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Washington, DC 20036  
Phone: 202-776-0544 | Fax 202-776-0545  
editorial@hematology.org

## Conformation of von Willebrand factor in shear flow revealed with stroboscopic single-molecule imaging

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Hans Bergal (Boston Children's Hospital, United States) Yan Jiang (Boston Children's Hospital, United States) Darren Yang (Wyss Institute, United States) Timothy Springer (Boston Children's Hospital, United States) Wesley Wong (Boston Children's Hospital and Harvard Medical School, United States)

### Abstract:

von Willebrand factor (VWF) is a multimeric blood protein that acts as a mechanical probe, responding to changes in flow to initiate platelet plug formation. Previously, our labs had shown using single-molecule imaging that shear stress can extend surface-tethered VWF, but paradoxically we found that the required shear stress was higher than reported for free-in-flow VWF—an observation inconsistent with basic physical principles. To resolve this inconsistency critical to VWF's molecular mechanism, we measured free VWF extension in shear flow using PULSIS—Pulsed Laser Stroboscopic Imaging of Single molecules. Here, laser pulses of different durations are used to capture multiple images of the same molecule within each frame, enabling accurate length measurements in the presence of motion blur. At high shear stresses, we observed a mean shift in VWF extension of less than 200 nm, much shorter than the multiple-micron extensions previously reported with no evidence for the predicted sharp globule-stretch conformational transition. Modeling VWF with a Brownian dynamics simulation, our results are consistent with VWF behaving as an uncollapsed polymer rather than the theorized compact ball. The muted response of free VWF to high shear rates implies that 1) the tension experienced by free VWF in physiological shear flow is lower than indicated by previous reports and 2) that tethering to platelets or the vessel wall is required to mechanically activate VWF adhesive function for primary hemostasis.

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1 **Conformation of von Willebrand factor in shear flow revealed with stroboscopic single-molecule**  
2 **imaging**

3 Hans T. Bergal<sup>1-3</sup>, Yan Jiang<sup>2-4</sup>, Darren Yang<sup>2,3,5</sup>, Timothy A. Springer<sup>2-4</sup>, and Wesley P. Wong<sup>2-5\*</sup>

4 Affiliations:

5 <sup>1</sup>Harvard Biophysics; <sup>2</sup>Program in Cellular and Molecular Medicine, Boston Children's Hospital;  
6 <sup>3</sup>Department of Biological Chemistry and Molecular Pharmacology, Blavatnik Institute at Harvard  
7 Medical School; <sup>4</sup>Department of Pediatrics, Harvard Medical School; <sup>5</sup>Wyss Institute for Biologically  
8 Inspired Engineering, Harvard University  
9

10  
11 \*Correspondence: Wesley P. Wong, Center for Life Sciences, 3rd floor, Boston Children's Hospital, 3  
12 Blackfan Circle, Boston, MA 02215; e-mail: wesley.wong@childrens.harvard.edu

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17 **Key points:**

- 18 • Free von Willebrand factor in flow extends gradually as shear stress increases, not abruptly with  
19 the presumed globule stretch transition.  
20 • Polymer simulations suggest that VWF behaves as an uncollapsed, random chain with minimal  
21 monomer-monomer interactions.

22

23 **Abstract:**

24 von Willebrand factor (VWF) is a multimeric blood protein that acts as a mechanical probe, responding  
25 to changes in flow to initiate platelet plug formation. Previously, our labs had shown using single-  
26 molecule imaging that shear stress can extend surface-tethered VWF, but paradoxically we found that  
27 the required shear stress was higher than reported for free-in-flow VWF—an observation inconsistent  
28 with basic physical principles. To resolve this inconsistency critical to VWF’s molecular mechanism, we  
29 measured free VWF extension in shear flow using PULSIS—**P**ulsed **L**aser **S**troscopic **I**maging of **S**ingle  
30 molecules. Here, laser pulses of different durations are used to capture multiple images of the same  
31 molecule within each frame, enabling accurate length measurements in the presence of motion blur. At  
32 high shear stresses, we observed a mean shift in VWF extension of less than 200 nm, much shorter than  
33 the multiple-micron extensions previously reported with no evidence for the predicted sharp globule-  
34 stretch conformational transition. Modeling VWF with a Brownian dynamics simulation, our results are  
35 consistent with VWF behaving as an uncollapsed polymer rather than the theorized compact ball. The  
36 muted response of free VWF to high shear rates implies that 1) the tension experienced by free VWF in  
37 physiological shear flow is lower than indicated by previous reports and 2) that tethering to platelets or  
38 the vessel wall is required to mechanically activate VWF adhesive function for primary hemostasis.

## 39 Introduction

40 von Willebrand factor (VWF) is a multimeric glycoprotein that circulates in blood and helps regulate  
41 hemostasis<sup>1,2</sup>. Consisting of 40-250 monomeric units arranged end-to-end, each VWF concatemer can  
42 have a contour length up to  $15\ \mu\text{m}^{3-5}$ . Hydrodynamic forces regulate VWF's molecular mechanisms via  
43 tension-dependent binding. Binding partners include GPIb $\alpha$  for platelet recruitment<sup>6-10</sup>, collagen for  
44 immobilization to damaged blood vessels<sup>11,12</sup>, other VWF molecules for amplifying activation<sup>13-15</sup>, and  
45 ADAMTS13 protease for VWF size-regulation<sup>15-19</sup>. VWF activation is premised upon its sensitivity to  
46 force, with conformational changes expected above a critical shear threshold. Extension is thought to  
47 expose binding sites, but sufficient tension is also required to allosterically activate binding to recruit  
48 platelets and initiate hemostasis.

49 Recently, Fu et al.<sup>6</sup> tethered VWF to a surface and measured VWF response to shear flow at the single-  
50 molecule level, monitoring extension and ability to bind the platelet-protein GP1b $\alpha$ . Surface-tethered  
51 VWF (figure 1A red) showed shear-dependent increases in extension up to the maximum shear stress  
52 applied ( $1280\ \text{dyn}/\text{cm}^2$ ). For reference, normal arterial shear stress is between  $10\text{-}70\ \text{dyn}/\text{cm}^2$  but is  
53 estimated to reach higher than  $400\ \text{dyn}/\text{cm}^2$  in injured arterioles<sup>20</sup>.

