**Supplementary Figure 1** | Conversion of metastable \( P\)-SOPV (obtained upon quenching from molecularly dissolved state) to thermodynamically stable \( M\)-SOPV with opposite helicity. (methylcyclohexane, 100 \( \mu\)M, \( T = 298 \) K, \( \lambda = 466 \) nm, \( l = 1 \) mm).

**Supplementary Discussion 1: Kinetic stopped-flow studies on self-assembly of SOPV**

The molecular dissolved state of SOPV in chloroform at the start of the stopped-flow experiment is experimentally based on the absence of a Cotton effect in circular dichroism (CD) spectra, and the absence of the band at 490 nm in UV-vis absorption which is characteristic for aggregation\(^29\). To verify the molecular dissolved state of SOPV in chloroform at the start of the kinetic experiment, concentration-dependent \(^1\)H-NMR experiments are performed on SOPV in CDCl\(_3\) in the concentration regime 0.15 – 8.3 mM at \( T = 298 \) K. As stacking of SOPV changes the local magnetic field of the aromatic protons, formation of small oligomers is expected to result in shifted resonances in the aromatic regime (7 – 8 ppm) of the \(^1\)H-NMR spectra. The shift for the peak corresponding to \( H_c \) (\( d \), 8.4 ppm) is related to the formation of SOPV dimers due to hydrogen-bonding (Supplementary Fig. 2a). No shifts are observed for the peaks corresponding to \( H_a \) (\( s \), 6.74 ppm) and \( H_b \) (\( d \), 7.4 ppm) (Supplementary Fig. 2b). Besides,
no broadening of peaks in the aromatic regime is observed, indicating that in chloroform no stacking of hydrogen-bonded SOPV dimers occurs in this concentration regime, which largely covers the concentrations used in the kinetic experiments.

Based on the SOPV dimerization constant \( K_{\text{dim}} = (2.1 \pm 0.3) \cdot 10^4 \text{ M}^{-1} \) at \( T = 298 \text{ K} \), the fraction of hydrogen-bonded SOPV dimer in chloroform is estimated to be \( >70 \% \) for all kinetic experiments\(^{29} \). However, upon addition of the chloroform solution to methylcyclohexane (MCH), the dimerization constant of SOPV increases considerably\(^{30} \), resulting in a full conversion of the remaining SOPV molecules into hydrogen-bonded SOPV dimers and the concomitant formation of helical stacks. As hydrogen-bonding occurs via a diffusion-controlled reaction\(^{31} \), the fraction of hydrogen-bonded SOPV dimers is expected to approach 100% immediately after mixing of the chloroform solution with MCH.

The influence of chloroform on the self-assembly of SOPV is assessed by temperature-dependent CD measurements (\( \lambda = 466 \text{ nm} \)) of solutions of SOPV in MCH containing varying amounts of chloroform (0 – 5 v/v\%). The addition of small percentages of chloroform leads to a reduction in the critical elongation temperature \( T_c \) and hence, stability of the helical stacks (Supplementary Fig. 3a). However, the shape of the cooling curves is similar as in pure MCH, indicating that the addition of chloroform does not affect the cooperative growth mechanism (Supplementary Fig. 3b). Furthermore, full CD spectra of SOPV in MCH/chloroform solutions obtained at 273 K demonstrate that the shape of the CD signal is not affected by addition of chloroform (Supplementary Fig. 3c), a clear sign that the supramolecular organization of the SOPV chromophores within the stack is similar as in pure MCH.
To verify if the mixing efficiency in the stopped-flow setup is sufficient for the diffusion-controlled formation of hydrogen-bonded SOPV dimers to be completed before the mixture reaches the cuvet, the complexation of $\alpha$-cyclodextrin with $p$-nitrophenolate in water is probed after mixing in the stopped-flow setup. At pH $\sim$ 11, the complexation occurs with a rate constant $k_c$ of $10^8$ M$^{-1}$s$^{-1}$ and is thereby close to diffusion-controlled$^{32}$. The complexation of $p$-nitrophenolate with $\alpha$-cyclodextrin is probed in UV-vis ($\lambda = 410$ nm, DC Voltage of CD spectrometer is used as measure for UV-vis absorption). Apart from the first data point, no time-dependent changes in UV-vis are observed after mixing (Supplementary Fig. 4), demonstrating that the efficiency of mixing is high enough to complete the diffusion-controlled formation of hydrogen-bonded SOPV dimers before the start of the kinetic experiment.

**Supplementary Figure 2** | **a**, Molecular structure of SOPV, with protons H$_a$, H$_b$ and H$_c$ indicated. **b**, Aromatic region of $^1$H-NMR spectra of solutions of SOPV in CDCl$_3$ in the concentration regime 0.15 – 8.3 mM at $T = 298$ K. The additional peak at 7.46 ppm is not related to SOPV, but is a satellite peak that belongs to chloroform. These satellite peaks
are caused by a coupling between $^1$H and $^{13}$C. At 7.04 ppm, the right satellite peak can be observed.

**Supplementary Figure 3** | **a**, Cooling curves acquired by measuring CD absorption at 466 nm as a function of temperature for solutions of SOPV in MCH with different volume fractions of chloroform. **b**, Cooling curves as a function of $T - T_e$, where $T_e$ is the elongation temperature, for solutions of SOPV in MCH with different volume fractions of chloroform. ($\lambda = 466$ nm, $dT/dt = -3$ K/hr). **c**, CD spectra of solutions of OPV in MCH with different volume fractions of chloroform at 273 K ($c = 10.3$ μM, $l = 1$ cm).

