Electronic Supplementary Material (ESI) for Organic & Biomolecular Chemistry.

Molecular Recognition Controlled Stereomutation Cycle in a Dynamic Helical Assembly

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1. General Methods

Transmission Electron Microscopy (TEM): TEM measurements were performed on a JEOL, JEM 3010 operated at 300 kV. Samples were prepared by placing a drop of the solution on carbon coated copper grids followed by drying at room temperature. The images were recorded with an operating voltage 300 kV. In order to get a better contrast sample was stained with uranyl acetate (1 wt % in water) before the measurements. For TEM, water was used instead of aq. HEPES solution to avoid masking of nanostructures due to HEPES deposition upon drying.

Optical Measurements: Electronic absorption spectra were recorded on a Perkin Elmer Lambda 900 UV-Vis-NIR Spectrometer and emission spectra were recorded on Perkin Elmer Ls 55 Luminescence Spectrometer. UV-Vis and emission spectra were recorded in 10 mm path length cuvettes. Fluorescence spectra of solutions were recorded with 470 nm excitation wavelength. Circular Dichroism measurements were performed on a Jasco J-815 spectrometer where the sensitivity, time constant and scan rate were chosen appropriately.

Sample Preparation: All samples for spectroscopic measurements were prepared by injecting the stock solution of **PDPA** (solvent MeCN) into required volume of solvent (aq. HEPES buffer in MeCN, wherever applicable). To that required amount of phosphates were injected and the solution was mixed by manual mixing before measurements.

Aq. HEPES buffer was prepared by making 10 mM solution of the compound in water.

Phosphates stock solutions were prepared in 10^{-2} M concentration by dissolving the required amount of compound in HEPES buffer solution.

Association Constant Measurement: All association constants were obtained using "GraphPad PRISM" software.[1] For Ka (AMP) i.e. association constant of AMP binding, the AMP binding titration was fit using the model "One site-specific binding with saturation". The obtained Kd (dissociation constant) was used to determine the Ka of AMP binding.

For ATP binding, due to its sigmoidal titration curve with cooperative binding, it could not be fit into the standard model for obtaining Ka (ATP). Even ITC (Isothermal Titration Calorimetry) measurements failed to provide reliable data due to binary mixture of solvent (MeCN and water), where enthalpy of solvent mixing interferes with the binding parameters. Thus, it was indirectly obtained by competitive binding experiment where AMP with known Ka is replaced by ATP. This titration was fit using "GraphPad PRISM" with the corresponding "Competitive Binding" with "One site-Fit Ki" model.

Materials: All chemicals / solvents were purchased from the commercial sources and were used as such. Spectroscopic grade solvents were used for all optical measurements.

Legends in graphs represent molar equivalents with respect to **PDPA**.

2. Synthesis

PDPA was synthesized and characterized according to the literature procedure.[2]

Supporting Figures

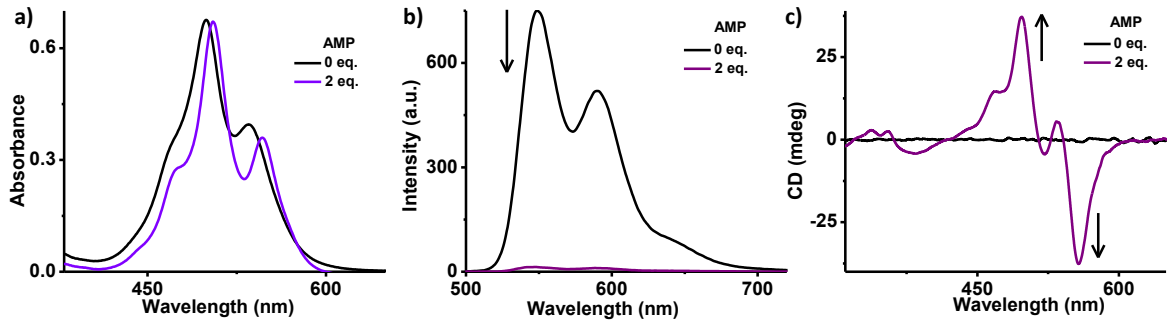

Fig. S1 Variation in the a) absorption spectra, b) emission spectra (λ_{ex} = 470 nm) and c) CD signal of **PDPA** upon addition of adenosine monophosphate (AMP) (90% aq. HEPES in MeCN, c = 2 x 10^{-5} M).

