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Bugs in the genome

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There is much speculation about how [lateral transfer](#) - the exchange of genes between distantly related species - has shaped the evolution of the human genome. A recent publication estimated that as many as [223 bacterial genes](#) can be found within the human genome sequence. In the May 17 [ScienceExpress](#), Salzberg *et al.* report a careful re-evaluation of the number of putative bacterial-to-vertebrate transfers (BVTs; *ScienceXpress* 2001, 10.1126/science.1061036). The authors performed careful similarity searches to compare the proteomes from human, fruitfly, nematode worm, yeast, mustard weed, eukaryotic parasites and [all completed prokaryotic genomes](#). They included both the [Ensembl](#) and [Celera](#) proteome sets (containing 31,780 and 26,544 proteins, respectively). Although their initial analysis revealed similar numbers to earlier estimates, careful statistical examination of the results whittled the final number of BVTs down to 41 (Ensembl) and 46 (Celera). Salzberg et al. show that the calculations are highly dependent on the number of non-vertebrate genomes screened (the number of BVTs decreases as the number of genomes rises). They conclude that gene loss and evolutionary rate variation are more likely to explain the sequence similarities than are true BVT events.

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