54 In an earlier study<sup>21</sup>, free VWF in pure shear flow was directly imaged. There appeared to be an  
55 extension of free VWF from a collapsed ball to an elongated filament  $\sim 15\ \mu\text{m}$  in length, with abrupt  
56 extension at  $\sim 50\ \text{dyn}/\text{cm}^2$ . Vascular injury was proposed to increase shear stress above this critical  
57 threshold, causing free-in-flow VWF to extend and adhere to the vessel wall at injury sites. A coarse-  
58 grained polymer model calibrated to match the extending behavior was used to model VWF<sup>21,22</sup>. The  
59 basic model of a collapsed polymer has been subsequently updated to simulate VWF behavior on a  
60 surface<sup>23-25</sup>, in elongational flow<sup>26-28</sup>, in shear flow<sup>29-31</sup> and size regulation through enzymatic  
61 cleavage<sup>17,32,33</sup>.

62 These tethered and free VWF single-molecule experiments present a paradox: the putative shear stress  
63 required to extend free VWF was *lower* than the shear stress required to extend surface-tethered VWF  
64 (figure 1B). Simulations (figure 1C), based on Schneider et al's.<sup>21</sup> model were applied to both free and  
65 surface-tethered scenarios. They predict surface-tethered VWF should extend at shear stresses 100x  
66 lower than free VWF. Independent of simulations, basic physical arguments predict a lower shear stress  
67 to extend tethered vs. free polymers<sup>30,34,35</sup>.

68 To resolve this discrepancy, we experimentally investigated the response of free VWF in shear flow using  
69 a new method to properly account for motion blur. Additionally, we updated the coarse-grained  
70 polymer model to match our new results and previously published single-molecule experiments. We find  
71 an uncollapsed polymer is sufficient to describe mesoscopic VWF behavior in flow, which complements  
72 a recent study that found evidence for a random coil description of VWF<sup>36</sup>. In contrast, models  
73 representing VWF as a collapsed polymer are difficult to reconcile with single-molecule data.

74 Our results indicate that single molecules of free VWF in physiological shear flow experience much lower  
75 internal tension than previous experiments and models predicted. This has major consequences for  
76 understanding the molecular mechanisms of hemostasis initiation, including the tension-dependent  
77 activation of VWF binding in flow and VWF size regulation, and further clinical significance for von  
78 Willebrand disease (VWD), thrombotic thrombocytopenic purpura (TTP), and Heyde's syndrome<sup>4</sup>.

## 79 **Methods**

### 80 **VWF and control preparation**

81 Recombinant, therapeutic grade VWF was size-fractionated to select for longer multimers and labeled  
82 with Alexa 488 NHS-ester as described in Fu et al<sup>6</sup>. For the positive control, M13mp18RF DNA was  
83 labeled with YOYO-1. Fluorescent beads (diameter=0.11  $\mu$ m determined by manufacturer) were used for  
84 the negative control. Imaging buffer was 60% (w/w) sucrose with 20 mM HEPES (pH 7.4), 150 mM NaCl,  
85 0.02% Tween-20 and 0.5 mg/ml BSA.

### 86 **Pulsed Laser Stroboscopic Imaging of Single molecules (PULSIS)**

87 Molecules were imaged with a lab built TIRF microscope (60x oil immersion objective). A pressure-  
88 driven flow system was used to flow VWF through microfluidic channels (figure 2A). To correct for  
89 motion blur, we developed PULSIS (figure 2B-D), which images each molecule multiple times with  
90 different duration laser pulses. This enables us to build a relationship between the laser pulse duration  
91 and the observed streak length on a per molecule basis which is used to determine a “zero-pulse” or  
92 motion blur corrected length. Molecules were imaged with pulsed laser illumination, which followed a  
93 pattern of 1-on,3-off,1-on,3-off,2-on,3-off,3-on,3-off with the frequency of the pulse pattern tuned to  
94 the fluid velocity. (See supporting text section 1).

### 95 **Image Analysis**

96 PULSIS trajectories were analyzed with custom MATLAB scripts. Trajectories were manually selected,  
97 streak lengths were measured, and pulse duration (1,2,3) was assigned. A linear regression of pulse  
98 duration and measured lengths with fitting errors was performed, giving the particle velocity (slope) and  
99 the corrected molecule length (y-intercept).

### 100 **Simulation**

101 VWF multimers are represented by spherical beads, connected by a finitely extensible nonlinear elastic  
102 (FENE) potential with relevant hydrodynamic interactions<sup>22</sup>. Bead positions are updated according to a  
103 discretized Langevin equation based on the applied forces and random fluctuations from Brownian  
104 motion. The simulation uses a non-specific Lennard-Jones (LJ) potential, which accounts for a cohesive  
105 monomer-monomer attraction and excluded volume. (See supporting text S2).

### 106 **Data Sharing**

107 For data, contact [wesley.wong@childrens.harvard.edu](mailto:wesley.wong@childrens.harvard.edu)

## 108 **Results**

### 109 **Pulsed Laser Stroboscopic Imaging of Single molecules (PULSIS)**

110 To resolve the discrepancy between force scales of free and tethered VWF experiments, we developed a  
111 new single-molecule approach to investigate the length response of free VWF to shear flow. The primary  
112 experimental challenge is accurately measuring the lengths of molecules rapidly flowing through the  
113 field of view. The movement of molecules during image exposure causes motion blur, which is difficult  
114 to distinguish from molecule extension.

115 To correct motion blur at high shear rates we developed PULSIS, which images each molecule multiple  
116 times using a series of different duration laser pulses (figure 2A,B). The pulse pattern creates a series of  
117 fluorescent streaks that encode the length and velocity (dependent on distance from the vessel wall) of  
118 the molecule within a single frame. Based on the pulse duration and measured streak lengths, a linear  
119 regression gives the particle velocity (slope) and the length for a “zero-duration” pulse (y-intercept), i.e.,  
120 the true length of the molecule. Example experimental PULSIS trajectories (figure 2C) show a  
121 fluorescently-labeled DNA molecule flowing across a single frame illuminated with the laser pulse  
122 pattern. The measured streak lengths at the corresponding pulse durations are fit to a line (streak length  
123 vs pulse duration), with the corrected extension given by the y-intercept (figure 2D). The corresponding  
124 linear fits of the image trajectories in figure 2C show linearized M13 DNA captured in two different  
125 orientations that differ in apparent length during tumbling in shear flow.

