

FIRMICUTES

GRAM +

***Staphylococcus aureus***

GCF\_000013425.1 • NCTC 8325

Genome size (Mb)	<b>2.82</b>
Total CDS	<b>2767</b>
Pseudogenes	<b>30</b>
tRNA	<b>59</b>
GC content (%)	<b>32.87</b>
IS elements / Mb	<b>0.71</b>
Release date	<b>2006-02-18</b>

Gram-positive coccus commonly used as a laboratory strain for studying staphylococcal biology.

FIRMICUTES

GRAM +

***Streptococcus pneumoniae***

GCF\_001457635.1 • NCTC7465

Genome size (Mb)	<b>2.11</b>
Total CDS	<b>1930</b>
Pseudogenes	<b>187</b>
tRNA	<b>58</b>
GC content (%)	<b>39.73</b>
IS elements / Mb	<b>37.90</b>
Release date	<b>2015-03-22</b>

Encapsulated bacterium associated with pneumonia and meningitis.

FIRMICUTES

GRAM +

***Enterococcus faecium***

GCF\_009734005.1 • SRR24

Genome size (Mb)	<b>2.92</b>
Total CDS	<b>2722</b>
Pseudogenes	<b>86</b>
tRNA	<b>70</b>
GC content (%)	<b>37.88</b>
IS elements / Mb	<b>48.64</b>
Release date	<b>2020-02-05</b>

Gut commensal that can cause hospital-acquired infections and is known for antibiotic resistance.

CAMPYLOBACTEROTA

GRAM -

***Campylobacter armoricus***

GCF\_013372105.1 • CCUG 73571

Genome size (Mb)	<b>1.64</b>
Total CDS	<b>1595</b>
Pseudogenes	<b>26</b>
tRNA	<b>46</b>
GC content (%)	<b>28.58</b>
IS elements / Mb	<b>0</b>
Release date	<b>2020-06-24</b>

Campylobacter species associated with animal hosts and foodborne transmission.

PROTEOBACTERIA

GRAM -

***Pseudomonas aeruginosa***

GCF\_000006765.1 • PAO1

Genome size (Mb)	<b>6.26</b>
Total CDS	<b>5572</b>
Pseudogenes	<b>19</b>
tRNA	<b>63</b>
GC content (%)	<b>66.56</b>
IS elements / Mb	<b>1.12</b>
Release date	<b>2006-07-24</b>

Opportunistic pathogen and model strain for studying biofilms and antibiotic resistance.

PROTEOBACTERIA

GRAM -

***Enterobacter asburiae***

GCF\_007035805.1 • 17Nkkm-UP2

Genome size (Mb)	<b>4.77</b>
Total CDS	<b>4400</b>
Pseudogenes	<b>59</b>
tRNA	<b>83</b>
GC content (%)	<b>55.79</b>
IS elements / Mb	<b>4.82</b>
Release date	<b>2019-05-14</b>

Member of the Enterobacter cloacae complex; can be an opportunistic pathogen.

PROTEOBACTERIA

GRAM -

***Acinetobacter baumannii***

GCF\_009035845.1 • ATCC 19606

Genome size (Mb)	<b>4.00</b>
Total CDS	<b>3683</b>
Pseudogenes	<b>54</b>
tRNA	<b>74</b>
GC content (%)	<b>39.15</b>
IS elements / Mb	<b>2.25</b>
Release date	<b>2019-10-16</b>

Opportunistic pathogen notable for survival on surfaces and multidrug resistance.

PROTEOBACTERIA

GRAM -

***Neisseria gonorrhoeae***

GCF\_013030075.1 • TUM19854

Genome size (Mb)	<b>2.17</b>
Total CDS	<b>1969</b>
Pseudogenes	<b>238</b>
tRNA	<b>55</b>
GC content (%)	<b>52.60</b>
IS elements / Mb	<b>37.76</b>
Release date	<b>2020-05-01</b>

Causative agent of gonorrhea; a human-specific pathogen.

