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## Pneumococcus genome

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*Streptococcus pneumoniae* (pneumococcus) was the bacterial strain used in the historic studies of Avery, MacLeod and McCarty more than half a century ago to demonstrate that DNA is the material of inheritance. The Gram-positive bacterium causes over 3 million infant deaths each year from pneumonia, bacteremia and meningitis. In the July 20 [Science](#), Tettelin and colleagues from [The Institute for Genome Research](#) (TIGR) report the [complete genome](#) sequence of *S. pneumoniae* (*Science* 2001, **293**:498-506). The genome is a single circular chromosome, 2.1 megabases long with a GC content of 39.7%. They identified 2,236 putative genes, many of which (64%) could be assigned a biological function. About half of the predicted proteins were most similar to proteins from other low-GC Gram-positive species, while 20% of the genes did not match genes in the databases. The *S. pneumoniae* genome is rich in insertion sequences (about 5% of the genome). The genome encodes many ATP-dependent transporters and sugar transporters (30% of transporters), which may reflect its adaptation to sugar-rich environments such as the oral cavity. Iron and phosphate transporters may also contribute to virulence. Pathogenicity may be influenced by extracellular enzyme systems that control the metabolism of polysaccharides and hexosamines, and by a 13-gene cluster involved in capsular biosynthesis. Sixty-nine proteins are predicted to be expressed on the bacterial surface and the authors identified a putative signal peptide motif. Tettelin *et al.* predict that further [comparative analysis](#) will highlight genes regulating virulence and pathogenicity and indicate candidate vaccine targets.

## References

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