126 To test if PULSIS can distinguish between compact and elongated particles, we measured fluorescently  
127 labeled double-stranded DNA, in both the supercoiled and linearized states (figure 2E). Each molecule  
128 gives a motion-blur corrected length; these are aggregated together to build up a distribution of lengths  
129 (figure 2E). For example, the two trajectories (figure 2C-D) are single statistics from the distribution for  
130 linearized DNA in figure 2E. Supercoiled DNA remained compacted, giving a normal distribution with  
131 mean length  $L=0.26\pm 0.25\ \mu\text{m}$ . In contrast, linearized DNA had a broader distribution, with molecules up  
132 to  $\sim 1.7\ \mu\text{m}$  and a shifted mean length  $L=0.58\pm 0.38\ \mu\text{m}$ , comparable to expected distributions for DNA in  
133 shear flow<sup>37</sup>. Broadening of the length distribution arises from the rotational component of shear flow,  
134 which causes polymers to tumble in cycles of extension and relaxation<sup>38</sup>, with sampling of these states  
135 resulting in a broad distribution. To further validate PULSIS, fluorescent beads were imaged at shear  
136 stresses between 20-200 dyn/cm<sup>2</sup> (figure 2F). The average measurement at each shear stress was within  
137 10 nm of the manufacturer’s reported diameter of 110 nm and had no dependence on the applied shear  
138 stress.

139 Distinguishing collapsed vs. extended free-VWF can be difficult due to motion blur. One approach  
140 imaged fiduciary beads to subtract out motion-blur effects for VWF in shear flow<sup>21</sup>. However, small  
141 deviations in distance from the flow vessel wall between molecules and their fiducials (even less than  
142 the depth of field, supporting text S3) can result in large errors in perceived VWF length. In contrast,  
143 PULSIS uses each molecule as its own reference, without requiring comparison to other objects or  
144 precise knowledge of distance from the surface. Another approach used single short-illumination pulses  
145 to minimize the motion blur of VWF in flow<sup>39</sup>. However, this method has limited signal-to-noise ratio  
146 and retains some motion blur artifacts. By contrast, PULSIS can fully account for motion blur by  
147 extrapolation to infinitesimally short pulses while maintaining a strong signal-to-noise ratio. While  
148 others have used short, stroboscopic pulses to limit motion blur and track molecules<sup>39-41</sup>, to our  
149 knowledge PULSIS is novel in using a pattern of different duration pulses to measure molecule lengths in  
150 flow.

151 Additionally, we used a 60% (w/w) sucrose solution to increase the viscosity of the imaging buffer by  
152  $\sim 58$  times compared to water<sup>42</sup> to study higher shear rates. This high-viscosity buffer applies equivalent  
153 shear stress at a 58-fold lower flow rate with correspondingly lower motion blur<sup>6,39</sup>. Surface-tethered  
154 VWF was imaged in both aqueous buffer and high-viscosity sucrose buffer at equivalent applied shear  
155 stresses (figure S2)<sup>6</sup>. Similar to previous studies<sup>7</sup>, no differences in length were observed between  
156 molecules in the aqueous and sucrose buffer at the same shear stress, suggesting sucrose has minimal  
157 effects on the energetics of VWF extension. With the sucrose buffer and PULSIS, we can measure the

158 lengths of free VWF molecules at shear stresses up to 200 dyn/cm<sup>2</sup>, double the limit of previous  
159 experiments<sup>39</sup>.

### 160 **Measurement of VWF free in shear flow**

161 Purified, fluorescently labeled VWF molecules were imaged with PULSIS at shear stresses of 20-200  
162 dyn/cm<sup>2</sup>(figure 3A), ranging from low arterial to pathological shear stresses<sup>43</sup>. Above 200 dyn/cm<sup>2</sup>, the  
163 signal-to-noise ratio was too low for reliable data. However, this is still twice the highest shear stress  
164 imaged in previous studies of VWF free in flow<sup>39</sup>. The underlying size-distribution of VWF was estimated  
165 based on the length of tethered VWF molecules, with some molecules at least 6 μm in length (figure  
166 S2B).

167 At the lowest shear stress, the measured length distribution was Gaussian with mean and standard  
168 deviation  $L=0.15\pm 0.17$  μm. We interpret this distribution as containing compact VWF molecules, with  
169 the variance resulting primarily from measurement error. At 50 dyn/cm<sup>2</sup>, the measured mean increased  
170 by 30 nm to 0.18 μm, dramatically less than the ~10 μm increase suggested<sup>21</sup> (figure 3B). At 200  
171 dyn/cm<sup>2</sup>, the highest shear stress measured, the mean length had shifted to 0.29 μm. Between 20 and  
172 200 dyn/cm<sup>2</sup>, the standard deviation increased from 0.16 to 0.41 μm, indicating the distributions were  
173 broadening. Like linearized DNA, the length distributions broaden at higher shear stresses as the VWF  
174 tumbles. The distributions are convolutions of the measurement error, the underlying VWF size  
175 distribution, and the tumbling of individual molecules.

176 The distributions at each shear stress were compared using the nonparametric Mann-Whitney U test for  
177 statistical significance. The test calculates the probability that the length distributions at two given  
178 shears are the same (figure 3D). Distributions at similar shear (80 dyn/cm<sup>2</sup> vs. 100 dyn/cm<sup>2</sup>) are  
179 statistically similar ( $p=0.91$ ). Large changes in shear stress, for example, 50 vs. 150 dyn/cm<sup>2</sup>, give  
180 statistically different distributions ( $p<0.001$ ), indicating the length distribution changes a marginal but  
181 statistically significant amount over the shear range explored.

182 We observed a small population of VWF molecules with a measured length of ~2 μm (figure 3A, E-F),  
183 consistent with length heterogeneity in the VWF concatemers and suggesting some elongation in this  
184 subset at 100-200 dyn/cm<sup>2</sup>. Comparing the 90<sup>th</sup> percentile of lengths between the 20 and 200 dyn/cm<sup>2</sup>  
185 shear stresses demonstrates a doubling in length (350 to 800 nm), while the median length changes by  
186 <100 nm (figure 3C).

### 187 **Brownian Dynamics polymer simulations for VWF**

188 Previous attempts to model VWF in flow have relied on coarse-grained Brownian Dynamics polymer  
189 simulations, as the massive size of VWF and the long timescales of physiological processes make full MD  
190 simulations unfeasible. The original free VWF in shear studies put forth a widely used Brownian  
191 dynamics model<sup>22</sup>. With more single-molecule experiments for VWF, we now have orthogonal  
192 experiments to test the model against<sup>6,24,39</sup>.

193 The two parameters  $u$  (Lennard-Jones (LJ) interaction strength) and  $r$  (bead radius), make up a phase  
194 space which represents possible realizations of the simulation (figure 4A). Used to model basic  
195 intermolecular interactions<sup>44</sup>, the Lennard-Jones potential is non-specific, meaning beads interact with  
196 all other beads. The LJ well-depth determines the strength of intermolecular interactions. With a large  
197 value ( $u > 0.314 k_B T$ ), beads favorably interact to form a collapsed globule resistant to extension up to a

198 critical shear stress, above which a sudden globule-stretch transition occurs<sup>22,30,35</sup>. VWF was proposed to  
 199 behave like a collapsed polymer because a sharp transition was reported to occur in shear flow<sup>21</sup>. The  
 200 simulation has been updated in more recent work to include features like A2 unfolding but continues to  
 201 use collapsed polymers with LJ potentials between 0.52-1.44  $k_B T$ <sup>23-25,29,45</sup>.