PROTEOBACTERIA

GRAM -

***Escherichia coli***

GCF\_000008865.2 • O157:H7 Sakai

Genome size (Mb)	<b>5.59</b>
Total CDS	<b>5155</b>
Pseudogenes	<b>136</b>
tRNA	<b>103</b>
GC content (%)	<b>50.48</b>
IS elements / Mb	<b>28.42</b>
Release date	<b>2018-06-08</b>

Shiga toxin-producing E. coli associated with severe foodborne illness.

PROTEOBACTERIA

GRAM -

***Klebsiella pneumoniae***

GCF\_000240185.1 • HS11286

Genome size (Mb)	<b>5.68</b>
Total CDS	<b>5779</b>
Pseudogenes	<b>0</b>
tRNA	<b>62</b>
GC content (%)	<b>57.12</b>
IS elements / Mb	<b>10.38</b>
Release date	<b>2011-12-27</b>

Opportunistic pathogen associated with pneumonia and bloodstream infections.

PROTEOBACTERIA

GRAM -

***Escherichia coli***

GCF\_022354085.1 • SWHEFF\_49

Genome size (Mb)	<b>5.19</b>
Total CDS	<b>4748</b>
Pseudogenes	<b>140</b>
tRNA	<b>88</b>
GC content (%)	<b>50.62</b>
IS elements / Mb	<b>17.72</b>
Release date	<b>2022-02-22</b>

Pathogen that causes bacillary dysentery; highly infectious.

PROTEOBACTERIA

GRAM -

***Haemophilus influenzae***

GCF\_020736045.1 • FDAARGOS\_1560

Genome size (Mb)	<b>1.89</b>
Total CDS	<b>1756</b>
Pseudogenes	<b>50</b>
tRNA	<b>59</b>
GC content (%)	<b>38.23</b>
IS elements / Mb	<b>3.70</b>
Release date	<b>2021-11-03</b>

Human respiratory tract bacterium that can cause invasive disease in some strains.

PROTEOBACTERIA

GRAM -

***Salmonella enterica***

GCF\_000006945.2 • LT2

Genome size (Mb)	<b>4.95</b>
Total CDS	<b>4554</b>
Pseudogenes	<b>39</b>
tRNA	<b>85</b>
GC content (%)	<b>52.24</b>
IS elements / Mb	<b>5.25</b>
Release date	<b>2016-01-13</b>

Model strain for studying Salmonella pathogenesis and metabolism.

FIRMICUTES

GRAM +

***Bacillus subtilis***

GCF\_000009045.1 • 168

Genome size (Mb)	<b>4.22</b>
Total CDS	<b>4237</b>
Pseudogenes	<b>88</b>
tRNA	<b>86</b>
GC content (%)	<b>43.51</b>
IS elements / Mb	<b>6.64</b>
Release date	<b>2009-08-12</b>

Gram-positive soil bacterium widely used as a model organism for studying sporulation and gene regulation.

FIRMICUTES

GRAM +

***Clostridioides difficile***

GCF\_000009205.2 • 630

Genome size (Mb)	<b>4.30</b>
Total CDS	<b>3806</b>
Pseudogenes	<b>51</b>
tRNA	<b>88</b>
GC content (%)	<b>29.06</b>
IS elements / Mb	<b>6.28</b>
Release date	<b>2017-09-29</b>

Anaerobic spore-forming bacterium that causes antibiotic-associated diarrhea and colitis.

PROTEOBACTERIA

GRAM -

***Escherichia coli***

GCF\_000005845.2 • K-12 substr. MG1655

Genome size (Mb)	<b>4.64</b>
Total CDS	<b>4290</b>
Pseudogenes	<b>145</b>
tRNA	<b>86</b>
GC content (%)	<b>50.79</b>
IS elements / Mb	<b>24.34</b>
Release date	<b>2013-11-03</b>

Non-pathogenic laboratory strain that is one of the most extensively studied organisms in biology.