**Supplementary Figure 4** | **a**, UV-vis spectra of α-cyclodextrin, $p$-nitrophenolate and α-cyclodextrin + $p$-nitrophenolate complex (water, $T = 293$ K, $l = 1$ cm, pH = 11, HPO$_4^{2-}$ / PO$_4^{3-}$ buffer, 0.25 M). **b**, Stopped-flow experiment on mixing of α-cyclodextrin (water,
10 mM) with p-nitrophenolate (5 mM), DC voltage vs. time (T = 293 K, λ = 410 nm, Δλ = 1 nm, l = 1 cm, Δt = 1 s, injection volume ratio 100:1).

**Supplementary Figure 5 |** The cooperative growth of metastable P-SOPV aggregates is demonstrated by rapidly quenching of a solution of SOPV in MCH from different temperatures at which a significant fraction of M-SOPV is already present under equilibrium conditions. a, CD spectra of SOPV at different temperatures under equilibrium conditions (MCH, 13 μM). b, Corresponding CD spectra acquired after quenching SOPV from different temperatures to 273 K, compared to CD spectrum of SOPV at 273 K under equilibrium conditions. c, Simulations of linear combinations of the CD spectra of pure P-SOPV (obtained via the two-step non-covalent synthetic methodology, Additional Methods Section, Supplementary Discussion 3) and M-SOPV aggregates to CD spectra acquired after quenching SOPV (ice bath) from different temperatures to 273 K. d, Fraction of free SOPV monomer (φ_{monomer}) present under
equilibrium conditions before quenching (derived from the CD spectra before quenching assuming $\phi_{\text{monomer}} = 1 - \phi_{\text{helical aggregate}}$), and fraction of $P$-SOPV present after quenching at 273 K. Fractions $P$-SOPV obtained after quenching from different temperatures are evaluated from the ratio in which $P$- and $M$-type CD spectra are combined to describe the respective CD spectra obtained after quenching. Only quenching from the highest temperatures (> 303 K) results in the formation of $P$-SOPV aggregates. This indicates a critical temperature and hence a critical free monomer concentration in the self-assembly of metastable $P$-SOPV aggregates, which is a hallmark of a cooperative growth mechanism.$^{33}$

Supplementary Figure 6 | (a) UV-vis and (b) linear dichroism (LD) spectra of SOPV in MCH (100 $\mu$M) in disassembled state (343 K, black), thermodynamically stable $M$-SOPV state (cooling 60 K/hr, 273 K, blue) and mixture of $M$-SOPV and metastable $P$-SOPV state (quenched in icebath, 273 K, red). Previous studies revealed that the cooperative formation of long helical $M$-SOPV aggregates is reflected in the changes of the extinction coefficient at $\lambda = 335$ nm$^{34}$. Hence, the coinciding UV-vis spectra of $P$- and $M$-SOPV aggregates at 273 K further demonstrate the cooperative growth of long $P$-SOPV aggregates. No LD artifacts are observed$^{35}$ ($l = 1$ mm).
Supplementary Discussion 2: Kinetic model describing competition between two cooperative aggregation pathways.

The reactions for the aggregation of monomer $X$ into two aggregates of different helicities ($P$-type and $M$-type) are given by:

$$
X + X \xrightleftharpoons_{k_i^{P-\text{M}}}^{k_i^{\text{P-M}}} M_2 \quad X + X \xrightleftharpoons_{k_i^{M-\text{P}}}^{k_i^{\text{M-P}}} P_2
$$

$$
M_2 + X \xrightleftharpoons_{k_i^{M-\text{M}}}^{k_i^{\text{M-M}}} M_3 \quad P_2 + X \xrightleftharpoons_{k_i^{P-\text{P}}}^{k_i^{\text{P-P}}} P_3
$$

\[ \vdots \]

$$
M_i + X \xrightleftharpoons_{k_i^{M-\text{M}}}^{k_i^{\text{M-M}}} M_{i+1} \quad P_i + X \xrightleftharpoons_{k_i^{P-\text{P}}}^{k_i^{\text{P-P}}} P_{i+1}
$$

(1)

Two important assumptions in this model are that the aggregates can change size only by monomer association or dissociation and that the helicity of the aggregate is determined at the dimer stage and does not change until the aggregate is completely dissociated into monomers.

Assuming mass-action kinetics, the corresponding rate equations for this model including two competitive growth pathways are given by:

$$
\frac{d[X]}{dt} = -[X]\left(2k_i^{\text{P-M}}[X] + \sum_{i=2}^{\infty} k_i^{\text{P-M}}[M_i] + 2k_i^{\text{P-P}}[P_i] + \sum_{i=3}^{\infty} k_i^{\text{P-P}}[P_i]\right)
$$

$$
-\left[X\right]\left(2k_i^{\text{M-P}}[X] + \sum_{i=2}^{\infty} k_i^{\text{M-P}}[P_i] + 2k_i^{\text{M-M}}[M_i] + \sum_{i=3}^{\infty} k_i^{\text{M-M}}[M_i]\right),
$$

$$
\frac{d[M_2]}{dt} = [X](k_i^{\text{P-M}}[M_{i-1}] - k_i^{\text{P-M}}[M_i]) + (k_i^{\text{P-P}}[P_{i-1}] - k_i^{\text{P-P}}[P_i]),
$$

$$
\frac{d[P_2]}{dt} = [X](k_i^{\text{M-P}}[P_{i-1}] - k_i^{\text{M-P}}[P_i]) + (k_i^{\text{M-M}}[M_{i-1}] - k_i^{\text{M-M}}[M_i]),
$$

(2)

with $[P_1] = [M_1] = [X]$. In order to describe the cooperative supramolecular polymerization, we assume that all association (forward) rate constants for each
aggregate type are the same and that the dissociation rate constants only differ between pre- and postnucleus aggregates, where the nucleus size is denoted by \( n \) for the \( M \)-type polymers and \( n^* \) for the \( P \)-type polymers. This assumption has been used previously in other cooperative reversible association models\(^{36,37,38}\). However, we note that Hill\(^{39}\) has shown, in general, that the rate constants depend continuously on the polymer length, although this dependence is proven to be very weak when aggregates grow by monomer addition only.

