

Species	subgroup	Accumulation Rate (x10 ⁻⁷)	Included/ excluded/ recalculated	Reason for exclusion/recalculation	Reference
<i>Acinetobacter baumannii</i>	GC1	15.00	Included		[1]
<i>Acinetobacter baumannii</i>	GC2	24.70	Included		[2]
<i>Bordetella pertussis</i>		2.24	Included		[3]
<i>Buchnera aphidicola</i>		1.10	Included		[4]
<i>Buchnera aphidicola</i>		0.09	Excluded	Very long divergence (50 million years)	[5]
<i>Burkholderia dolosa</i>		3.28	Included		[6]
<i>Campylobacter jejuni</i>		323.00	Included		[7]
<i>Chlamydia psittaci</i>		174.00	Included		[8]
<i>Clostridium difficile</i>		3.20	Included		[9]
<i>Clostridium difficile</i>	27	1.70	Included		[10]
<i>Clostridium difficile</i>	027/BI/NAP1	1.88	Included		[11]
<i>Enterococcus faecium</i>	ST17/ST252	15.00	Included		[12]
<i>Escherichia coli</i>		1.44	Recalculated	Unsure about the rationale related to timepoints used in the calculation. We recalculated by running SNP alignment through BEAST	[13]
<i>Helicobacter pylori</i>		410.00	Excluded	SNPs might be recombinant	[14]
<i>Helicobacter pylori</i>		29.35	Excluded	Upper limit on estimate of the divergence time is arbitrary	[15]
<i>Helicobacter pylori</i>		138.00	Excluded	Synonymous rate	[16]
<i>Helicobacter pylori</i>		54.5	Recalculated	Cannot be sure that 3yr isolates are a direct descendant of Oyr isolates	[17]
<i>Klebsiella pneumoniae</i>	CC258 Clade1	2.56	Included		[18]
<i>Klebsiella pneumoniae</i>	CC258 Clade2	2.99	Included		[18]
<i>Legionella pneumophila</i>		1.39	Included		[19]
<i>Mycobacterium abscessus</i>	subsp abscessus	3.63	Included		[20]
<i>Mycobacterium abscessus</i>	subsp massiliense	0.95	Included		[20]

<i>Mycobacterium bovis</i>		0.34	Included		[21]
<i>Mycobacterium leprae</i>		0.09	Included		[22]
<i>Mycobacterium tuberculosis</i>		0.49	Included		[23]
<i>Mycobacterium tuberculosis</i>		1.80	Included		[24]
<i>Mycobacterium tuberculosis</i>		1.14	Included		[25]
<i>Mycobacterium tuberculosis</i>		1.93	Included		[18]
<i>Mycobacterium tuberculosis</i>		1.00	Included		[26]
<i>Mycobacterium ulcerans</i>		0.63	Included		[27]
<i>Mycoplasma gallisepticum</i>		102.00	Included		[28]
<i>Neisseria gonorrhoeae</i>		2.50	Included		[29]
<i>Neisseria meningitidis</i>		0.61	Included		[18]
<i>Pseudomonas aeruginosa</i>	DK2	3.95	Included		[30]
<i>Pseudomonas aeruginosa</i>	DK1	2.11	Included		[31]
<i>Pseudomonas aeruginosa</i>	DK2	4.30	Excluded	Synonymous rate	[32]
<i>Pseudomonas aeruginosa</i>		154.50	Excluded	Hypermutator strains	[33]
<i>Renibacterium salmoninarum</i>		3.80	Included		[34]
<i>Salmonella enterica</i>	Kentucky	5.35	Included		[18]
<i>Salmonella enterica</i>	Typhi H58	1.78	Included		[18]
<i>Salmonella enterica</i>	paratyphi A	1.94	Included		[35]
<i>Salmonella enterica</i>	Agona	0.93	Included		[36]
<i>Salmonella enterica</i>	Typhimurium Lineage II	1.90	Included		[37]
<i>Salmonella enterica</i>	Typhimurium Lineage I	3.90	Included		[37]
<i>Salmonella enterica</i>	Typhimurium	3.35	Included		[38]
<i>Salmonella enterica</i>	Typhimurium	3.40	Included		[39]
<i>Salmonella enterica</i>	Enteritidis	100.00	Excluded	Hypermutator strain	[40]

<i>Shigella dysenteriae</i>	Sd1	8.70	Included	[41]
<i>Shigella sonnei</i>		6.00	Included	[42]
<i>Staphylococcus aureus</i>	ST93	4.50	Included	[43]
<i>Staphylococcus aureus</i>	ST239	16.00	Included	[44]
<i>Staphylococcus aureus</i>	CC398	16.80	Included	[45]
<i>Staphylococcus aureus</i>	ST22	13.00	Included	[46]
<i>Staphylococcus aureus</i>	USA300	12.20	Included	[47]
<i>Staphylococcus aureus</i>	USA300	12.50	Included	[48]
<i>Staphylococcus aureus</i>	ST239	32.50	Included	[49]
<i>Staphylococcus aureus</i>	ST239	33.00	Included	[50]
<i>Staphylococcus aureus</i>	ST239	37.90	Included	[51]
<i>Staphylococcus aureus</i>	ST225	20.00	Included	[52]
<i>Staphylococcus aureus</i>	MSSA	27.20	Included	[53]
<i>Streptococcus agalactiae</i>	CC1	6.40	Included	[54]
<i>Streptococcus agalactiae</i>	CC17	5.60	Included	[54]
<i>Streptococcus agalactiae</i>	CC19	9.30	Included	[54]
<i>Streptococcus agalactiae</i>	CC23	7.50	Included	[54]
<i>Streptococcus equi</i>		5.22	Included	[55]
<i>Streptococcus pneumoniae</i>	PMEN1	15.70	Included	[56]
<i>Streptococcus pyogenes</i>	Emm M1	8.06	Included	[57]
<i>Streptococcus pyogenes</i>	emm12	11.00	Included	[58]
<i>Treponema pallidum</i>		6.60	Included	[59]
<i>Vibrio cholerae</i>		9.60	Included	[18]
<i>Vibrio cholerae</i>		8.30	Included	[60]
<i>Vibrio cholerae</i>		2.35	Excluded	Synonymous rate [61]
<i>Yersinia pestis</i>		0.07	Included	[62]
<i>Yersinia pestis</i>		0.20	Included	[63]
<i>Yersinia pestis</i>		0.16	Included	[18]
<i>Yersinia pestis</i>		0.23	Included	[18]
<i>Yersinia pseudotuberculosis</i>	ST19	3.87	Included	[64]

<i>Yersinia pseudotuberculosis</i>	ST43	5.63	Included	[64]
<i>Yersinia pseudotuberculosis</i>	ST9	20.10	Included	[64]
<i>Yersinia pseudotuberculosis</i>	ST42	3.57	Included	[64]
<i>Yersinia pseudotuberculosis</i>	ST14	8.67	Included	[64]

Supplementary Table 1. 81 estimates of the rate at which bacteria accumulate mutations per site per year (the accumulation rate) for 34 species of bacteria.