Binding of adenosine monophosphates (AMP) to **PDPA** stacks i.e. **PDPA-AMP** (90% aq. HEPES in MeCN, 2 x 10^{-5} M) led to complete quenching of monomeric emission band at 549 nm and 590 nm indicates further ordering of stacks.

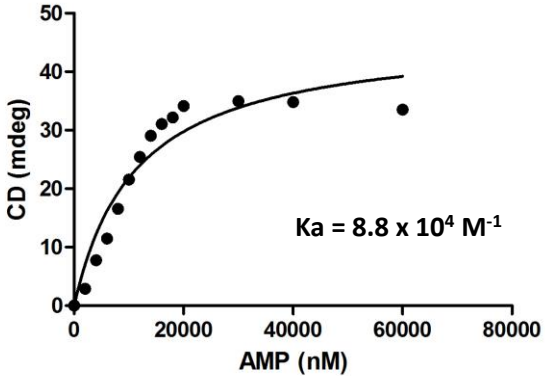

Fig. S2 Evolution of CD signal upon titration with AMP (90% aq. HEPES in MeCN, c = 2 x 10^{-5} M PDPA). AMP is reported in nM concentration unit. This titration curve was fit using "GraphPad Prism" software with the model "One site-specific binding with saturation". The obtained Kd (dissociation constant) was used to determine the Ka of AMP binding which was obtained to be 8.8 x 10^4 M^{-1}.