Under these assumptions, the reactions reduce to:

\[
\begin{align*}
X + X & \xrightleftharpoons[]{a \atop b} M_2 & X + X & \xrightleftharpoons[]{a^* \atop b^*} P_2 \\
M_2 + X & \xrightleftharpoons[]{a \atop b} M_3 & P_2 + X & \xrightleftharpoons[]{a^* \atop b^*} P_3 \\
& \quad \vdots & & \quad \vdots \\
M_{n-1} + X & \xrightleftharpoons[]{a \atop b} M_n & P_{n-1} + X & \xrightleftharpoons[]{a^* \atop b^*} P_{n^*} \\
M_n + X & \xrightleftharpoons[]{a \atop c} M_{n+1} & P_n + X & \xrightleftharpoons[]{a^* \atop c^*} P_{n^*+1} \\
& \quad \vdots & & \quad \vdots \\
M_i + X & \xrightleftharpoons[]{a \atop c} M_{i+1} & P_i + X & \xrightleftharpoons[]{a^* \atop c^*} P_{i+1} \\
& \quad \vdots & & \quad \vdots 
\end{align*}
\]

in which \( M_n \) represents the oligomer with a size that corresponds to the critical nucleus size for the \( M \)-type aggregates, and \( P_{n^*} \) represents the oligomer with a size that corresponds to the critical nucleus size for the \( P \)-type aggregates. Although only monomer association and dissociation are taken into account, the number of rate equations is in principle infinite. In previous kinetic models the required number of rate
equations has been reduced either by truncating at a certain polymer length\textsuperscript{38}, or by using a lumped set of reaction-rate equations under the assumption of irreversible monomer association to the nucleus\textsuperscript{36}. A drawback of truncating the rate equations is that the concentration of high-molecular species is assumed to be zero, which is unrealistic in a cooperative growth mechanism. A lumped set of reaction-rate equations successfully describes the formation of a single type of supramolecular polymer. However, if off-pathway aggregation is included, the assumption of irreversible monomer association to the nucleus is unrealistic as off-pathway aggregates have to depolymerize in order for the thermodynamically stable aggregates to grow in length. An insightful model analyzed by Powers and Powers describes the off-pathway aggregation as an isodesmic growth process in which all species are assumed to be in fast (pre)equilibrium with the free monomer\textsuperscript{40}. The cooperative on-pathway reactions are described by a lumped set of rate equations under the assumption of irreversible monomer addition.

Here, we introduce an alternative approach to describe competition between two cooperative aggregation pathways. All aggregates up to a certain length $N$, with $N$ much larger than the nucleus sizes ($n$ and $n^*$) are described explicitly. The aggregates with size larger than $N$ are described per type together as fibrils by considering both the fibril number concentrations,

$$\left[ F^M \right] = [M_{N+1}] + [M_{N+2}] + [M_{N+3}] + \ldots$$  \hspace{1cm} (4)

similarly for the $P$-type fibrils:

$$\left[ F^P \right] = [P_{N+1}] + [P_{N+2}] + [P_{N+3}] + \ldots.$$  \hspace{1cm} (5)
and the fibril mass concentrations,

\[
[Z^M] = (N + 1) [M_{N+1}] + (N + 2) [M_{N+2}] + (N + 3) [M_{N+3}] + \ldots
\]  

(6)
similarly for the \( P \)-type fibrils:

\[
[Z^P] = (N + 1) [P_{N+1}] + (N + 2) [P_{N+2}] + (N + 3) [P_{N+3}] + \ldots
\]  

(7)

In order to keep the fibril formation reversible, an estimation is needed for the number of fibrils of length \( N+1 \), the species that upon monomer dissociation results in the explicitly described aggregate of length \( N \). Assuming that for all \( i > N \), \([M_{i+1}] = \alpha_i [M_i]\), one obtains

\[
[F^M] = \sum_{i=0}^{\infty} (\alpha_M)^i [M_{N+1}],
\]

\[
[Z^M] = \sum_{i=0}^{\infty} (N + 1 + i)(\alpha_M)^i [M_{N+1}].
\]

(8)

Using the standard series \( \sum_{i=0}^{\infty} x^i = \frac{1}{1-x} \) and \( \sum_{i=0}^{\infty} i \cdot x^i = \frac{x}{(1-x)^2} \) for \( x < 1 \), this yields

\[
[F^M] = [M_{N+1}] \frac{1}{1-\alpha_M}, \quad [Z^M] = [M_{N+1}] \left( \frac{N + 1}{1-\alpha_M} + \frac{\alpha_M}{(1-\alpha_M)^2} \right).
\]

(9)

Substituting the equation for \([F^M]\) in \([Z^M]\) yields

\[
[Z^M] = [F^M] \left( N + 1 + \frac{\alpha_M}{(1-\alpha_M)} \right),
\]

(10)

from which \( \alpha_M \) can be solved as

\[
\alpha_M = 1 - \frac{[F^M]}{[Z^M] - N[F^M]}.
\]

(11)
The estimated concentration of $M$-type aggregates of length $N+1$ is thus

$$[M_{N+1}] = (1 - \alpha_M) \left[ F^M \right].$$  \hfill (12)

