

TABLE 1 Coverage of completely-sequenced genomes by conserved families of orthologs

Species ^a	Number of genes	
	Total	In COGs (% of total)
Bacteria		
<i>Aquifex aeolicus</i>	1526	1265 (83%)
<i>Thermotoga maritima</i>	1852	1437 (78%)
<i>Rickettsia prowazekii</i>	834	632 (76%)
<i>Mycoplasma genitalium</i>	480	366 (76%)
<i>Haemophilus influenzae</i>	1694	1246 (74%)
<i>Chlamydia trachomatis</i>	895	612 (68%)
<i>Treponema pallidum</i>	1033	677 (66%)
<i>Escherichia coli</i>	4292	2752 (64%)
<i>Bacillus subtilis</i>	4100	2600 (63%)
<i>Helicobacter pylori</i>	1577	996 (63%)
<i>Mycoplasma pneumoniae</i>	678	408 (60%)
<i>Chlamydia pneumoniae</i>	1053	629 (60%)
<i>Synechocystis</i> sp.	3168	1883 (59%)
<i>Borrelia burgdorferi</i>	1256	656 (52%)
Archaea		
<i>Archaeoglobus fulgidus</i>	2411	1703 (71%)
<i>Methanobacterium</i>	1871	1319 (70%)
<i>Methanococcus jannaschii</i>	1747	1227 (70%)
<i>Pyrococcus horikoshii</i>	2072	1276 (62%)
Eukaryotes		
<i>Saccharomyces cerevisiae</i>	5932	2052 (35%)

^aWithin bacteria and archaea, the species are ordered by the percentage of genes included in clusters of orthologous groups of proteins (COGs).