PROTEOBACTERIA

GRAM -

***Vibrio cholerae***

GCF\_000006745.1 • N16961

Genome size (Mb)	<b>4.03</b>
Total CDS	<b>3485</b>
Pseudogenes	<b>99</b>
tRNA	<b>98</b>
GC content (%)	<b>47.49</b>
IS elements / Mb	<b>6.94</b>
Release date	<b>2001-09-18</b>

Causative agent of cholera known for producing cholera toxin and causing severe watery diarrhea.

PROTEOBACTERIA

GRAM -

***Helicobacter pylori***

GCF\_000008525.1 • 26695

Genome size (Mb)	<b>1.67</b>
Total CDS	<b>1450</b>
Pseudogenes	<b>108</b>
tRNA	<b>36</b>
GC content (%)	<b>38.87</b>
IS elements / Mb	<b>6.00</b>
Release date	<b>2001-09-18</b>

Spiral-shaped bacterium that colonizes the human stomach and is linked to ulcers and gastric cancer.

BACTEROIDETES

GRAM -

***Bacteroides fragilis***

GCF\_000025985.1 • NCTC 9343

Genome size (Mb)	5.24
Total CDS	4160
Pseudogenes	70
tRNA	73
GC content (%)	43.11
IS elements / Mb	3.82
Release date	2005-03-03

Common gut commensal that plays a role in digestion but can cause infections if displaced from the

ACTINOBACTERIA

ACID-FAST

***Mycobacterium tuberculosis***

GCF\_000195955.2 • H37Rv

Genome size (Mb)	4.41
Total CDS	3906
Pseudogenes	30
tRNA	45
GC content (%)	65.61
IS elements / Mb	80.47
Release date	2013-02-01

Slow-growing pathogen responsible for tuberculosis and a key reference strain in TB research.

ACTINOBACTERIA

GRAM +

***Rhodopseudomonas palustris CGA009***

GCF\_000195775.1 • CGA009

Genome size (Mb)	5.47
Total CDS	4913
Pseudogenes	51
tRNA	49
GC content (%)	65.03
IS elements / Mb	2.74
Release date	2003-12-11

Versatile photosynthetic bacterium used to study carbon and nitrogen fixation.

ACTINOBACTERIA

GRAM +

***Streptomyces violaceolatus***

GCF\_000203835.1 • A3(2)

Genome size (Mb)	9.05
Total CDS	7996
Pseudogenes	192
tRNA	66
GC content (%)	72
IS elements / Mb	11.93
Release date	2003-05-06

Soil-dwelling bacterium famous for producing antibiotics and for its complex developmental life cycle.

CHLAMYDIOTA

GRAM -

***Chlamydia trachomatis***

GCF\_000008725.1 • D/UW-3/CX

Genome size (Mb)	1.04
Total CDS	887
Pseudogenes	3
tRNA	37
GC content (%)	41.31
IS elements / Mb	0
Release date	2001-09-13

Obligate intracellular pathogen and leading cause of bacterial sexually transmitted infections worldwide.

MYCOPLASMATOTA

NO CELL WALL

***Mycoplasma genitalium***

GCF\_000027325.1 • G-37

Genome size (Mb)	0.58
Total CDS	504
Pseudogenes	20
tRNA	36
GC content (%)	31.69
IS elements / Mb	0
Release date	2006-01-09

Extremely small bacterium with a minimal genome used to study the limits of cellular life.

PSEUDOMONADOTA

GRAM -

***Yersinia pestis***

GCF\_000009065.1 • CO92

Genome size (Mb)	4.83
Total CDS	4094
Pseudogenes	217
tRNA	69
GC content (%)	47.64
IS elements / Mb	51.76
Release date	2001-10-15

Plague-causing bacterium responsible for historic pandemics.