Similarly, for the $P$-type aggregates

$$\alpha_P = 1 - \frac{\left[ F^P \right]}{\left[ Z^P \right] - N \left[ F^P \right]},$$  \hfill (13)

and

$$[P_{N+1}] = (1 - \alpha_P) \left[ F^P \right].$$  \hfill (14)

The rate equations for our aggregation pathway competition model then finally become:

- for the monomers

$$\frac{d[X]}{dt} = -a[X] \left( 2[X] + \sum_{j=2}^{N} [M_j] + [F_M] \right) + b \left( 2[M_2] + \sum_{i=3}^{N} [M_i] + [F_M] \right) + c \left( \sum_{j=1}^{N} [M_i] + [F_M] \right) - a^* [X] \left( 2[X] + \sum_{i=2}^{N} [P_i] + [F_P] \right) + b^* \left( 2[P_2] + \sum_{i=3}^{N} [P_i] \right) + c^* \left( \sum_{i=1}^{N} [P_i] + [F_P] \right),$$  \hfill (15)

- for the oligomers

$$\frac{d[M_i]}{dt} = a[X] \left( [M_{i-1}] - [M_i] \right) + b \left( [M_{i-1}] - [M_i] \right),$$  \hfill (16)

$$\frac{d[P_j]}{dt} = a^* [X] \left( [P_{j-1}] - [P_j] \right) + b^* \left( [P_{j-1}] - [P_j] \right),$$

- for the nucleus

$$\frac{d[M_{n+1}]}{dt} = a[X] \left( [M_{n+1}] - [M_n] \right) + c \left( [M_{n+1}] - [M_n] \right),$$  \hfill (17)

$$\frac{d[P_{n+1}]}{dt} = a^* [X] \left( [P_{n+1}] - [P_n] \right) + c^* \left( [P_{n+1}] - [P_n] \right).$$
- for polymers larger than the nucleus size $n$ (M-type) or $n^*$ (P-type)

\[
\frac{d[M]}{dt} = a[X]([M_{i-1}] - [M_i]) + c([M_{i+1}] - [M_i]),
\]
\[
\frac{d[P]}{dt} = a^*[X]([P_{i-1}] - [P_i]) + c^*([P_{i+1}] - [P_i]),
\]

- for the last explicitly considered aggregate with length $N$

\[
\frac{d[M_N]}{dt} = a[X]([M_{N-1}] - [M_N]) + c((1 - \alpha_M)[F_M] - [M_N]),
\]
\[
\frac{d[P_N]}{dt} = a^*[X]([P_{N-1}] - [P_N]) + c^*((1 - \alpha_P)[F_P] - [P_N]),
\]

- for the fibril number concentration

\[
\frac{d[F_M]}{dt} = a[X][M_N] - c(1 - \alpha_M)[F_M],
\]
\[
\frac{d[F_P]}{dt} = a^*[X][P_N] - c^*(1 - \alpha_P)[F_P],
\]

- and finally for the fibril mass concentration

\[
\frac{d[Z_M]}{dt} = (N + 1)(a[X][M_N] - c(1 - \alpha_M)[F_M]) + a[X][F_M] - c([F_M] - (1 - \alpha_M)[F_M]),
\]
\[
\frac{d[Z_P]}{dt} = (N + 1)(a^*[X][P_N] - c^*(1 - \alpha_P)[F_P]) + a^*[X][F_P] - c^*([F_P] - (1 - \alpha_P)[F_P]),
\]

which can be rewritten into

\[
\frac{d[Z_M]}{dt} = a[X]((N + 1)[M_N] + [F_M]) - c([F_M] + N(1 - \alpha_M)[F_M]),
\]
\[
\frac{d[Z_P]}{dt} = a^*[X]((N + 1)[P_N] + [F_P]) - c^*([F_P] + N(1 - \alpha_P)[F_P]).
\]

The resulting system of differential equations, combined with the relation between $a$, $F$ and $Z$ for both $P$-type as well as $M$-type aggregates, is solved using the ode15s solver in Matlab.
We assess the influence of $N$ on the simulated aggregation kinetics by comparing kinetic curves simulated with different values of $N$, using the rate constants and nucleus sizes corresponding to the concentration-dependent kinetic simulations shown in the main text. No differences in the simulated curves are found upon increasing $N$ to a value of 200, demonstrating that, at least if $N > 50$, the size of the largest aggregate that is explicitly described in a rate equation does not affect the simulated growth kinetics as shown in Fig. 3 (Supplementary Fig. 7a, b). To verify the influence of truncating the differential equations at a specific length (i.e. excluding the filaments), simulations are performed with a maximum aggregate size of 50. The differences at low concentrations clearly demonstrate the necessity of including reversible fibril formation in the kinetic model (Supplementary Fig. 7c,d). However, if the differential equations are truncated at a larger aggregate size, the simulations approach the simulated kinetics with filaments included.

To investigate the assumption of irreversible monomer association to the nucleus on the simulated aggregation kinetics, we compare kinetic simulations using a single type of supramolecular polymer assuming a cooperative growth mechanism. The kinetic simulations in which reversible monomer addition to the nucleus occurs are performed using the ODE model discussed above and assuming only one type of supramolecular polymer (i.e. off-pathway aggregation is ignored). The kinetic simulations assuming irreversible monomer addition to the nucleus are performed using a lumped set of reaction-rate equations$^{36}$. The concentration-dependent kinetic simulations show only small differences at the lowest concentration, demonstrating the limited influence of
reversibility in case of a single type of fiber aggregation mechanism (Supplementary Fig. 7e, f).