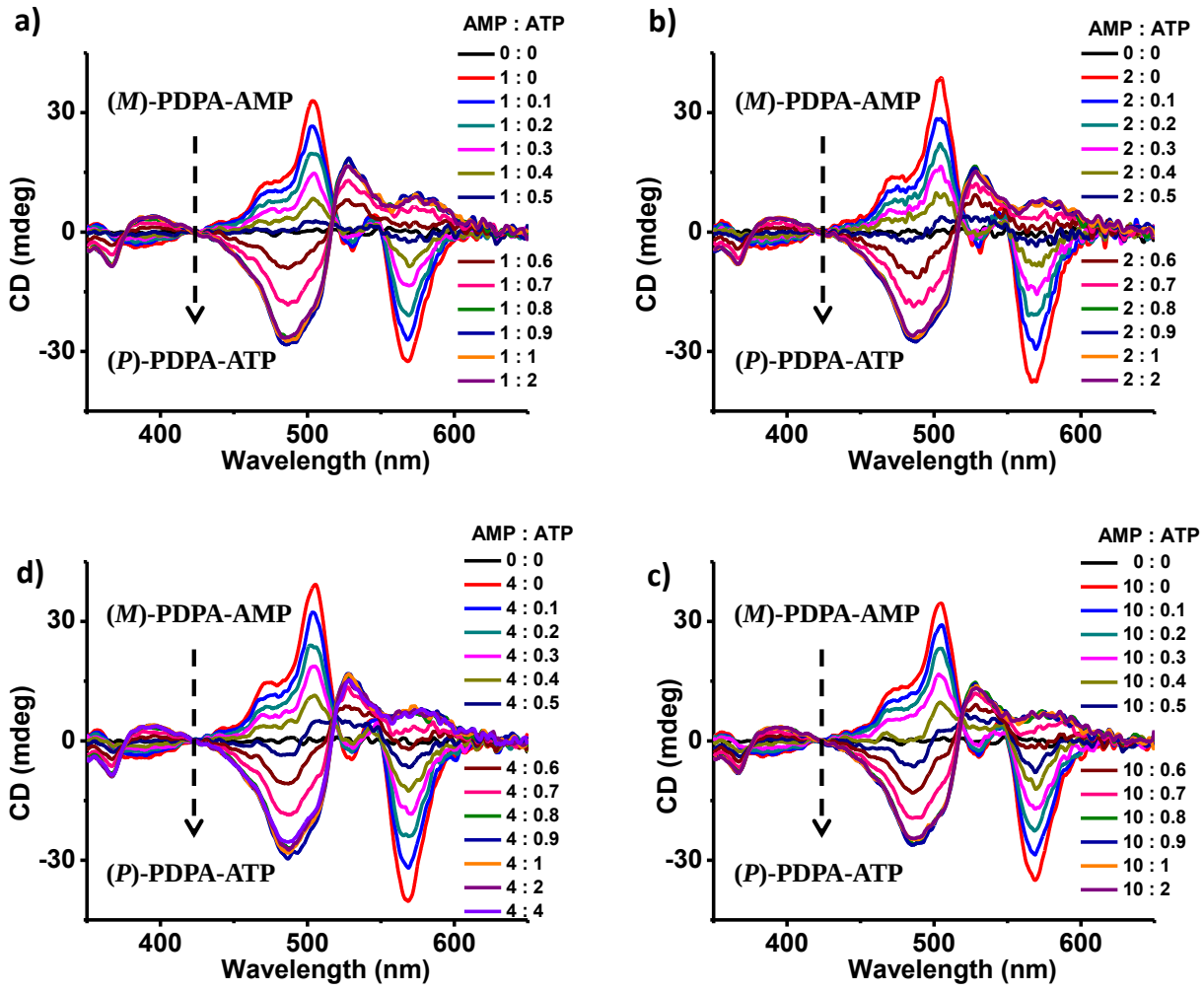

Fig. S3 . Variation in CD spectra upon addition of ATP to **(*M*)-PDPA-AMP** solution with a) 1 eq. AMP, b) 2 eq. AMP, c) 4 eq. AMP and d) 10 eq. AMP (90% aq. HEPES in MeCN, c = 2 x 10^{-5} M).

The replacement of AMP by ATP is very efficient as seen from the fact that even in the presence of excess AMP like 10 eq., the stoichiometric amount of ATP is enough to replace all AMP (Fig. S4). This competitive binding titration of ATP with varying amount of AMP was used to obtain the association constant of ATP. This titration curve with log [ATP] on x-axis and CD signal on y-axis was fit using "GraphPad PRISM" with the corresponding "Competitive Binding" with "One site-Fit Ki" model. Thus, by feeding in the Ka (AMP) value, we could indirectly determine the Ka of ATP binding.[3] Highest Ka (ATP) obtained was 1.2 x 10^6 M^{-1} which is more than an order higher than the Ka (AMP), thus reiterating the fact that the bound AMP can be easily replaced by ATP.

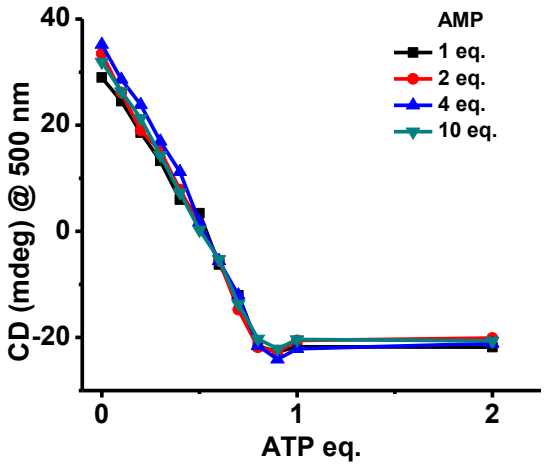

Fig. S4 Plot of variation in CD signal of **(*M*)-PDPA-AMP** upon titration with ATP at different concentration of initial AMP (90% aq. HEPES in MeCN, c = 2 x 10^{-5} M). This data was obtained from Fig. S3.

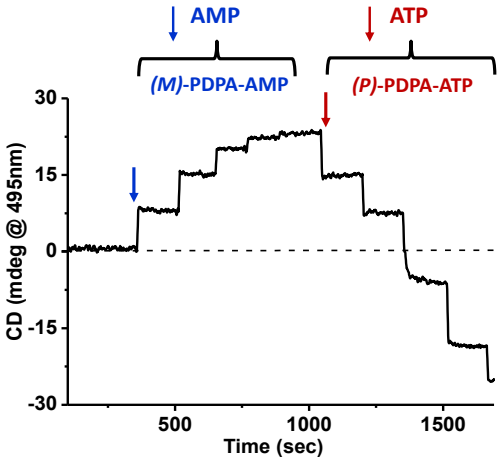

Fig. S5 Plot of variation in CD signal (495 nm) with time upon sequential addition of AMP (blue arrow) followed by ATP (red arrow). These data show sharp jumps in CD intensity confirming very fast response to change of binding phosphates (90% aq. HEPES in MeCN, c = 2 x 10^{-5} M).

