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**Eric J Rawdon\*** (ejrawdon@stthomas.edu), Dept of Mathematics, University of St. Thomas,  
Saint Paul, MN 55105. *Knotted Arcs*. Preliminary report.

Some proteins have been classified recently as being knotted. However, proteins have free ends and knotting, traditionally, has only been defined formally for closed curves. How should we define the existence of knotting within open chains? Once we settle on a definition, we can search for smallest knotted arcs within knotted open and closed chains. We discuss generating polymer models and show recent results for classifying the knotting within models and within proteins. This is joint work with Ken Millett, Andrzej Stasiak, and Joanna Sulowska. (Received July 27, 2011)