FIRMICUTES

GRAM +

***Listeria monocytogenes***

GCF\_000196035.1 • EGD-e

Genome size (Mb)	2.94
Total CDS	2867
Pseudogenes	6
tRNA	67
GC content (%)	37.98
IS elements / Mb	2.72
Release date	2003-05-06

Foodborne pathogen that grows at low temperatures and infects humans.

PROTEOBACTERIA

GRAM -

***Legionella pneumophila***

GCF\_000008485.1 • Philadelphia 1

Genome size (Mb)	3.40
Total CDS	2976
Pseudogenes	23
tRNA	44
GC content (%)	38.27
IS elements / Mb	10.30
Release date	2004-09-29

Waterborne pathogen that causes Legionnaires' disease.

CAMPYLOBACTEROTA

GRAM -

***Campylobacter jejuni***

GCF\_000009085.1 • NCTC 11168

Genome size (Mb)	<b>1.64</b>
Total CDS	<b>1572</b>
Pseudogenes	<b>40</b>
tRNA	<b>43</b>
GC content (%)	<b>30.55</b>
IS elements / Mb	<b>14.01</b>
Release date	<b>2001-09-27</b>

Leading cause of bacterial gastroenteritis worldwide.

PROTEOBACTERIA

GRAM -

***Shigella flexneri***

GCF\_000007405.1 • 2457T

Genome size (Mb)	<b>4.60</b>
Total CDS	<b>3834</b>
Pseudogenes	<b>674</b>
tRNA	<b>100</b>
GC content (%)	<b>50.91</b>
IS elements / Mb	<b>111.32</b>
Release date	<b>2003-04-23</b>

Highly infectious pathogen causing bacillary dysentery.

FIRMICUTES

GRAM +

***Clostridium botulinum***

GCF\_000022765.1 • Kyoto

Genome size (Mb)	<b>4.16</b>
Total CDS	<b>3783</b>
Pseudogenes	<b>78</b>
tRNA	<b>81</b>
GC content (%)	<b>28.21</b>
IS elements / Mb	<b>2.89</b>
Release date	<b>2009-04-15</b>

Bacterium that produces botulinum toxin

PROTEOBACTERIA

GRAM -

***Haemophilus influenzae***

GCF\_000027305.1 • Rd KW20

Genome size (Mb)	<b>1.83</b>
Total CDS	<b>1604</b>
Pseudogenes	<b>117</b>
tRNA	<b>57</b>
GC content (%)	<b>38.15</b>
IS elements / Mb	<b>7.10</b>
Release date	<b>1999-12-22</b>

Model strain of a human respiratory tract bacterium.

PROTEOBACTERIA

GRAM -

***Rickettsia rickettsii***

GCF\_000018225.1 • Sheila Smith

Genome size (Mb)	<b>1.26</b>
Total CDS	<b>1290</b>
Pseudogenes	<b>102</b>
tRNA	<b>34</b>
GC content (%)	<b>32.47</b>
IS elements / Mb	<b>9.54</b>
Release date	<b>2007-10-02</b>

Tick-borne intracellular pathogen causing Rocky Mountain spotted fever.

PROTEOBACTERIA

GRAM -

***Coxiella burnetii* RSA 493**

GCF\_000007765.1 • RSA 493

Genome size (Mb)	<b>2.03</b>
Total CDS	<b>1853</b>
Pseudogenes	<b>0</b>
tRNA	<b>42</b>
GC content (%)	<b>42.60</b>
IS elements / Mb	<b>14.76</b>
Release date	<b>2005-07-22</b>

Highly infectious intracellular pathogen that causes Q fever.

FIRMICUTES

GRAM +

***Staphylococcus aureus***

GCF\_000013465.1 • FPR3757

Genome size (Mb)	<b>2.92</b>
Total CDS	<b>2774</b>
Pseudogenes	<b>82</b>
tRNA	<b>52</b>
GC content (%)	<b>32.69</b>
IS elements / Mb	<b>12.00</b>
Release date	<b>2006-02-11</b>

Community-associated MRSA strain linked to severe skin infections.