# On the Mechanism of Crystalline Polymorph 

## Selection by Polymer Heteronuclei

Vilmalí López-Mejías, ${ }^{\dagger}$ Jennifer L. Knight, ${ }^{\dagger}$ Charles L. Brooks III, ${ }^{*}{ }^{\dagger,}{ }^{\square}$ Adam J. Matzger ${ }^{*}, \uparrow, \S$ Department of Chemistry, ${ }^{\dagger}$ Department of Biophysics, ${ }^{\square}$ and the Macromolecular Science and Engineering Program, ${ }^{\S}$ University of Michigan, 930 North University Avenue, Ann Arbor MI 48109-1055.<br>brookscl@umich.edu; matzger@umich.edu

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## SI 1. Optical Microscopy.

Images of monoclinic and orthorhombic ACM crystals grown from aqueous supersaturated solution onto PBMA and PMMA, respectively, were collected using a Spot Flex Mosaic 15.2 camera coupled to a Leica DMLP microscope. Images were processed using Spot Advanced software (version 4.6).


Figure SI 1. Optical microscopy of monoclinic ACM grown on PBMA (left) and orthorhombic ACM (right) grown on PMMA.

## SI 2. Powder X-ray Diffraction (PXRD).

PXRD analysis was performed using a Bruker D8 Advance diffractometer equipped with a LynxEye detector and graphite monochromated $\mathrm{Cu}-\mathrm{K} \alpha$ radiation ( $1.5406 \AA, 40 \mathrm{kV}, 40 \mathrm{~mA}$ ). Diffractograms were collected at room temperature from $5^{\circ}$ to $50^{\circ}$ with a $0.05^{\circ}$ step size while the sample was rotated at 60 rpm . All powder patterns were processed in Jade Plus version 8.2.


Figure SI 2. PXRD pattern of monoclinic ACM grown on Nylon 6/9 (a) Nylon 6/12 (b), and Nylon 11 (c) from a supersaturated acetonitrile solution.


Figure SI 3. PXRD pattern of monoclinic ACM grown on Nylon 6/9 (a) Nylon 6/12 (b), and Nylon 11 (c) from a supersaturated acetone solution.


Figure SI 4. PXRD pattern of monoclinic ACM grown on Nylon $6 / 9$ (a) Nylon $6 / 12$ (b), and Nylon 11 (c) by sublimation.


Figure SI 5. PXRD pattern of orthorhombic ACM grown on Nylon 6/9 (a) Nylon 6/12 (b), and Nylon 11 (c) from a supersaturated ethanol solution.

## SI 3. Molecular Dynamics Simulations.

3.1 General. All of the binding energy $\left(\Phi_{\mathrm{BE}}\right)$ calculations, including molecular dynamic simulations, were performed using the CHARMM macromolecular modeling package version c36a4 ${ }^{1,2}$ on dual 2.66 GHz Intel Quad Core Xeon CPUs. Molecular structures of the oriented faces were obtained by cleaving the room temperature crystal structures of ACM (CSD reference codes HXACAN and HXACAN01), ${ }^{3,4}$ along each preferred crystallographic plane using Materials Studio v4.3. Based on previously reported Bravais-Friedel-Donnay-Harker (BFDHE) and attachment energy (AE) morphology predictions for $\mathrm{ACM},{ }^{5}$ additional faces were chosen as suitable negative controls due to their morphological prevalence. Each crystal face had dimensions of $\sim 60 \times 40 \AA^{2}$ and contained $\sim 285$ molecules. Parameters and partial charges for ACM molecules were taken from the CHARMM Generalized Force Field (CGenFF). ${ }^{6}$ PBMA $\left(\mathrm{C}_{24} \mathrm{H}_{44} \mathrm{O}_{6}, \mathrm{MW}=428.6 \mathrm{~g} / \mathrm{mol}\right)$ and $\operatorname{PMMA}\left(\mathrm{C}_{15} \mathrm{H}_{26} \mathrm{O}_{6}, \mathrm{MW}=302.4 \mathrm{~g} / \mathrm{mol}\right)$ were represented as trimers with syndiotactic configuration ${ }^{7}$ and capped with hydrogen atoms at the terminal sites. The molecular structure of each trimer was constructed using Material Studio v4.3. Parameters and partial charges for each trimer were assigned from our in-house automated parameterization tool. ${ }^{8}$
3.2 Molecular Modeling. Vapor phase crystallization of ACM utilizing PMMA and PBMA as heteronucleants was mimicked by annealing models of each polymer onto seven different faces of the monoclinic ACM crystal lattice ((001), (21-1), (020), (021), (120), (110), and (002) faces) and onto seven different faces of the orthorhombic ACM crystal lattice, ((002), (121), (201), (212), (222), (221), and (220) faces). The trimer was placed $\sim 20 \AA$ above the surface of the ACM face and the temperature was cooled to 150 K with an exponential cooling schedule of $T(\mathrm{t})$ $=T_{\mathrm{o}} \exp ^{-k t}$, where $k$ is the cooling rate constant and $t$ is the iteration number. In each iteration, the polymer model was lowered by $1 \AA$ towards the face of the ACM face, a molecular dynamics simulation was performed with a center of mass restraint on the trimer, and a minimization of the polymer model without restraints was carried out. Three annealing protocols were explored using different cooling schedules and dynamics lengths with an initial temperature, $T_{o}$, of 600 K : (i) $k=$ 0.05 with 50 ps dynamics for each iteration, (ii) $\mathrm{k}=0.01$ with 50 ps dynamics for each iteration, and (iii) $\mathrm{k}=0.005$ with 100 ps dynamics for each iteration. During the dynamics phase, a nonbonded cutoff of $15 \AA$ was used and van der Waals switching and electrostatic force shifting functions were implemented between $10 \AA$ and $12 \AA$. All ACM atoms were fixed, hydrogen bonds were restrained using the SHAKE $^{9}$ algorithm and the time step was 2 fs. Final energy minimizations were performed with no constraints on the ACM hydrogen atoms and no nonbonded cutoffs.

