polymer chemistries to reduce unwanted biological effects. In addition, monodisperse polymer preparations are beginning to emerge in the form of dendrimers [1] and polyamides [2] and the field should soon witness an increase in the molecular weights of these preparations such that they become useful in drug delivery. Methods for the facile preparation of such polymers would assist in the rational characterization of the biological effects of polymers and enable more rapid design and development of polymers toward desired therapeutic goals.

Although the biological effects of apparently innocent polymers are unknown and monodisperse polymer preparations are unavailable, Hunter and Moghimi [3] are correct to call for more work in these areas and suggest that the field of polymer therapeutics will otherwise take a long time to reach its full potential.

References

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Pharmaceutical companies need to broaden research

Attending the 14th International Genome Sequencing and Analysis Conference in Boston (2–5 October 2002) made me wonder whether pharmaceutical companies are taking advantage of the latest developments in mammalian, model-organism and microbial genomics. I will limit myself to three examples from the meeting.

Kelly Frazer of Perlegen Sciences (http://www.perlegen.com/) commented that numerous novel human transcripts are not conserved in the mouse, and cited examples of novel transcripts with intriguing origins (e.g. a breast cancer cell line) and even more intriguing structures (e.g. endogenous cis-antisense to a known protein-coding gene).

Victor Ambros of the Dartmouth Medical School (http://www.dartmouth.edu/dms/) spoke about the importance of noncoding micro-RNAs in *Caenorhabditis elegans* gene expression regulation, and noted that several developmentally regulated micro-RNA candidates are not conserved in the related worm *C. briggsae*.

David Relman of Stanford University (http://www.stanford.edu/) reported that over 1500 species of bacteria (and, surprisingly, even archaea) found in human subgingival crevices are novel and that disrupted microbial ecologies are likely to be relevant not only to gingivitis, but also to more serious conditions such as inflammatory bowel disease. These findings underscore the need for a human 'environmental genome' (microbiome survey) project.

Given these developments, why do many in the industry limit their database mining efforts to the identification of evolutionarily conserved proteins? Why is the lack of research on non-conserved, and non-protein, targets seldom lamented? Perhaps most importantly, why is work on the pathogenesis of common human diseases largely synonymous with analyzing human SNPs, or with identifying 'druggable' protein targets of human origin, when it is becoming increasingly clear that all genetic material and all proteins found on and in the human body – regardless of whether their origin is human or microbial – might be relevant to the pathogenesis of these common conditions? After all, treatments for common, mixed-etiology disorders are precisely what post-genomic medicine has promised, and so far failed, to deliver.

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Corrigendum

Please note a correction to the article *Mining the human 'kinome'* by David A. Dunn, published in *Drug Discovery Today*, 15th November 2002, Volume 7, No. 22, 1121–1123.

On page 1122, in the second column, the article references the company Kinexis: this should have read Kinexus, and the correct web address for this company is http://www.kinexus.ca.

We would like to apologize for this inaccuracy and for any confusion that this might have caused.

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