We investigate the influence of irreversible monomer association to the nucleus in combination with off-pathway aggregation kinetics. Concentration-dependent aggregation kinetics are simulated using the ODE model discussed above, and using a model\(^4\) that includes a lumped set of reaction-rate equations for the cooperative on-pathway reactions (assuming irreversible monomer association to the nucleus). Off-pathway reactions are in both models assumed to follow an isodesmic mechanism in which the rate constants do not change as a function of chain length. Although both models show similar behaviour, significant differences in the simulated aggregation kinetics can be observed. (Supplementary Fig. 7g, h).
Supplementary Figure 7 | Normalized difference between concentration of monomers assembled in $M$- and $P$-type aggregates vs. time (a) and $t$-50 vs. concentration (b) for cooperative aggregation pathway competition with different values for $N$, including filaments. Normalized difference between concentration of monomers assembled in $M$- and $P$-type aggregates vs. time (c) and $t$-50 vs. concentration (d) for cooperative aggregation pathway competition with different values for $N$, either with or without filaments taken into account. (parameters in a-d: $n = n^* = 5$; $a = 2.9 \cdot 10^4 \text{ M}^{-1}\text{s}^{-1}$; $K_e = 1.52 \cdot 10^6 \text{ M}^{-1}$; $K_n/K_e = 0.0526$; $K_n^*/K_n = 1.38$, $K_e^*/K_e = 0.164$ and $a^*/a = 3.79$, concentration increases along the arrow from $10^{-5.8}$ to $10^{-4}$ M). Conversion (concentration of aggregated monomers divided by final concentration of aggregated monomers) of aggregates larger than the nucleus vs. time (e) and $t$-50 vs. concentration (f) for single-type aggregate growth kinetics assuming either irreversible or reversible monomer association to the nucleus, respectively (parameters in e and f: $n = 6$; $a = 1 \text{ M}^{-1}\text{s}^{-1}$; $b = 1000 \text{ s}^{-1}$; $c = 1 \text{ s}^{-1}$, concentration increases along the arrow from $10^{0.5}$ to $10^6$ M). Conversion of on-pathway aggregates larger than the nucleus vs. time (g) and $t$-50 vs. concentration (h) simulated using the off-pathway model assuming either irreversible or reversible monomer addition to the on-pathway nucleus. (parameters in g and h: $n = 4$; $a^* = 1 \cdot 10^7 \text{ M}^{-1}\text{s}^{-1}$; $b^* = 10 \text{ s}^{-1}$; $c^* = 10 \text{ s}^{-1}$; $a = 1 \cdot 10^6 \text{ M}^{-1}\text{s}^{-1}$; $b = 1 \cdot 10^2 \text{ s}^{-1}$; $c = 1 \cdot 10^{-1} \text{ s}^{-1}$, concentration increases along the arrow from $10^{-6.5}$ to $10^{-1}$ M).
Supplementary Figure 8 | a, Normalized CD vs. enantiomeric excess (e.e.) for mixtures of S- and ROPV (298 K, MCH, 200 µM). Majority-rules model (including mismatch penalty \(MMP\) and helix reversal penalty \(HRP\)) developed by van Gestel is fitted to the data by non-linear least-squares optimization\(^{41,42}\). b, Error landscape with sum of least-squares examined as a function of dimensionless energy penalties \(\omega (= \exp(-MMP/RT))\) and \(\sigma (= \exp(-2HRP/RT))\). Minimum sum of least-squares is obtained at \(HRP = 8.12 \, RT\) and \(MMP = 0.31 \, RT\).
Supplementary Figure 9 | Simulations with pathway competition model to analyze the formation of P-SOPV during the initial stages of the assembly process. (1) at critical concentration of P-SOPV; $K_e^* = 1/c_{tot}$, $(K_n^*/K_n = 1; K_e^*/K_e = 0.065; \alpha^*/\alpha = 1)$; (2) with larger forward rate constant for the off-pathway aggregates; $\alpha^* > \alpha$, given $K_n^* = K_n$ $(K_e^*/K_e = 0.3; \alpha^*/\alpha = 10)$; (3) with kinetically more stable P-SOPV prenucleus oligomers compared to M-SOPV prenucleus oligomers; $K_n^* > K_n$, given $\alpha^* = \alpha$ $(K_n^*/K_n = 1.2; K_e^*/K_e = 0.3)$. \(a\), Calculated Gibbs free energy diagram for formation of P-SOPV and M-SOPV,
assuming the total concentration $c_{tot}$ as reference state, whereas the standard state is defined at 1 M$^{43}$.  

**b.** Fraction of P-SOPV formed vs. time, calculated with $K_e^* = 1/c_{tot}$ (1), $a^* > a$ (2) and $K_n^* > K_n$ (3, *vide supra*).  

**c.** Normalized difference between concentration of monomers assembled in M-SOPV and P-SOPV aggregates vs. time, calculated with $K_e^* = 1/c_{tot}$ (1), $a^* > a$ (2) and $K_n^* > K_n$ (3, *vide supra*). Significant amounts of metastable P-SOPV are only formed if $K_e^* > 1/c_{tot}$, if $a^* > a$ or $K_n^* > K_n$. (parameters for a-c: $n = n^* = 5; K_n/K_e = 0.052; a = 2.9 \times 10^4 \text{ M}^{-1}\text{s}^{-1}, K_e = 1.52 \times 10^6 \text{ M}^{-1}, c_{tot} = 1 \times 10^{-5} \text{ M}$).  

