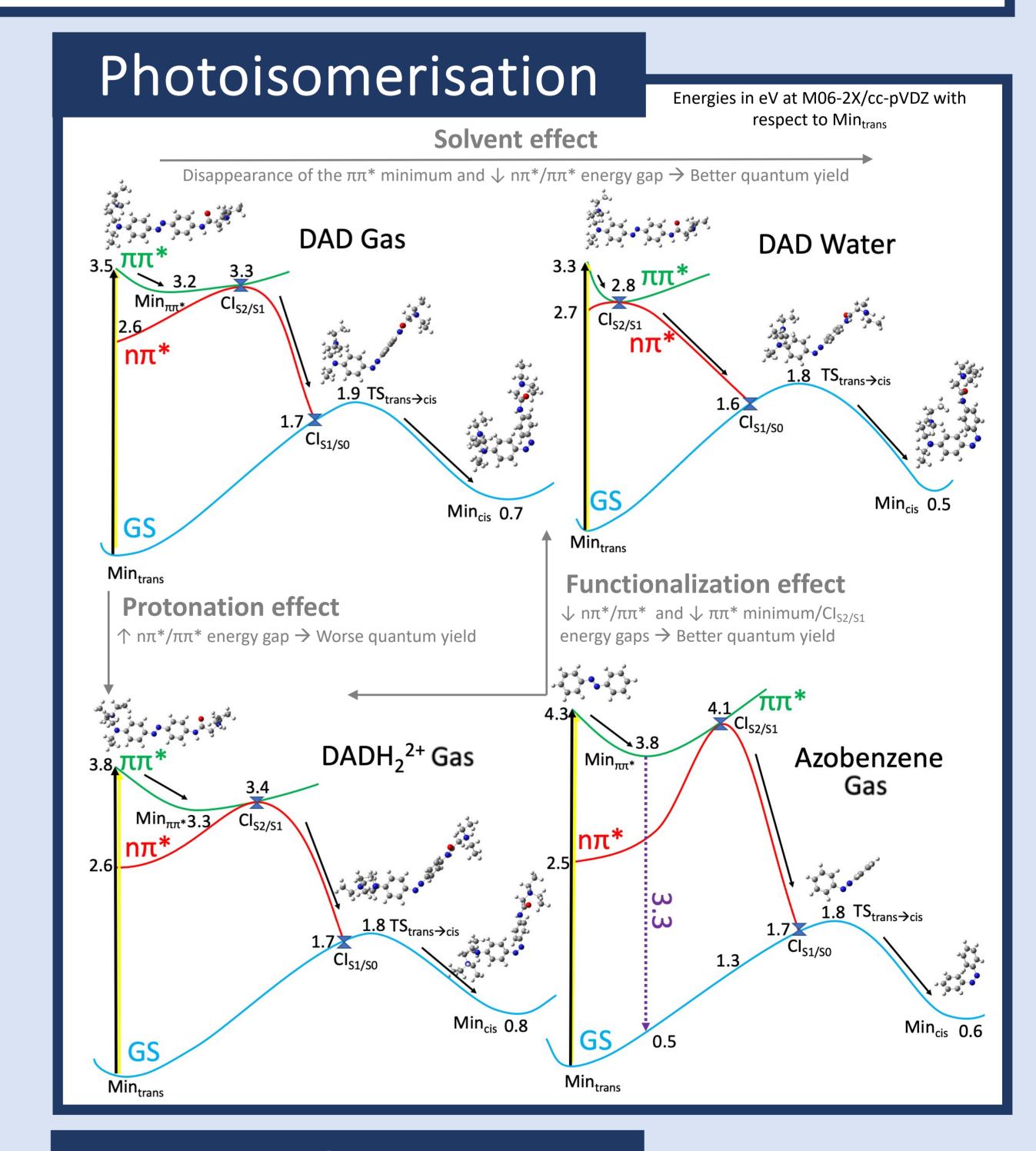
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Conclusions

- Pocket 1 is the most favourable pocket for *trans*-DADH₂²⁺.
- The $n\pi^*/\pi\pi^*$ gap $\left\{ \begin{array}{l} \downarrow \text{ Polar solvents, Derivation of azobenzene} \\ \uparrow \text{ DAD protonation} \end{array} \right.$
- Among the considered systems, the most favourable photoisomerization occurs for DAD in water.
- The QM region will be increased to describe the protein environment more accurately.