## SI 4. Binding Energy Calculation.

One hundred independent iterations of each of the three annealing protocols were performed for each combination of oligomer and ACM face using different initial random seed values in establishing initial velocities for the molecular dynamics steps. The initial trimer position was sufficiently far away from the ACM face that the trimer could freely rotate about its center of
mass during the initial dynamics phase and, thus, the final results are not sensitive to the initial orientation of the trimer. The overall surface binding energies $\left(\Phi_{\mathrm{BE}(\mathrm{h}, \mathrm{k}, \mathrm{l}}\right)$ were estimated from the energy difference between the most favorable energy complex in vacuum ( $\Phi_{\mathrm{IE}}$ ), and the minimized energy of the free components ( $\Phi_{\mathrm{PM}}$, polymer model and $\Phi_{\mathrm{CF}}$, crystal face) in vacuum (Equation 1). ${ }^{10}$

$$
\begin{equation*}
\Phi_{\mathrm{BE}(\mathrm{~h}, \mathrm{k}, \mathrm{l})}=\Phi_{\mathrm{IE}}-\left(\Phi_{\mathrm{PM}}+\Phi_{\mathrm{CF}(\mathrm{~h}, \mathrm{k}, \mathrm{l})}\right) \tag{1}
\end{equation*}
$$

Table SI 1. Surface binding energies ( $\Phi_{\mathrm{BE}(\mathrm{hkl}), \mathrm{kcal} / \mathrm{mol}) \text { of PO faces of ACM crystals interacting }}$ with PBMA and PMMA trimers estimated from molecular docking simulations.

| $\Phi_{\text {BE( } \mathrm{l}, \mathrm{k}, \mathrm{l})}(\mathrm{kcal} / \mathrm{mol})$ | PBMA | PMMA |
| :---: | :---: | :---: |
| $\boldsymbol{\Phi}_{\text {BE(001)monoclinic }}$ | -43.0 | -35.3 |
| $\Phi^{\text {BE(110)monoclinic }}$ | -38.9 | -25.8 |
| $\Phi_{\text {BE(020) monoclinic }}$ | -44.5 | -26.1 |
| $\boldsymbol{\Phi}_{\text {BE(021)monoclinic }}$ | -40.8 | -28.3 |
| $\Phi_{\text {BE(120)monoclinic }}$ | -40.4 | -26.3 |
| $\boldsymbol{\Phi}_{\text {BE(21-1)monoclinic }}$ | -43.9 | -28.9 |
| $\boldsymbol{\Phi}_{\text {BE(002) monoclinic }}$ | -35.7 | -26.0 |
| $\boldsymbol{\Phi}_{\text {BE(002) orthorhombic }}$ | -33.7 | -20.7 |
| $\boldsymbol{\Phi}_{\text {BE(121)orthorhombic }}$ | -38.6 | -26.5 |
| $\boldsymbol{\Phi}_{\text {BE(201)orthorhombic }}$ | -39.1 | -27.3 |
| $\boldsymbol{\Phi}_{\text {BE(212)orthorhombic }}$ | -39.5 | -28.3 |
| $\boldsymbol{\Phi}_{\text {BE(222)orthorhombic }}$ | -39.8 | -27.6 |
| $\boldsymbol{\Phi}_{\text {BE(221)orthorhombic }}$ | -40.4 | -28.5 |
| $\boldsymbol{\Phi}_{\text {BE(220) orthorhombic }}$ | -36.5 | -22.9 |



Figure SI 6. Lowest energy snapshot for PBMA interacting with (001) monoclinic ACM.


Figure SI 7. Lowest energy snapshot for PMMA interacting with (001) monoclinic ACM.


Figure SI 8. Lowest energy snapshot for PBMA interacting with (002) orthorhombic ACM.


Figure SI 8. Lowest energy snapshot for PMMA interacting with (002) orthorhombic ACM.

## SI 5. References.

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