**d.** Although a difference in the stability of the prenucleation aggregates (i.e. $K_n^* > K_n$) is sufficient to explain the initial formation of P-SOPV followed by the concomitant formation of M-SOPV, a difference in forward rate constants (i.e. $a^* > a$) is required to obtain the experimentally observed inverted dependence of $t-50$ on concentration. ($n = n^* = 5, a = 2.9 \times 10^4 \text{ s}^{-1}, K_e = 1.52 \times 10^6 \text{ M}^{-1}, K_n / K_e = 0.0526, K_n^*/K_n = 1.38, K_e^*/K_e = 0.164$).  

**e.** Although the experimental aggregation kinetics could be described using a diffusion-limited forward rate-constant, this consequently results in very low values for the cooperativity parameter sigma ($\sigma = K_n / K_e < 10^{-4}$). (the diffusion-controlled rate constant is calculated via $k_d = 8RT/3\eta$, where $\eta$ displays the viscosity of MCH, at 293 K $0.736 \times 10^{-3}$ Pa.s.$^{44}$, $K_e = 1.52 \times 10^6 \text{ M}^{-1}, a = a^* = 8.9 \times 10^9 \text{ M}^{-1}\text{s}^{-1}, K_n^*/K_n = 2, K_e^*/K_e = 0.2, n = n^* = 5, c_{tot} = 7.5 \mu\text{M}, \sigma$ increases from $10^{-5}$ to $10^{-2}$ along the arrow). To rationalize whether such low sigma values give a realistic description of the aggregation process we perform additional simulations using the cooperative supramolecular polymerization model developed by Goldstein and Stryer (Supplementary Discussion 3) for a single type of aggregate. Simulations of the weight and z-average degree of polymerization using very low values of sigma result in extremely high degrees of polymerization (*vide infra*),
which is not in correspondence with dynamic light scattering (DLS)\textsuperscript{45} and small angle neutron scattering (SANS) data measured under thermodynamically controlled conditions. Hence we can rule out a diffusion-limited forward rate constant for monomer addition to the SOPV aggregates. 

\textbf{f.} Simulations of weight and z-average degree of polymerization ($DP_w$ and $DP_z$) vs. dimensionless concentration $K_c c_{\text{tot}}$ with $\sigma = 0.0001$ and $\sigma = 0.0526$. The dashed line indicates $K_c c_{\text{tot}}$ at which DLS data are reported\textsuperscript{45}. The (approximate) z-average\textsuperscript{47} aggregate size based on DLS studies (~300 nm, $DP_z \sim 900$), acquired at $T = 350$ K and $c_{\text{tot}} = 3.35 \cdot 10^{-4}$ M deviates orders of magnitude from the degree of polymerization calculated with $\sigma = 0.0001$, but approximates the degree of polymerization calculated with $\sigma = 0.0526$. This indicates that the value of $\sigma$ that is used to describe the kinetics predicts more realistic aggregate sizes compared to the very low value of $\sigma$ that is needed to describe the kinetics using diffusion-limited forward rate constants. 

\textbf{g.} The equilibrium constant which describes the elongation of $M$-SOPV aggregates, $K_e$, can be determined independently. The temperature-dependent degree of aggregation $\phi$ of SOPV in a MCH/chloroform mixture (50/1 v/v, $c_{\text{tot}} = 10.3$ $\mu$M) is probed using CD spectroscopy ($\lambda = 466$ nm) under thermodynamically controlled conditions. The data is analyzed using a non-linear least-square procedure via a model developed by Van der Schoot\textsuperscript{34}: $\phi = 1 - \exp\left(\frac{-\Delta H_e^0}{RT_e} (T - T_e)\right)$, with gas constant $R$, temperature $T$, enthalpy of elongation $\Delta H_e^0$, and critical temperature of elongation $T_e$. To avoid the influence of LD artifacts at low temperatures, data below 298 K are ignored in the analysis. It can be shown\textsuperscript{48} that at $T = T_e$, $1 = c_{\text{tot}} \exp\left(\frac{-\Delta G_e^0}{RT_e}\right)$, where $c_{\text{tot}}$ represents the total SOPV-dimer concentration. The Gibbs free energy of elongation can be
calculated using the enthalpy and entropy of elongation $\Delta G_e^0 = \Delta H_e^0 - T \Delta S_e^0$. Combination of the above equations allows calculating $\Delta S_e^0$ based on $\Delta H_e^0$ and $T_e$, which can be extracted from the fit: \[
\ln \frac{1}{c_{\text{tot}}} = \frac{-\Delta G_e^0}{RT_e} = \frac{-\Delta H_e^0}{RT_e} + \frac{\Delta S_e^0}{R}; \quad \Delta S_e^0 = R \ln \frac{1}{c_{\text{tot}}} + \frac{\Delta H_e^0}{T_e}. \] 
With $c_{\text{tot}} = 5.15 \cdot 10^{-6}$ M, $\Delta H_e^0 = -133760$ J/mol and $T_e = 308.97$ K, this yields $\Delta S_e^0 = -331.68$ J/Kmol. Based on $\Delta H_e^0$ and $\Delta S_e^0$ obtained via the temperature-dependent data, $K_e$ at 293 K can be calculated: \[
K_e = \exp \left( -\frac{\Delta H_e^0 - T \Delta S_e^0}{RT} \right) = 3.32 \cdot 10^6 \text{ M}^{-1}, \] 
which approaches the value of $K_e$ used to simulate the kinetic data ($1.52 \cdot 10^6$ M$^{-1}$). The minor difference can be explained by a small temperature-dependence of $\Delta H_e^0$ and $\Delta S_e^0$, which is not taken into account in the calculation of $K_e$.