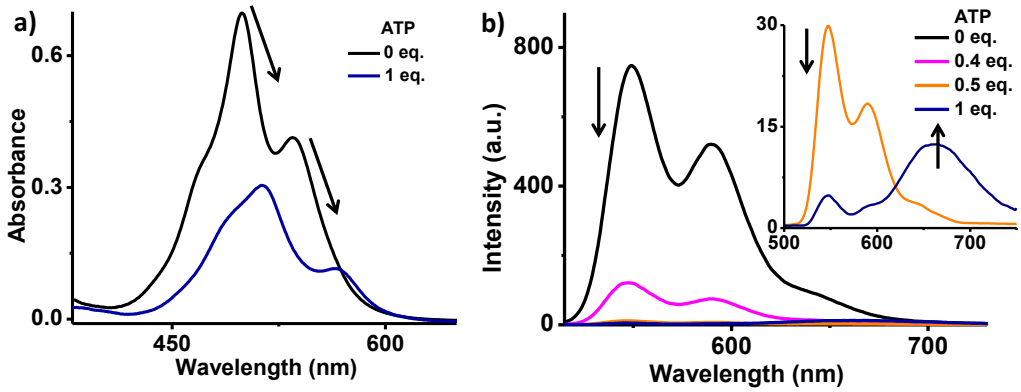

Fig. S6 Variation in the a) absorption spectra and b) emission spectra (λ_{ex} = 470 nm) of **PDPA** upon interaction with ATP (90% aq. HEPES in MeCN, c = 2 x 10^{-5} M). Inset in b) is obtained by magnifying a portion of the fluorescence spectra.

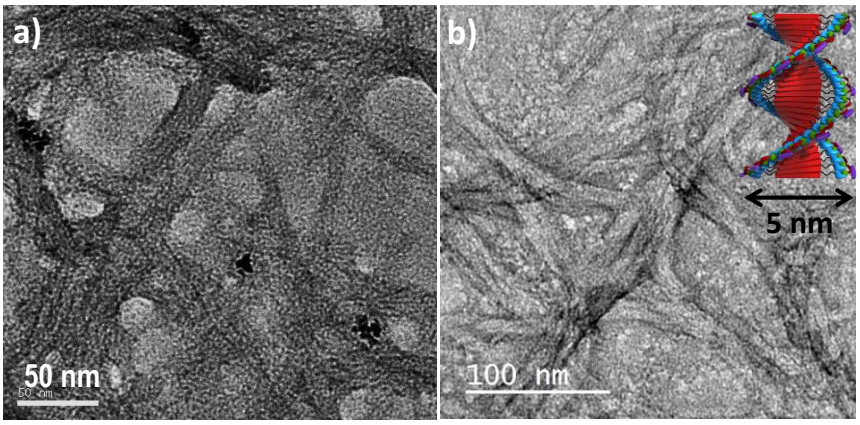

Fig. S7 TEM micrographs of **PDPA** assembly in presence of a) 1 eq. ATP, b) 4 eq. AMP followed by 1 eq. ATP showing morphological similarity of aggregates forming well-defined 1-D nanofibers, confirming replacement of bound AMP by ATP (90% water in MeCN, 2 x 10^{-5} M). Inset in b) is a schematic illustration of the supramolecular organization in **(*P*)-PDPA-ATP** assembly.

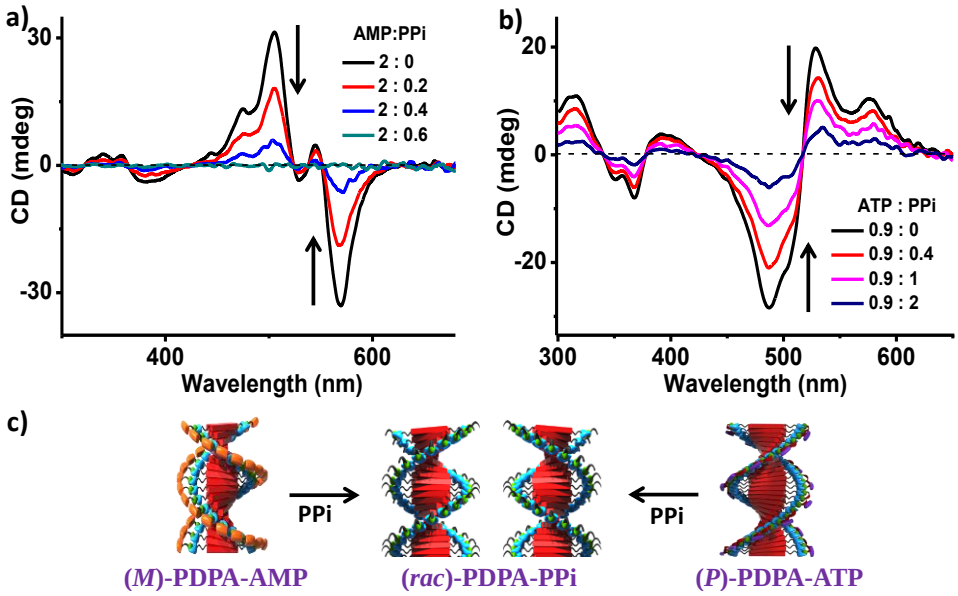

Fig. S8 Variation in CD signal upon addition of achiral PPi to a) **(*M*)-PDPA-AMP** and b) **(*P*)-PDPA-ATP** (90% aq. HEPES in MeCN, c = 2 x 10^{-5} M). Schematic in c) shows the transition from helical to racemic assembly by competitive replacement of AMP and ATP by PPi.

