

Supplementary Figure 1: Crystallographic structure of compound *Z-***1**. Ellipsoids enclose 50% probability. Front perspective view of the molecule (top) and view in the plane of the indanylidene moiety (bottom). Single yellow crystals of compound *Z-***1** were obtained from a dichloromethanemethanol solution (9: 1 v/v) upon slow evaporation of the solvents in the dark. Single crystal of *Z*-**1** was submitted to X-ray data collection via an Oxford-Diffraction Xcalibur Sapphire 3 diffractometer by using a graphite monochromated Mo-Kα radiation ($λ = 0.71073$ Å) at 293 K in orthorhombic space group. The structure was solved by direct methods, implemented on SHELXS-2014 program. The refinement was carried out by full-matrix anisotropic least squares on F^2 for all reflections for non-H atoms by means of the SHELXL-2014 program (R1(orb data)=0.11). Unfortunately, the data quality is not suitable for a crystallographic deposit, as several atoms are affected by thermal disorder. Presently, it has not been possible to address this issue. However, the acquired data confirm the chemical structure of *Z*-**1** with the distortion of the pyrroline ring placed outside the plane of the molecule, in line with the computational data (compare with Figure 4a). A comparison between the most relevant computed and observed dihedral angles is given in Supplementary Figure 2a.

Values of the C9'-C1'=C4-C5 and C2'-C1'=C4-C3 torsional parameters from the computed (in brackets, see Supplementary Notes 1 and 2 and Supplementary Figures 3 to 5) and available structural data (Supplementary Figure 1) for *Z*-**1**. **b** The same data for *E*-**2**. Notice that, in this case however, the computed parameters (in brackets) are compared with a previously reported [1] precursor of *E*-**2** which is "sterically close" to *E*-**2** (i.e. a H atom is replaced with an O atom)**,** since *E***-2** could not be crystallized.

Supplementary Note 1: Investigation of the room temperature thermal equilibrium in methanol

In order to theoretically describe the spectroscopic and dynamic properties of the studied molecular switches a QM/MM-based protocol oriented to generate an *average configuration* of the *solvent environment* at the *desired temperature* was used to optimize the ground state geometries and generate initial conditions to initiate exited states dynamics. The proposed protocol [2] is based on the idea of Herbert *et al*. [3,4] of combining the Average Solvent Electrostatic Configuration (ASEC) model [5,6] and the free energy gradient method proposed by M. Nagaoka *et. al.* to optimize solvated molecular systems.[7-9] In this QM/MM model the solute is considered quantum mechanically (QM) while a molecular mechanic force field is used to describe the solvent environment (MM).

As stated by M. Nagaoka *et. al.*, [7-9] the free energy gradient, or the forces *F(q)* acting on the QM part of the system, can be computed as:

$$
F(q) = -\frac{\partial G(q)}{\partial q} = -\langle \frac{\partial V}{\partial q} \rangle \approx -\frac{\partial \langle V \rangle}{\partial q},
$$

where *q* represents the coordinates of the QM part and *G* is the free energy of the system, which can be computed, in a very good approximation, as the average of the potential interaction, $\langle V \rangle$, between the QM and MM subsystems. In this context, the ASEC model [6,7] is used to compute, in a very efficient way, the average potential interaction $\langle V \rangle$. ASEC model is a mathematical construct called "ASEC configuration" created from a selected sampling of configurations, obtained via extensive molecular dynamics (MD), to mimic the effect of thermodynamic equilibrium conditions at a selected temperature. The solute is kept fixed along the MD in order to sample the environment, being subsequently optimized in the presence of the average external configuration (Supplementary Figure 3a). The GROMACS code [10] was used for the MD, performing an initial thermalization of 1 ns, followed by 4 ns of production in the *NPT* ensemble and standard room conditions. The QM/MM geometry optimization is performed using the quasi-Newton-Raphson method implemented in the MOLCAS-TINKER interface.[11, 12] The QM subsystem is described using Complete Active Space Self Consistent Field (CASSCF) method.[13] For the MM subsystem, OPLS force field parameters are used.[14] Finally, the absorption energies of optimized structures are re-computed using second order perturbation theory (CASPT2)[15] with ionization potential electronic affinity (IPEA) set to zero. An active space comprising of 12 electrons in 11 orbitals is used for all QM calculations in current study.