**Supplementary Figure 10** | **a**, Normalized CD vs. time squared ($t^2$) for initial stages (up to 5% conversion) of supramolecular polymerization of SOPV (293 K, 6.5 µM). The linear relation indicates a homogeneous nucleated mechanism$^{49}$. **b**, Autocorrelation $\psi(\tau)$ of residual sequence (data – fit) estimated via $\psi(\tau) = \frac{1}{L} \sum_{i=1}^{L} \xi(i) \xi(i+\tau)$, where $L$
represents half of the length of the dataset and $\zeta$ the residual sequence. The red lines indicating the boundaries of the 95% confidence interval are computed via $\pm 1.96 \cdot \sigma_{\zeta}^2 \cdot L^{-0.5}$, where $\sigma_{\zeta}^2$ is the estimated variance of the residual. 96.7% of the autocorrelation estimates are in between the boundaries.

**Supplementary Figure 11** | Temperature-dependent simulations with pathway competition model show that the optimum rate shifts to higher concentrations and lower $t$-50 values upon increasing temperature. Parameters: $A = 2.38 \cdot 10^{13}$ M$^{-1}$s$^{-1}$, $E_{\text{act}} = 50$ kJ/mol, $\Delta H_e^0 = -100$ kJ/mol, $\Delta S_e^0 = -223$ J/K.mol, $K_n^*/K_n = 0.052$, $K_n^*/K_n = 1.38$, $K_e^*/K_e = 0.16$, $a^*/a = 3.8$. 
Supplementary Discussion 3: Isolation of metastable P-SOPV via two-step non-covalent synthetic methodology

To isolate pure metastable P-SOPV, S-chiral dibenzoyl tartaric acid (DTA) is applied, which transfers its chirality to the SOPV monomer via two-fold hydrogen-bonding between the carboxylic acid group of DTA and SOPV. Previous studies on helicity induction in SOPV aggregates through hydrogen-bonded chiral acids have shown that the carboxylic acid group can bind to the free amine proton and the neighboring non-central nitrogen of the triazine ring of SOPV via hydrogen-bonding\(^50\). \(^1\)H-NMR studies have demonstrated that the binding of a chiral acid via two-fold hydrogen-bonding does not affect the formation of SOPV dimers via quadruple hydrogen-bonding\(^50\).

The binding of DTA to SOPV is demonstrated by changes in CD, UV-vis absorption, fluorescence and an increase in the elongation temperature \(T_e\) compared to pure SOPV (Supplementary Figure 12a-c). Upon binding of DTA to SOPV, P-DTA-SOPV with opposite helicity compared to the equilibrium state M-SOPV is obtained. Besides, an additional shoulder appears in UV-vis absorption at 525 nm, whereas the emission spectrum (\(\lambda_{ex} = 425\) nm) is quenched and shows a red shift to 640 nm. The higher \(T_e\) for P-DTA-SOPV indicates that binding of DTA increases the stability of the stacks. This suggests the possibility of the diacid functionality of DTA to act as a clip between adjacent SOPV hydrogen-bonded dimers, providing additional stabilization. DTA can be removed from the SOPV aggregates by aqueous extraction at 273 K using an excess of ethylene diamine which complexes with the carboxylic acid. The resulting P-SOPV aggregates are transiently stable at 273 K (Supplementary Fig. 12d), however at higher
temperatures *M*-SOPV appears in time. The rate of this conversion increases with temperature (Supplementary Fig. 12d, e).

To simulate the stereomutation kinetics with the kinetic aggregation pathway competition model as derived in Supplementary Discussion 2, the concentration of each species $P_i$ at $t = 0$ is required. To compute the initial concentrations $[P_i]$ of the metastable $P$-type stacks, we use the concentration-dependent cooperative supramolecular polymerization model developed by Goldstein and Stryer\textsuperscript{37}. The model describes the supramolecular polymerization as a sequence of monomer addition equilibria. Monomer addition to all species smaller than the nucleus takes place with equilibrium constant $K_n^*$, and monomer addition to larger species with equilibrium constant $K_e^*$:

\[ X + X \xrightleftharpoons{K_n^*} P_2 \quad [P_2] = K_n^* [X]^2 \]
\[ P_2 + X \xrightleftharpoons{K_n^*} P_3 \quad [P_3] = K_n^* [P_2][X] \]
\[ \vdots \]
\[ P_{n-1} + X \xrightleftharpoons{K_n^*} P_n \quad [P_n] = K_n^* [P_{n-1}][X] \]
\[ P_n + X \xrightleftharpoons{K_n^*} P_{n+1} \quad [P_{n+1}] = K_e^* [P_n][X] \]
\[ \vdots \]
\[ P_{i-1} + X \xrightleftharpoons{K_n^*} P_i \quad [P_i] = K_e^* [P_{i-1}][X]. \]  

(23)

The concentration of each species $P_i$ can be expressed as a function of $K_n^*$, $K_e^*$ and monomer concentration $[X]$. For $i \leq n$, $[P_i] = K_n^{*i-1} [X]^i$, while for $i > n$ $[P_i] = K_e^{*n-n} K_n^{*n-1} [X]^i$. These equations can be made dimensionless, which improves the accuracy of numerically solving the resulting mass balance. With dimensionless concentration $p_i = K_e^{*i} [P_i]$, dimensionless monomer concentration $x = K_e^{*} [X]$, and cooperativity $\sigma = K_n^{*} / K_e^{*}$
\[ p_i = \sigma ^{i-1} x^i \quad \text{for } i \leq n, \]  
\[ p_i = \sigma ^{n-1} x^i \quad \text{for } i > n, \]  

the mass balance (with \( x_{\text{tot}} = K_e^* c_{\text{tot}} \)) results in

\[ x_{\text{tot}} = \sigma ^{i-1} \sum_{i=1}^{n} i (\sigma^* x) + \sigma ^{n-1} \sum_{i=n+1}^{\infty} i x^i. \]  