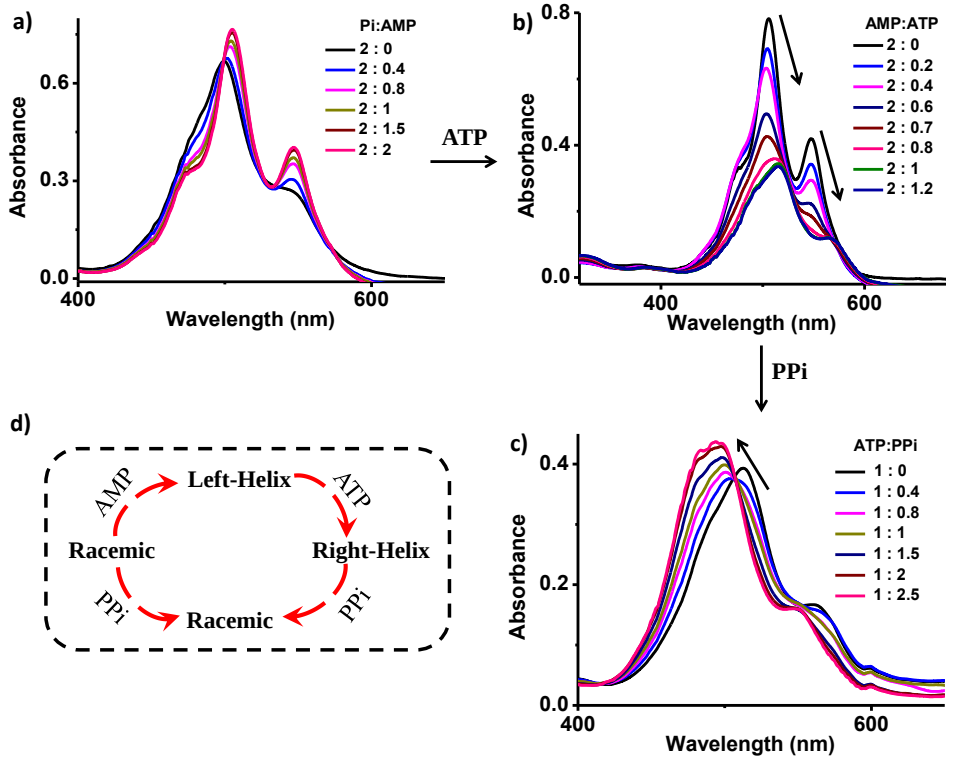

Fig. S9 Variation in absorption spectra upon sequential addition of a) AMP to (*rac*)-**PDPA**-Pi followed by b) ATP and subsequently c) PPi (90% aq. HEPES in MeCN, c = 2 x 10^{-5} M). d) Pictorial representation of transformation over one complete helix cycle.

1 All nonlinear regression analysis and curve fitting to obtain the association constants Ka (AMP) and Ka (ATP) were performed using GraphPad Prism version 5.00 for Windows, GraphPad Software, San Diego California USA, www.graphpad.com.

2 X. Chen, M. J. Jou and J. Yoon, *Org. Lett.,* 2009, **11**, 2181.

3 Although this is not the most accurate model because of the complex binding of ATP with multiple site of attachment, this gives a fair comparative value. Moreover, due to the inability to obtain the association constant with other standard methods like fitting the titration curve (due to its sigmoidal nature) and ITC measurements (due to binary solvent composition and enthalpy of mixing interfering with the binding parameters), this was the best available method. As evident from the fact that Ka (ATP) varied with concentration of AMP, demonstrates the limitation of the model, however it provides useful insight about the relative association constant of ATP. Ka of ATP varied from 3.0×10^5 M^{-1} (for AMP 1 eq.), 5.5×10^5 M^{-1} (for AMP 2 eq.), 9.2×10^5 M^{-1} (for AMP 4 eq.) to 1.2×10^6 M^{-1} (for AMP 10 eq.) but in any case it was higher than the Ka of AMP binding.