202 At smaller interaction potentials ( $u < 0.314 k_B T$ ), a polymer behaves as an uncollapsed polymer. At the  $\Theta$ -  
 203 point ( $u = 0.314 k_B T$ ), the attractive and repulsive forces cancel out, and the polymer's dimensions match  
 204 that of a simple ideal chain<sup>46,47</sup>. Unlike a collapsed polymer, an uncollapsed polymer's extension changes  
 205 smoothly with increasing shear and does not have a sharp transition<sup>38,48</sup>.

206 Shear resistance is also dependent on bead size. Larger beads experience more hydrodynamic drag than  
 207 smaller beads causing elongation at lower shear stresses. In the original model, a large monomer  
 208 attraction was used to get a sharp transition, which required a large bead of  $r = 80$  nm to fit the critical  
 209 shear stress. Based on EM images from Fowler et al.<sup>49</sup> (figure 4B) and x-ray crystallography structures<sup>1</sup>, a  
 210 spherical radius of 80 nm overestimates two dimensions of VWF monomers. Recent models have  
 211 attempted to correct this and reduced the bead radius to  $r = 10-15$  nm<sup>23-25,29,45</sup> but still overestimate the  
 212 cross-section of VWF monomers ( figure 4B).

213 We tested a polymer at the  $\Theta$ -point ( $u = 0.314 k_B T$ ) and optimized the bead size to best match the single-  
 214 molecule experiments described below and found a radius of  $r = 3.7$  nm. This radius would require 8  
 215 spherical beads to make up a full monomer of 60 nm<sup>49</sup>. Notably, this bead size is similar to the size of  
 216 the 11 domains in each VWF monomer, which range from 1.5-3 nm in radius<sup>1,50</sup>. We also evaluated the  
 217 original Brownian dynamics model ( $u = 2.08 k_B T$ ,  $r = 80$  nm)<sup>21,22</sup> and a revised-LJ model ( $u = 2.08 k_B T$ ,  $r = 14$   
 218 nm) with a smaller radius representative of recent models<sup>23-25,45</sup>. The simulations are compared to three  
 219 single-molecule experiments: previous measurements of surface-tethered VWF stretching in shear flow  
 220 and subsequent relaxation<sup>6</sup> and measurements here of free VWF in shear flow. All simulations have a  
 221 contour length of  $\sim 3 \mu m$  based on the average maximum extension length from surface extension  
 222 experiments (figure S2B, expanded lengths in figures S3-4,S7,S9).

### 223 **Polymer simulations for surface-tethered VWF in shear flow**

224 Surface-tethered VWF in shear flow was simulated with the three models described above.  
 225 Experimental data from Fu et al.<sup>6</sup> shows VWF extends little between 10-40  $dyn/cm^2$ . Between 40-1280  
 226  $dyn/cm^2$ , VWF requires an exponential increase in shear to achieve a linear length increase. Shear flow  
 227 was applied to the tethered polymer models, then length in the flow direction was recorded and  
 228 normalized by the length at the highest shear stress. When normalized by maximum extension, shear-  
 229 extension curves of VWF are generally independent of length<sup>6</sup>.

230 With a small bead size, our uncollapsed polymer experiences less hydrodynamic extensional force than  
 231 other models and entropic effects are sufficient to resist extension without a cohesive potential. Like  
 232 VWF, the simulated uncollapsed polymer's fractional extension scales logarithmically with shear stress  
 233 and matches the data well (figure 4c). In contrast, due to large beads, the original LJ model unfolds  
 234 completely by 10  $dyn/cm^2$  when tethered to the surface, at a shear stress  $\sim 100$  times lower than  
 235 experimentally observed. Furthermore, independent of bead radius, models with strong LJ interactions  
 236 extend abruptly over a narrow range of shear stresses<sup>22,35</sup>. The revised-LJ model was optimized to reach  
 237 the proper half-maximal extension at the same shear as VWF. This collapsed polymer extends  $\sim 65\%$  of



238 its maximal length between 160 and 320 dyn/cm<sup>2</sup>, showing an abrupt transition not experimentally  
239 observed.

#### 240 **Polymer simulations for free VWF in shear flow**

241 The polymer simulations were further compared to our experimental measurements here of free VWF  
242 in shear flow. Shear flow was applied and the length distribution over time was recorded, as measured  
243 by the maximum length difference along the axis of flow. Since the contour length of the experimental  
244 VWF data is not known, the lengths are not normalized. The experimental data also represents a  
245 heterogenous distribution of sizes, making direct comparison difficult as polymer simulations have  
246 shown a size dependence for elongation in shear stress<sup>30,51</sup>. However, the qualitative behavior of each  
247 model is still informative.

248 Mean extensions of the simulated polymers in free shear were compared to the mean experimental  
249 length measurements (figure 4D). The original LJ model was specifically designed to exhibit large  
250 conformational changes in mean extension at shear stresses around 50-80 dyn/cm<sup>2</sup> and predicts a mean  
251 length change of 0.8 μm. The revised-LJ model, with parameters set to match the experimental surface  
252 stretching data, has a critical shear rate higher than the experiment and shows no change in mean  
253 length in the tested range. Our uncollapsed polymer model increases in mean extension by ~150 nm  
254 between 40-160 dyn/cm<sup>2</sup>, qualitatively matching the observed behavior. Based on the uncollapsed  
255 polymer model, the mean tension under physiological shear stress was estimated to be <0.1 pN  
256 (supporting text S4, figure S5).

#### 257 **Polymer simulations for VWF relaxation**

258 Polymer relaxation in the absence of flow provides orthogonal experimental VWF data to further test  
259 the predictions of models. Relaxation provides details on timescale and conformation. Experimental  
260 data was analyzed from Fu et al.<sup>6</sup> where VWF in a high-viscosity sucrose buffer is hydrodynamically  
261 stretched by a high shear stress and imaged as the molecule relaxes. Even in high viscosity buffer, VWF  
262 relaxes quickly in ~1 second. In our simulations (supporting text S5), we find the relaxation time scale is  
263 inversely correlated with the polymer bead size, consistent with a small bead radius to parameterize  
264 VWF (figure S6,S7). Furthermore, the relaxation conformation, based on the experimental fluorescence  
265 distribution of VWF, disagrees with the collapsed polymer simulation but is well-modeled by our  
266 uncollapsed polymer simulation (figure S8,S9).

