

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

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

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

Versatile photosynthetic bacterium used to study carbon and nitrogen fixation.

ACTINOBACTERIA

GRAM +

***Streptomyces violaceolatus***

GCF\_000203835.1 • A3(2)

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

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

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

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