Expanding both sums yields:

\[ x_{\text{tot}} = \sigma ^{i-1} \left( \frac{\sigma^* x^{n+1}}{(\sigma^* x-1)^2} + \frac{\sigma^* x}{(\sigma^* x-1)^2} \right) - \sigma ^{n-1} \left( \frac{x^{n+1} (nx - n - 1)}{(x-1)^2} \right), \]  

numerically solving this equation using Matlab yields the dimensionless free monomer concentration \( x \) at \( t = 0 \). Subsequently, the value of \( x \) is used to calculate the concentrations of each species up to \( i = N \), with \( N = 200 \). The larger \( P \)-type aggregates are described together as fibrils by considering both the dimensionless fibril number concentration \( f^P \) and the fibril mass concentration \( z^P \):

\[ f^P = \sigma ^{n-1} \left( \frac{x^{N+1}}{1-x} \right), \quad z^P = \sigma ^{n-1} \left( \frac{x^{N+1} (Nx - N - 1)}{(x-1)^2} \right). \]  

Using the dimensionless concentrations that follow from the dimensionless free monomer concentration, the initial concentrations of all aggregates \( P_i \) up to \( i = N \) can be calculated, as well as the fibril number and mass concentrations, respectively. However, to find \( x \) upon solving the mass balance, the value of \( K_e^* \) at 273 K is required, as well as the cooperativity \( \sigma ^* = \frac{K_n^*}{K_e^*} \). Since \( K_e^* \) and \( \sigma ^* \) at 273 K cannot be determined independently, \( \sigma ^*(273 \text{ K}) \) is estimated to be 0.05, in agreement with the value of \( \sigma \) used to simulate the kinetic data at 293 K in Figure 3b of the main text. The stereomutation kinetics have been simulated with values of \( K_e^*(273 \text{ K}) \) in the range \([10^5 \text{ - } 10^8] \text{ M}^{-1}\), using
the parameters that have been used to simulate the kinetics in Figure 3b \((n = n^* = 5; a = 2.9 \cdot 10^4 \text{M}^{-1}\text{s}^{-1}; K_e = 1.52 \cdot 10^6 \text{M}^{-1}, K_n/K_e = 0.0526, K_n^*/K_n = 1.38, K_e^*/K_e = 0.164 \text{ and } a^*/a = 3.79\)). The simulations show a decreasing rate with increasing value of \(K_e^*(273 \text{K})\) (Supplementary Figure 13a). This can be explained by the size of the \(P\)-type aggregates which increases with their stability before the stereomutation process (i.e. \(K_e^*(273 \text{K})\)). As stereomutation occurs via disassembly of \(P\)-type aggregates and subsequent assembly of \(M\)-type aggregates, the rate decreases with increasing length and stability of \(P\)-type aggregates. Based on the experimentally determined value of \(t_{-50} (12000 \text{s})\) at 293 K, the value of \(K_e^*(273 \text{K})\) is expected in the range \([10^6 - 10^7] \text{M}^{-1}\). To rationalize the values of \(K_e^*(273 \text{K})\) in this range, we compute \(K_e\) at 273 K, which equals \(1.85 \cdot 10^8 \text{M}^{-1}\) based on the values of \(\Delta H_e^0\) and \(\Delta S_e^0\) determined via non-linear least-square analysis of the temperature-dependent data as shown in Supplementary Figure 9g. This means that \(K_e^*/K_e\) at 273 K is smaller than 0.1, in agreement with the value of \(K_e^*/K_e\) used to describe the kinetic data at 293 K \((K_e^*/K_e = 0.164)\).

The experimental data on the stereomutation process can be approximated by first order kinetics \((y \sim 1 - \exp(-k \cdot (t - t_0)))\). Only at higher temperatures the kinetic data deviate from first order kinetics in the initial stages of the conversion process (Supplementary Figure 13b,c). This effect is most probably related to a delay in heating of the sample from 273 K to the temperature at which the stereomutation is probed. Furthermore the simulated kinetic curves are well described by first order kinetics (Supplementary Figure 13d), in agreement with the experimental data.
Supplementary Figure 12 | UV-vis (a) and fluorescence (b) spectra of P-DTA-SOPV and M-SOPV (298 K). c, Cooling curves of P-DTA-SOPV and M-SOPV (466 nm, dT/dt = – 60 K/hr). d-e, Conversion from P-SOPV to M-SOPV at different temperatures. (MCH, 100 µM, l = 1 mm).
**Supplementary Figure 13 |**

**a,** Conversion from \( P \)-SOPV to \( M \)-SOPV simulated with pathway competition model using different values of \( K_e^* \) at 273 K to compute distribution of \( P \)-type aggregates at \( t = 0 \). **b-c,** Stereomutation kinetics from \( P \)-SOPV to \( M \)-SOPV at different temperatures (MCH, 100 \( \mu \)M) fitted with first order kinetics. **d,** Simulated stereomutation kinetics using the pathway competition model and the result of non-linear least square analysis of the simulations using first order kinetics (parameters in a and d: \( n = n^* = 5 \); \( a = 2.9 \cdot 10^4 \text{ M}^{-1}\text{s}^{-1} \); \( K_e = 1.52 \cdot 10^6 \text{ M}^{-1} \), \( K_n/K_e = 0.0526 \), \( K_{n^*}/K_n = 1.38 \), \( K_{c^*}/K_c = 0.164 \) and \( a^*/a = 3.79 \), \( K_{n^*}/K_{c^*} = 0.05 \) at 273 K, concentration 50 \( \mu \)M).
References and Notes:


