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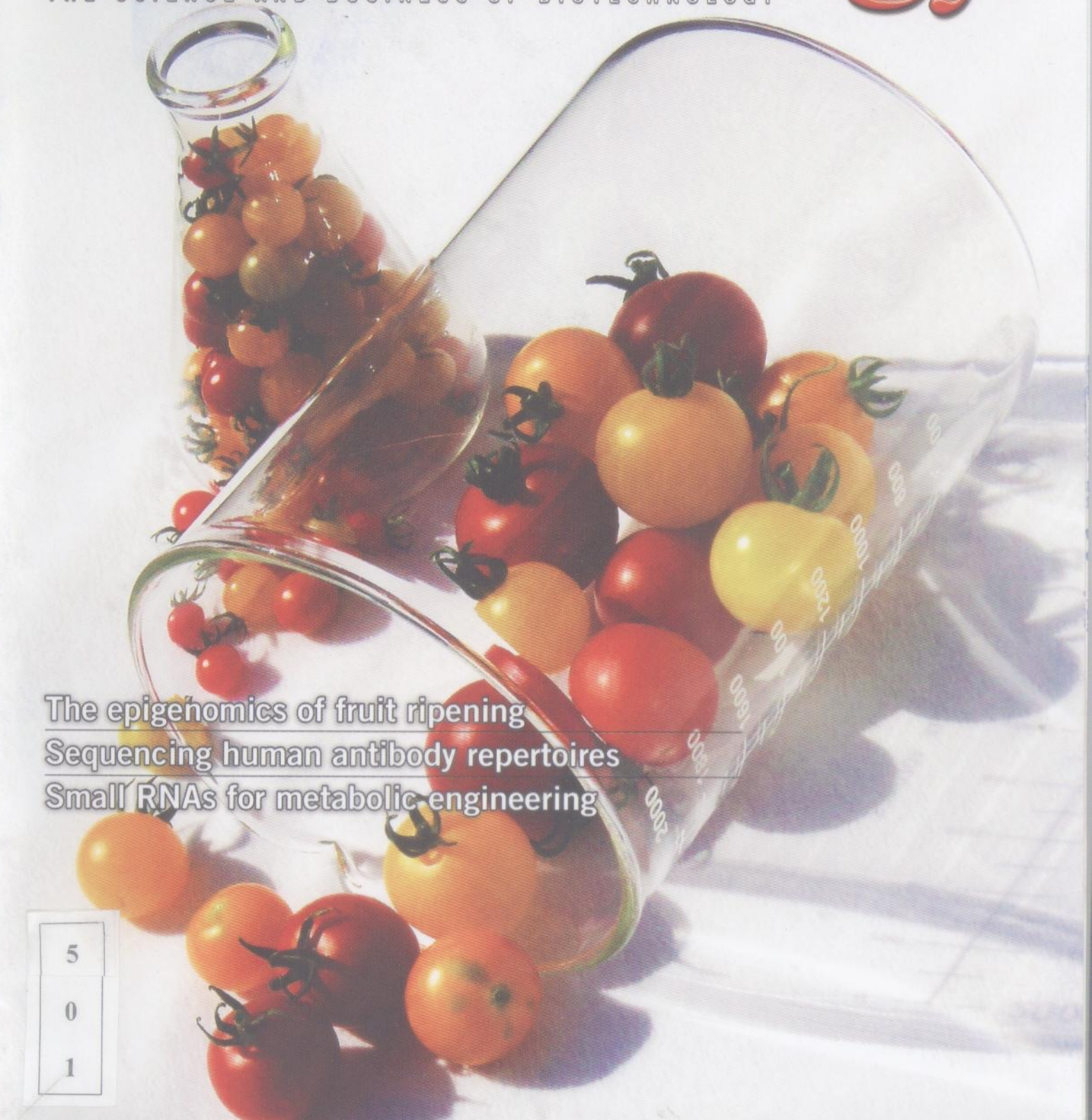

The epigenomics of fruit ripening

Sequencing human antibody repertoires

Small RNAs for metabolic engineering

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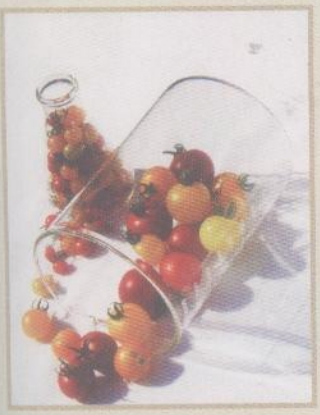

Cherry and currant tomatoes of varying ripeness. Zhong *et al.* use whole-genome cytosine methylation and transcription factor binding analyses to show that epigenome dynamics influence the developmental transition to ripening (p 154). Credit: Ryan McQuinn

Amgen buys gene hunter deCODE, p 87

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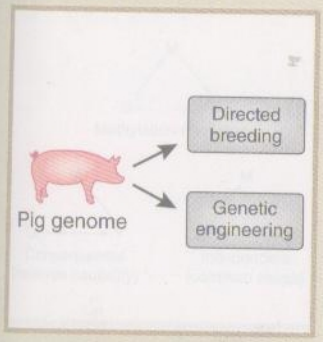
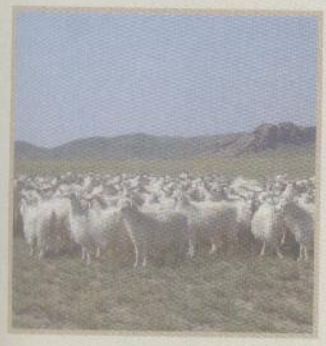


Swine reference genome, p 122



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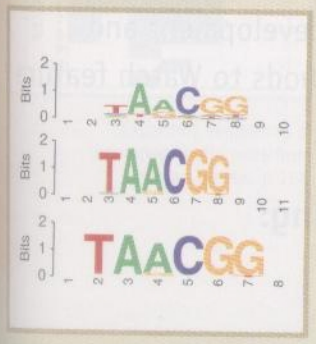

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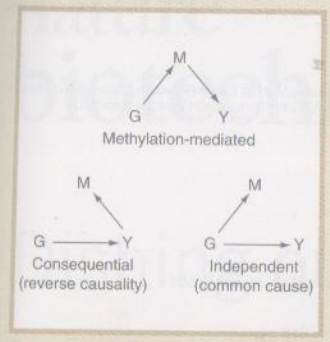

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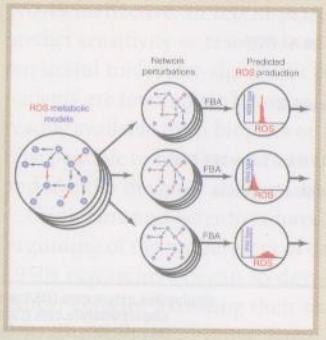

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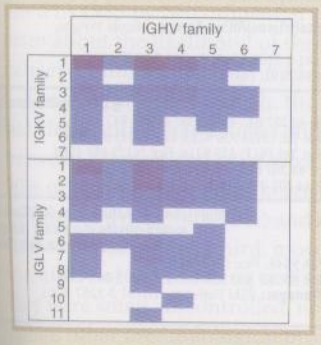

Extracting sequences of immunoglobulin pairs from human B cells, p 166

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