#### 267 **Discussion**

268 We developed PULSIS, an approach for measuring the lengths of molecules in high shear flow by  
269 measuring each molecule multiple times with different duration pulses. We then investigated VWF at  
270 shear stresses ranging from 20-200 dyn/cm<sup>2</sup>, representing physiological to pathological shear stresses to  
271 capture relevant changes *in vivo*<sup>20</sup>. Qualitatively, the VWF length distribution shows no sharp globule-  
272 stretch transition near the previously reported 50 dyn/cm<sup>2</sup> threshold. Quantitatively, the change in  
273 mean length between 20-200 dyn/cm<sup>2</sup> is two orders of magnitude less than the previously reported  
274 values (0.17 vs 13 μm)<sup>21</sup>. This discrepancy may have resulted from motion blur artifacts in the previous  
275 work<sup>21</sup>. High shear rates coupled with limited axial resolution would make it difficult to account for  
276 motion blur with fiducial beads.

277 The small response of VWF to pure shear flow is a departure from the current perception within the  
278 field but still consistent with a majority of VWF literature. Length distributions, with a long tail with low  
279 micrometer lengths, is consistent with VWF free-in-flow experiments from Vergauwe et al.<sup>39</sup>.  
280 Furthermore, the measured mean extension of free VWF is less than the extension of tethered VWF  
281 reported by Fu et al.<sup>6</sup> at the same shear stress, resolving the force paradox discussed in figure 1B. A  
282 small response of VWF to shear stress is also consistent with small-angle neutron scattering  
283 experiments<sup>52</sup> which found no large-scale rearrangement at 30 dyn/cm<sup>2</sup> as well as dynamic light  
284 scattering experiments<sup>7</sup> which found no evidence for individual VWF extension at 60 dyn/cm<sup>2</sup>.

285 Tension allosterically activates VWF binding to platelet proteins GPIb<sup>6</sup>. Furthermore, VWF cleavage by  
286 ADAMTS13 requires unfolding of the A2 domain for monomer cleavage, indicating that tension helps  
287 regulate VWF function<sup>16</sup>. Our results imply the tension experienced by free VWF in shear flow is lower  
288 than previously assumed; since tension depends on the difference in velocity between opposing ends of  
289 the molecule, a smaller extension should result in a comparably smaller tension<sup>53</sup>.

290 Studies have observed VWF cleavage accelerated with shear stress<sup>17,54</sup>. However, other studies have  
291 observed no increase in ADAMTS13 cleavage with either high shear or elongational flow<sup>55</sup> but find that  
292 high turbulent flow results in VWF cleavage<sup>56</sup>. Based on our polymer model, the average tension at 80  
293 dyn/cm<sup>2</sup>, high arterial stress, is estimated to be <0.1 pN (figure S5), much lower than the force scale  
294 measured for A2 unfolding ( $f_b=1.1\pm0.2$  pN)<sup>16</sup>. The estimated tension predicts that physiological shear  
295 does not dramatically bias on average the unfolded form of free-VWF A2 for VWF cleavage. However, it  
296 is unconfirmed whether physiological force could still play a role in accelerating the rate of cleavage or  
297 create a preference for cleavage of longer VWF molecules. The exact flow conditions and contributions  
298 from blood proteins like Factor VIII<sup>60</sup> needed for VWF cleavage require further experimental  
299 investigation.

300 VWF localizes to the area of vascular injury and recruits other clotting factors like platelets. VWF  
301 localization is likely driven by binding to collagen in the vessel wall that is exposed in injury<sup>1</sup>. Both flow-  
302 dependent<sup>12</sup> and flow-independent<sup>61,62</sup> VWF-collagen binding have been reported. Injury could expose  
303 collagen in the endothelium, allowing binding independent of flow. If the VWF-collagen binding rate has  
304 some tension dependence, shear stresses below 200 dyn/cm<sup>2</sup> are not predicted to have a significant role  
305 in accelerating binding. Supporting this, Colace and Diamond<sup>12</sup> observed minimal rates of VWF-collagen  
306 binding at a shear stress of 125 dyn/cm<sup>2</sup>.

307 Extension and tension ( $\sim 20$  pN)<sup>6</sup> are necessary to shift the VWF A1 domain from a low affinity to a high  
308 affinity state for platelet protein GP1b binding<sup>6</sup>. Our results suggest single-molecules of free VWF alone  
309 do not exhibit shear-stress dependent binding to GP1b at physiological shear rates. Recruitment of  
310 platelets is likely only after VWF is attached to a surface, where the flow directly stretches VWF and  
311 higher tensions are reached. Interestingly, Nesbitt et al.<sup>63</sup> predominantly observed platelet aggregation  
312 on vessel walls at the point of stenosis, supporting the idea that both high flow and surface attachments  
313 are important for platelet aggregation.

314 We found no evidence for the sharp transition for free-in-flow VWF predicted by the LJ collapsed  
315 polymer simulations. Furthermore, based on the relaxation conformation and surface stretching  
316 behavior, the LJ collapsed polymer is not a suitable model for VWF. Meanwhile, our uncollapsed  
317 polymer model was consistent with previous VWF surface stretching-in-flow experiments<sup>6</sup>, our own  
318 PULSIS data for free polymers in shear, and both time scale and conformation of relaxation from a

319 stretched state. While the good agreement of single-molecule experiments with our uncollapsed  
320 polymer models do not constitute proof, an uncollapsed polymer is a sufficient description of the  
321 observed mesoscopic VWF dynamics in flow. Optimal bead size is on a similar scale as VWF domains,  
322 giving further agreement with physical observations of VWF. Our model suggests that VWF does not  
323 adopt a globular, collapsed form and monomers have minimal attractive interactions. This supports  
324 recent ultracentrifuge experiments where VWF behaved like a random coil<sup>36</sup> and is consistent with EM  
325 images of VWF<sup>49</sup>.

326 The molecular mechanism of VWF activation is based on large conformational changes above a critical  
327 shear threshold to initiate hemostasis. However, we find no experimental evidence for a critical shear  
328 for large conformational changes in free-in-flow VWF—observed length changes are ~10 times smaller  
329 than previously thought. We find gradual length changes over a range of shear stress, consistent both in  
330 scale and shape with an uncollapsed polymer. Our results suggest free-flowing VWF molecules cannot  
331 act as a responsive sensor of shear stress for activation of hemostasis, invalidating a commonly held  
332 view of VWF activation. The field should investigate alternative initiation mechanisms, including the role  
333 of elongational flow near constriction sites, flow-independent binding to collagen in the vessel wall, and  
334 interaction with platelets.

