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Probing protein mechanical stability with controlled shear flows JONATHAN DUSTING, Experimental and Computational Laboratory for the Analysis of Turbulence (ECLAT), King's College London, Strand, London WC2R 2LS, UK, LORNA ASHTON, Manchester Interdisciplinary Biocentre, University of Manchester, Manchester, M1 7DN, UK, JUSTIN LEONTINI, FLAIR, Dept of Mechanical and Aerospace Engineering, Monash University, Australia, EWAN BLANCH, Manchester, UK, STAVROULA BALABANI, London, UK — Understanding and controlling protein aggregation or misfolding is of both fundamental and medical interest. The structural changes experienced by proteins in response to forces such as those generated within flows have not been well characterised, despite the importance of mechanics in many biological processes. By monitoring the structural conformation of proteins in different concentric cylinder flows using Raman Spectroscopy we have quantified the relative stability of β -sheet dominated proteins compared with those containing a greater proportion of α -helix. To ensure that the fluid stresses are quantified accurately, a combined DNS and PIV approach has been undertaken for flow cell characterisation across the full range of operating Re. This is important for practical concentric cylinder geometries where the shear components are non-zero and spatially dependent, with the peak stresses located near the endwalls. Furthermore, recirculation regions appear well below the crtical Reynolds number for Taylor vortex formation.

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