Since the configurations of the environment selected to generate the ASEC configuration (100 solute-solvent uncorrelated configurations in our case) are obtained from the system into thermodynamic equilibrium conditions, a Boltzmann distribution of the absorption energies is expected to be observed from those structure. Therefore, these 100 configurations can be used to initiate excited state dynamics. For the two molecular switches, absorption bands were constructed (Supplementary Figure 4). A single configuration from each band, representing the average was selected to map the potential energy surfaces. The selected two configurations were re-optimized on the ground state. The setup used for optimization and subsequent QM/MM calculations is shown in Supplementary Figure 3b. The vertical excitation energies and oscillator strengths were computed for the ground state optimized structures. According to oscillator strengths, the transition from ground state to second excited state (S_0 to S_2) was highly probable in both switches. Therefore, minimum energy path (MEP) calculation and Franck-Condon trajectory for each of the two switches were initiated from S_2 . The MEP calculation resulted in minima on S_2 and S_1 for Z -**1** and E -**2** switches respectively (Supplementary Figures 5c and 5d). Starting from these minima, torsional scans for each switch was performed by constraining the dihedrals C9'-C1'=C4-C5 and C2'-C1'=C4-C3 (see Supplementary Figure 6). The Franck-Condon trajectories were computed at 3-root-state-average CASSCF/6-31G*/OPLS level. This was performed using the Dynamix module implemented in the MOLCAS program and more details can be found in Schapiro et al.[16] Since the CASSCF method does not account for dynamic electron correlation, the energy profiles had to be recomputed using a method that doesn't suffer from this problem. Due to this reason, for each geometry along the trajectories, the energies were recomputed at 4-root-state-average CASPT2 and XMCQDPT2 levels (see Supplementary Note 3 for more details on the latter).

Supplementary Figure 3: QM/MM setups used in current study. a. ASEC cavity hosting *Z-***1** molecular switch. The switch (orange) is treated at QM level whereas the configurations (green) at MM level. **b.** QM/MM setup used to study the single configurations. The switch (orange) is treated at QM level. Solvent molecules within 4 Å distant are treated as MM active (light green) while the rest (gray) is kept frozen MM level.

Supplementary Figure 4: Distribution of energies of 100 configurations of *Z-***1 (a.) and** *E-***2 (b.)** switches. Red and green circles denote energies computed by ASEC and single S₀ configurations representing the ASEC result (see Supplementary Note 2 below) respectively. Notice that the simulated distributions consistently replicate the absorption bands displayed in Figure 1 both in λ_{max} and width.

Supplementary Note 2: Computation of a representative QM/MM structure in solution

Parts a. and b. of Supplementary Figure 5 illustrate the steric clash/pretwist in *Z-***1** and geared/planar conformation in *E-***2**. In *Z*-**1**, the steric clash of the nearly eclipsed hydrogens at C3 with the methyl groups at C2' as well as the clash of the methyl group and hydrogen at C5 and C8' respectively result in a strongly twisted S_0 equilibrium conformation. Instead structure E -2 displays a substantially planarized S_0 conformation, where the small H substituent at C5 assumes a geared configuration with respect to the two relatively bulky methyl groups at C2'. The corresponding equilibrium S_1 structures (see parts c. and d. in Supplementary Figure 5) are computed by optimizing on the S_1 state a single equilibrium S₀ configuration obtained in the following way: (i) Selecting from the ASEC configuration (composed by 100 overlapping configurations) a single configuration component featuring the absorption maximum closest to the ASEC absorption maximum and (ii) performing a QM/MM geometry optimization in S_0 starting from this structure and relaxing both the QM part and the mobile solvent cavity (the MM cavity of Supplementary Figure 3b). The resulting optimized structure has then an absorption maximum very close to the ASEC absorption (these two values are indicated with green and red circles in Supplementary Figure 4 respectively).