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### 340 **Author contributions**

341 H.T.B., W.P.W., Y.J., and D.Y designed the research. H.T.B and Y.J. performed the experiments. H.T.B and  
342 D.Y ran simulations. W.P.W and H.T.B. drafted the manuscript. W.P.W., D.Y, Y.J, and H.T.B. analyzed  
343 data. H.T.B., Y.J., D.Y., T.A.S., and W.P.W. discussed the results and commented on the manuscript.

### 344 **Conflict-of-interest Disclosure**

345 All the authors declare no competing financial interests.

346 **ORCID profiles** H.T.B., 0000-0002-5499-7833; Y.J., 0000-0002-2745-4323; D.Y., 0000-0002-2271-6910;  
347 T.A.S., 0000-0001-6627-2904; W.P.W., 0000-0001-7398-546X

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518



519 **Figure Captions**

520 **Figure 1. Free vs surface tethered VWF extension under flow.** **A** Diagram illustrating<sup>64</sup> free-in-flow VWF  
521 (blue) vs surface-tethered (red) with applied shear flow. **B** Data from Schneider et al.<sup>21</sup> (blue) showing  
522 normalized extension vs shear stress for free VWF and data from Fu et al.<sup>6</sup> (red) showing normalized  
523 extension vs shear for tethered VWF. Required shear stress for free VWF extension is expected to be  
524 higher than required shear stress for surface tethered extension but experimentally the opposite was  
525 observed. **C** Predictions of mean extension in response to shear stress based on a Brownian dynamics  
526 model with a strong Lennard-Jones interaction potential proposed by Schneider et al.<sup>21</sup> for both a free-  
527 in-flow (blue) and tethered (red) polymer. Lengths are normalized based on the maximum observed  
528 length in the direction of flow.

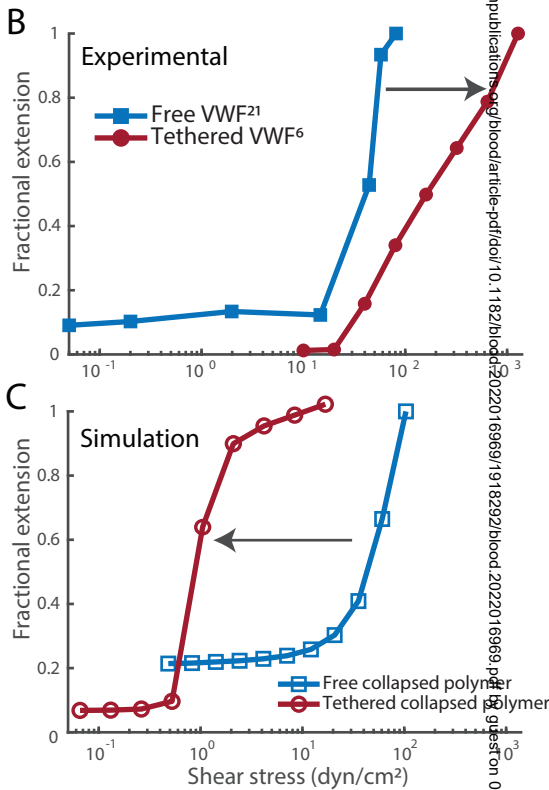
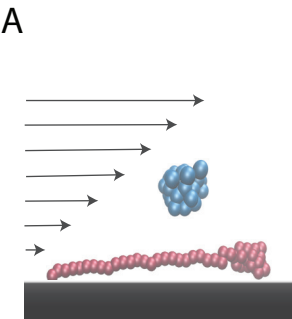
529 **Figure 2. Pulsed Laser Stroboscopic Imaging of Single molecules (PULSIS).** **A** Basic schematic of the  
530 pressure driven flow system and imaging set up, not to scale. **B** Cartoon depiction of PULSIS. Objects are  
531 imaged with different duration pulses and by comparing the relative lengths, we can accurately measure  
532 the lengths of moving objects, and distinguish point objects from elongated objects. **C** Example  
533 experimental PULSIS trajectories of fluorescently labeled linearized DNA at 50 dyn/cm<sup>2</sup>. **D** Example  
534 relationship between measured length of pulse  $L_m$  ( $\mu\text{m}$ ) vs relative pulse duration  $T_p$  (arbitrary time  
535 units) for the two DNA PULSIS trajectories in 2C. For each trajectory, streak lengths are measured and a  
536 linear regression performed of the form  $L_m=L_0+V*T_p$  with fitting errors according to York et al<sup>65</sup>.  $L_m$  is the  
537 illuminated streak length that we measure and  $T_p$  is the relative pulse duration defined by the pulse  
538 pattern (1, 2, or 3). The linear fit gives us the particle velocity  $V$ , and the y-intercept  $L_0$  represents the  
539 length of the molecule observed with an infinitesimally short pulse i.e with no motion blur. The first  
540 trajectory (yellow) has a corrected length of 0.29  $\mu\text{m}$  and resembles a compact object. The second  
541 trajectory has a corrected length of 1.03  $\mu\text{m}$  and represents an elongated object. Error bars on pulse  
542 length are based on goodness of fit to predicted pulse shape (Supplemental Methods). **E** Positive control  
543 showing histogram of PULSIS determined lengths of double stranded M13 DNA plasmid both in  
544 supercoiled (blue) and linearized (red) state at 50 dyn/cm<sup>2</sup> imaged in sucrose buffer. Histograms are of  
545 motion blur-corrected lengths of hundreds of single molecules. The examples (trajectories and analysis)  
546 from figure 2C-D are two statistics from the linearized (red) distribution. Histograms are displayed along  
547 with kernel density estimates. Kernel density estimation is a method for smoothing histograms by  
548 applying a gaussian kernel to each point<sup>66</sup>. A Gaussian kernel was used with bandwidth set by  
549 Silverman's rule<sup>67</sup> **F** Negative control showing kernel density estimate for PULSIS motion blur corrected  
550 beads at different shear stress (manufacture determined diameter of 0.11  $\mu\text{m}$ ). Raw histograms in figure  
551 S1. Number of measurements, mean length and standard deviation for each condition are shown in  
552 panels E and F.

