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Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence

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2171	Quantitative NTerminal Footprinting of Pathogenic Mycobacteria Reveals Differential Protein Acetylation.		
2170	2Mercapto-Quinazolinones as Inhibitors of Type II NADH Dehydrogenase and Mycobacterium tuberculosis: StructureActivity Relationships, Mechanism of Action and Absorption, Distribution, Metabolism, and Excretion Characterization.		
2169	.		
2168	Transposon mutagenesis in mycobacteria using conditionally replicating mycobacteriophages. 2001 , 54, 43-57		4
2167	Comparative genomics of Listeria species. 2001 , 294, 849-52		1189
2166	A self-compartmentalizing protease in Rhodococcus: the 20S proteasome. 1998 , 74, 83-7		7
2165	sigmaR, an RNA polymerase sigma factor that modulates expression of the thioredoxin system in response to oxidative stress in Streptomyces coelicolor A3(2). 1998 , 17, 5776-82		169
2164	ATP-dependent aggregation of single-stranded DNA by a bacterial SMC homodimer. 1998 , 17, 7139-48		101
2163	Blueprint for the white plague. <i>Nature</i> , 1998 , 393, 515-6	50.4	36
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2161	The genome sequence of Rickettsia prowazekii and the origin of mitochondria. <i>Nature</i> , 1998 , 396, 133-40	50.4	1381
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