Supplementary Figure 5: Comparison of S⁰ optimized and S¹ optimized geometries. Bond length values are in angstrom and dihedral angles are in degrees. The S_0 (ground state) structures are the geometrically optimized ASEC structures. The S_1 structures (excited state) are single configurations obtained by optimizing on S_1 state a specifically constructed single S_0 configuration. The corresponding Cartesian coordinates are given in the Supplementary Tables 1, 2, 4 and 5. Notice that the excited state structure of E -2 has actually been optimized on the S_2 state as this state is actually the spectroscopic state at the CASSCF level (see Supplementary Figures 6c and 6d).

Supplementary Figure 6: Energy and charge profiles along the relaxed scan. The energy profiles of *Z*-**1** and *E*-**2** are shown in (a) and (c) respectively. Notice the flat or slightly uphill *E-***2** reaction path region between -150 and -170 degrees (part c) which is absent in *Z-***1**. The corresponding charge profiles are shown in (b) and (d). The charges are computed for the pyrroline fragment (see Figure 4 in the main text). S_0 to S_3 states are represented by blue, green, red and yellow colors respectively. CASSCF and CASPT2 energy profiles are shown in solid and dashed lines.

Supplementary Note 3: XMCQDPT2 energy profiles of *Z***-1 and** *E***-2 trajectories.**

Although the CASPT2 method accounts for dynamic electron correlation and results in better energies with respect to CASSCF, it fails to describe near degeneracy regions [17-19]. Due to this reason, the energy profiles along the trajectories were also computed at the extended multiconfigurational quasidegenerate second order perturbation theory (XMCQDPT2) [19]. This was performed using the Firefly computer package [20]. The resulting XMCQDPT2 energy profiles are reported in the Supplementary Figure 7. By comparing these with the corresponding CASPT2 energies reported in Figure 4, one can clearly see that crossings between potential energy surfaces at CASPT2 level have now become avoided crossings.

Supplementary Figure 7: XMCQDPT2 energy profiles. Energies of *Z*-**1** and *E*-**2** trajectories recomputed at XMCQDPT2 level of theory are shown in (a) and (b) respectively. Note that the S₁/S₀ crossing of Z-1 at CASPT2 level is an avoided crossing at the XMCQDPT2 level.

Supplementary Figure 8: Excited state geometrical progression along the isomerization coordinate. Left. First 100 fs evolution of the bond length alternation stretching coordinate (BLA), double bond isomerization coordinate (-C9'-C1'=C4-C5-) and pyrroline out-of-plane deformation coordinate (=N-C2- C3-C4-) along the FC trajectory of *Z*-**1**. Right. Same data for the FC trajectory of *E*-**2**. The times given along the *Z*-**1** coordinate show that the BLA mode is populated immediately, that the -C9'-C1'=C4-C5 isomerization activate only after 11 fs and that the out of plane deformation becomes active only after 32 fs. In contrast, along the *E*-**2** deformation coordinate, only BLA is active during the first 100 fs.

Supplementary Figure 9: Contribution of the excited state out-of-plane ring deformations along the isomerization coordinate of *Z***-1 and** *E***-2.** Upper panels. Progression along the reaction coordinate of *Z*-**1** (left) and *E*-**2** (right) of the out-of-plane deformation of the indanylidene five-membered ring (described by the C1'-C2'-C3'-C4' dihedral. See dashed-dotted line). The BLA stretching coordinate (dashed line) and -C9'-C1'=C4-C5- isomerization coordinates (full line) are reported for comparison. Lower panel. The same diagram for the out-of-plane deformation of the pyrroline ring (reflected by the =N-C2-C3-C4- dihedral, dashed-dotted line). Note that the coordinate evolution represented in the left and right panels for the pyrroline ring are associated to the left and right diagrams of Supplementary Figure 8, respectively.

Supplementary Table 1: Cartesian coordinates of the *Z*-1 S₀ optimized structure

Supplementary Table 2: Cartesian coordinates of the *Z*-1 S₁ optimized structure

Supplementary Table 3: Cartesian coordinates of the *Z*-1 structure corresponding to S₁/S₀ CInt

Supplementary Table 4: Cartesian coordinates of the *E-***2** S₀ optimized structure

Supplementary Table 5: Cartesian coordinates of the *E-***2** S₁ optimized structure

Supplementary References

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