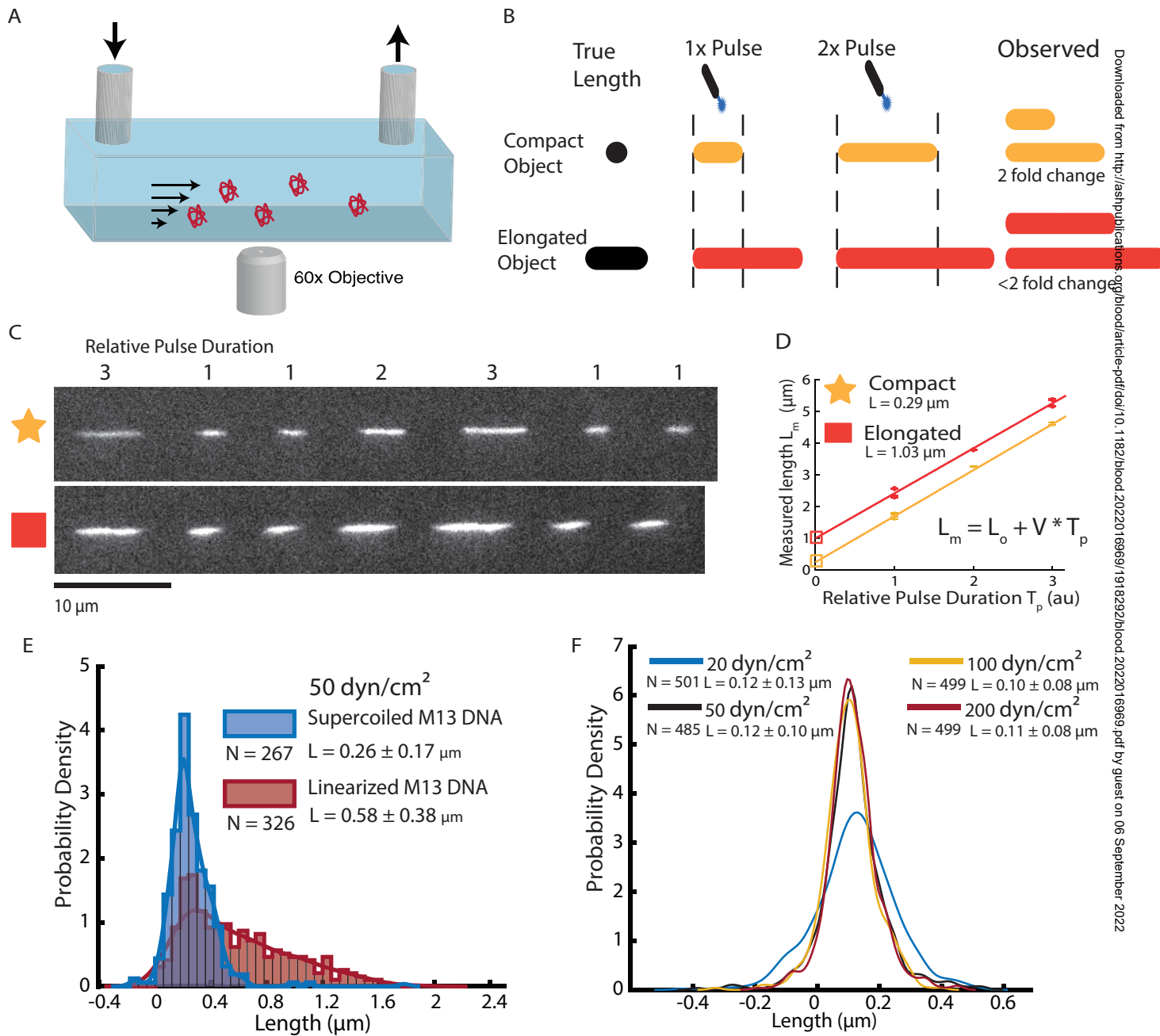
553 **Figure 3. Free-in-flow VWF extension in shear flow.** **A** Histogram of VWF length at 6 shear stresses (20,  
554 50, 80, 100, 150, 200 dyn/cm<sup>2</sup>). **B** Mean extension vs shear stress ( $\circ$ ) and standard deviation vs shear  
555 stress ( $\Delta$ ) of VWF molecules for histograms shown in 3A. Monotonic increases in mean and standard  
556 deviation are both consistent with molecules extending under flow. **C** Percentiles 50-90 of VWF length  
557 vs shear stress for histograms in 3A. **D** Nonparametric statistical significance testing using Mann-  
558 Whitney U test comparing each shear stress length distribution. Values for  $p<0.05$  indicate statistical  
559 significance. **E** Three example trajectories of VWF at 150 dyn/cm<sup>2</sup> with different PULSIS corrected  
560 lengths. Example molecules of a long, middle, and short extended molecule. **F** Corresponding plots of

561 pulse length vs relative pulse duration for trajectories in fig 3E. The y-intercept represents motion blur  
562 corrected lengths for VWF molecules.

