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Genome-scale design is complicated by scale; if you consider the removal of protein-coding genes for minimal genome designs using brute force and no assumptions, the number of possible genome-scale designs with M. genitalium's 525 genes is 2 525. This is infeasible in vivo; laboratories can only follow a small number of research avenues . High-quality computational models can investigate many more research avenues and model contextual essentiality, assuming that cellular interactions are ...

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