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► **COVER:** 'Slime trails' by Lara Crow, inspired by the Review on p9 on integrins. These molecules are important in all migration and adhesion and they enable cells to follow distinct trails.



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With the rush to translate new findings into more effective cancer drugs, alterations in basic biological mechanisms can sometimes be overlooked.

Inflammation is known to induce and maintain tumour development in several tissues, however, alterations to the immune system in cancer patients are likely to extend beyond the tissue in which the tumour is developing. Magdalena Chechlinska and colleagues on page 2 argue that failure to consider this can lead to bias in biomarker discovery.

Extensive changes to the genome also occur during tumorigenesis, and identifying which of the many genetic and epigenetic changes are important can be time consuming. In 2004 we published a census of the human cancer genes, in which six genes were shown to drive tumour development as a result of gene amplification and overexpression. Now, using an evidence-based model, Colin Cooper and colleagues on page 59 have identified a further 71 genes that are amplified and overexpressed in human tumours and are probably responsible for at least some of the underlying tumour biology.

Janet Rowley and colleagues have been investigating genetic changes in leukaemia for many years and over that time the complexity of this disease has become apparent. On page 23, Rowley and colleagues are now considering the epigenetic as well as genetic changes that occur in leukaemia, including changes in microRNAs that are important in the development of this disease.

As we embark on a new year and a new decade, the tools that we have for dissecting the biological complexity of tumour development are immense, but basic biological knowledge will need to be applied to ensure that we make the best of the data now at hand.

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