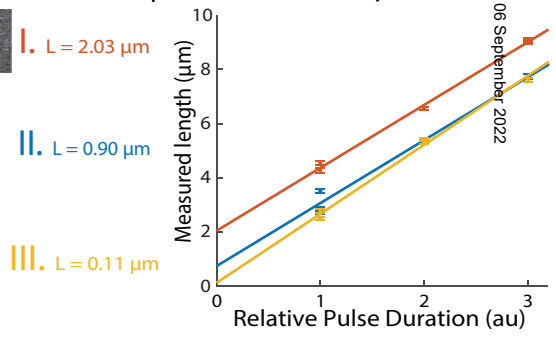
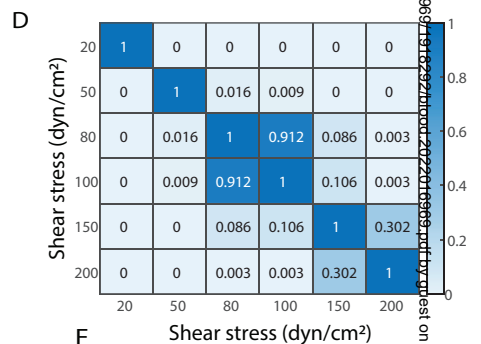
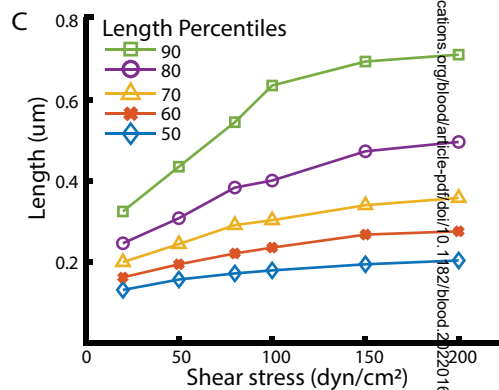
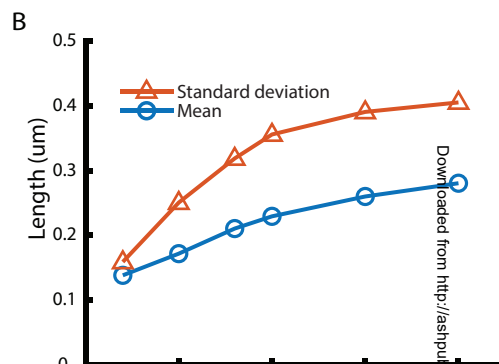
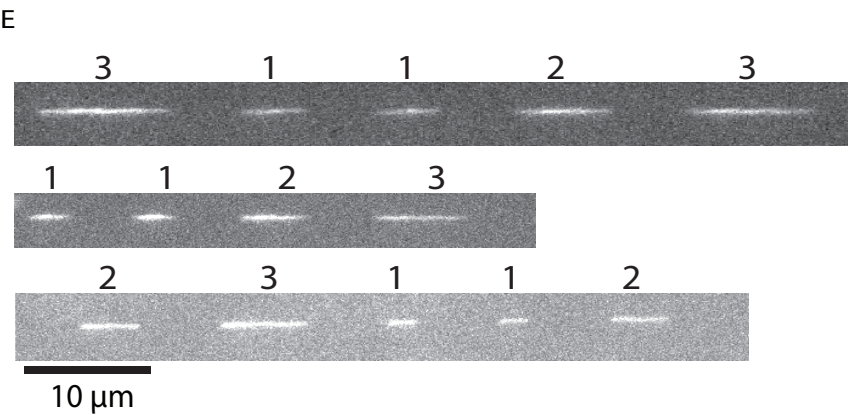
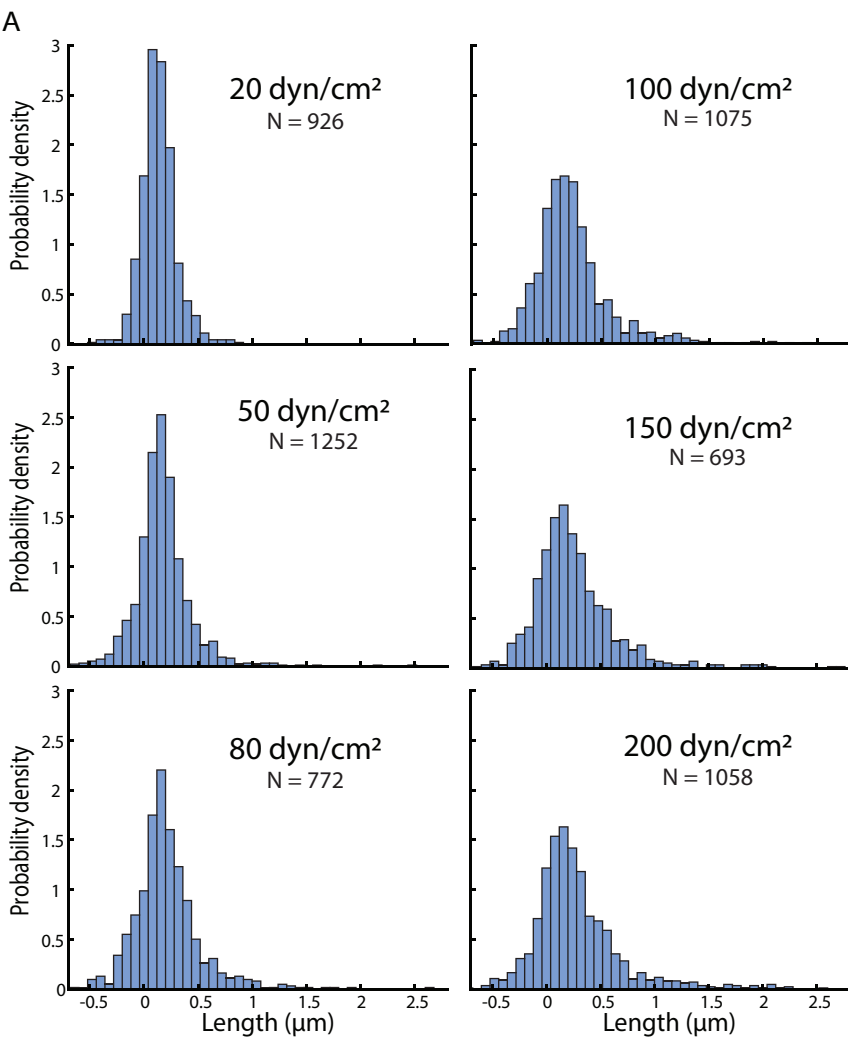
563 **Figure 4. Comparison of Brownian dynamics models for VWF.** **A** Parameter space of the simulation as a  
564 function of bead diameter and Lennard-Jones interaction strength. Comparison with the size of spheres  
565 representing monomers of the different models. Sizes of spheres are on the same scale as 4B. Blue  
566 space represents collapsed polymers, with yellow being uncollapsed polymers. Dotted line represents  
567 the  $\Theta$ -point where attractive and repulsive forces cancel out. **B** Electron microscopy images adapted  
568 from Fowler et al.<sup>49</sup> of VWF. **C** Comparison between Brownian dynamics simulation and experimental  
569 steady state extension for surface tethered polymers under shear flow. The three models are the  
570 original Lennard-Jones model ( $\diamond$ ), the revised Lennard-Jones model ( $\Delta$ ) and the uncollapsed polymer  
571 model ( $\square$ ). Simulations compared to experimental data from previous surface stretching experiments of  
572 2-3.5  $\mu\text{m}$  VWF molecules from Fu et al. (o, 156 molecules measured)<sup>6</sup>. For each model and shear stress,  
573 the equilibrium extension of five independent simulations were averaged together at each shear stress.  
574 Extension is normalized by maximum extension and plotted on a semi log plot. Shaded area shows  
575 standard deviation of the 5 simulations. **D** Comparison of Brownian dynamics simulation and  
576 experimental mean extension for free-in-flow VWF with applied shear flow as measured by PULSIS,  
577 plotted on a semi log plot. Since the contour length of the experimental data is unknown, simulations  
578 and data are not normalized. Polymer simulation extensions were averaged over a time window and  
579 independent runs. (LJ original runs=3, Revised LJ runs = 3, Uncollapsed polymer runs = 10). Absolute  
580 contour length of all simulations was  $\sim 3 \mu\text{m}$ .

Figure 1.



**Figure 2.**

**Figure 3.**



**Figure 4.**