



# Draft Genome Sequences of 64 Type Strains of 50 Species and 25 Subspecies of the Genus *Staphylococcus* Rosenbach 1884

Kevin Cole,<sup>a,b,c</sup> Dona Foster,<sup>d</sup> Julie E. Russell,<sup>f</sup> Tanya Golubchik,<sup>d,e</sup> Martin Llewelyn,<sup>b,c</sup> Daniel J. Wilson,<sup>d,g</sup> Derrick Crook,<sup>a,d</sup> John Paul,<sup>a,b</sup> Modernising Medical Microbiology Consortium

<sup>a</sup>National Infection Service, Public Health England, London, United Kingdom

<sup>b</sup>Brighton and Sussex University Hospitals NHS Trust, Brighton, United Kingdom

<sup>c</sup>Division of Medicine, Brighton and Sussex Medical School, Falmer, United Kingdom

<sup>d</sup>Nuffield Department of Medicine, University of Oxford, Oxford, United Kingdom

<sup>e</sup>Department of Statistics, University of Oxford, Oxford, United Kingdom

<sup>f</sup>National Collection of Type Cultures, Public Health England, London, United Kingdom

<sup>g</sup>Wellcome Trust Centre for Human Genetics, University of Oxford, Oxford, United Kingdom

**ABSTRACT** Members of the genus *Staphylococcus* have been isolated from humans, animals, and the environment. Accurate identification with whole-genome sequencing requires access to data derived from type strains. We provide sequence data for type strains of 64 taxa in the genus that at the time of this writing have standing in the nomenclature.

The term “*Staphylococcus*” was introduced by Sir Alexander Ogston in reference to the bunch-of-grapes-like appearance that distinguishes these organisms from streptococci (1). Friedrich Rosenbach subsequently described “*Staphylococcus pyogenes aureus*” and “*Staphylococcus pyogenes albus*” (2). At the time of this writing, the genus includes 51 species plus additional subspecies. They are nonmotile, facultatively or obligatory anaerobic, Gram-positive cocci (3–5). Most are catalase positive (4–6). Members of the genus include human and animal pathogens and commensals, and they have been isolated from foodstuffs and environmental sources (7, 8). *S. aureus* is a well-known human pathogen, and the genome sequence of the type strain was published by Kim et al. in 2014 (9) and Shiroma et al. in 2015 (10). Other staphylococci are increasingly becoming recognized as clinically important (7, 11) and are being investigated accordingly (12, 13).

Here we give information for genome sequences of 64 type strains (Table 1) representing 50 species in the genus *Staphylococcus* that have standing in the nomenclature at the time of writing plus a number of subspecies. This catalogue of sequences can be employed as a resource for taxonomic study and to identify test isolates.

Organisms were obtained from the National Collection of Type Cultures, United Kingdom (NCTC), Deutsche Sammlung von Mikroorganismen und Zellkulturen, Germany (DSMZ), and Culture Collection, University of Göteborg, Sweden (CCUG).

Isolates were cultured on a Columbia agar and horse blood (CBA) plate (Oxoid Ltd., Basingstoke, UK) and incubated aerobically or anaerobically at 35°C overnight. Bacterial biomass was scraped from cultured plates for DNA extraction. DNA was extracted and purified with a QuickGene DNA tissue kit (AutoGen, Holliston, MA, USA). Extracted DNA was prepared for sequencing following NexteraXT (Illumina, San Diego, CA, USA) protocols and sequenced as 150-bp paired-end reads on the Illumina MiSeq platform. Reads were stripped of adaptors with BBDuk 34.38 (14). Illumina reads were quality controlled by calling bases only when 5 or more were present at a position and supported by at least 1 high-quality read in forward and reverse directions. Reads were

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Address correspondence to Kevin Cole, [kevin.cole@phe.gov.uk](mailto:kevin.cole@phe.gov.uk).

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**TABLE 1** Accessions and genomic characteristics of 64 type strains of the genus *Staphylococcus* Rosenbach 1884

Species	Strain	No. of total reads	No. of contigs	Contig N <sub>50</sub> value (bp)	G+C content (%)	Depth (x)	Length (bp)	No. of genes
<i>Staphylococcus agnetis</i>	DSM 23656	1,978,702	164	38,640	34.6	66.4	2,491,359	2,514
<i>Staphylococcus argensis</i>	DSM 29875	1,430,626	19	98,914	40.8	24.75	2,452,468	2,350
<i>Staphylococcus argenteus</i>	DSM 28299	1,686,623	48	96,207	35.1	31.51	2,759,629	2,741
<i>Staphylococcus arlettae</i>	NCTC 12413	1,992,335	33	66,907	36.2	26.57	2,665,344	2,600
<i>Staphylococcus aureus</i> subsp. <i>anaerobius</i>	DSM 20714	1,949,112	400	14,564	33.2	56.12	2,575,746	2,738
<i>Staphylococcus aureus</i> subsp. <i>aureus</i>	NCTC 08532	2,207,024	41	66,458	34.9	32.75	2,749,019	2,887
<i>Staphylococcus auricularis</i>	NCTC 12101	1,517,960	103	39,462	37.6	38.94	2,201,622	2,416
<i>Staphylococcus capitis</i> subsp. <i>capitis</i>	NCTC 11045	2,331,749	51	101,914	36	38.76	2,434,909	2,419
<i>Staphylococcus capitis</i> subsp. <i>urealyticus</i>	DSM 6717	1,467,277	184	42,481	35.7	35.79	2,468,245	2,500
<i>Staphylococcus caprae</i>	NCTC 12196	2,647,473	101	62,212	33.6	62.25	2,606,761	2,551
<i>Staphylococcus carnosus</i> subsp. <i>carnosus</i>	DSM 20501	1,442,326	70	247,399	37.7	90.42	2,434,039	2,447
<i>Staphylococcus carnosus</i> subsp. <i>utilis</i>	DSM 11676	1,834,824	444	11,755	33.4	36.49	2,622,255	2,702
<i>Macrococcus caseolyticus</i>	DSM 20597	1,614,157	122	46,917	35.5	70.8	2,171,833	2,341
<i>Staphylococcus chromogenes</i>	NCTC 10530	1,169,641	117	55,359	38.5	35.94	2,276,768	2,265
<i>Staphylococcus cohnii</i> subsp. <i>cohnii</i>	NCTC 11041	1,727,741	69	107,943	34.9	26.83	2,637,875	2,588
<i>Staphylococcus cohnii</i> subsp. <i>urealyticus</i>	DSM 6718	1,780,154	189	26,500	33.8	49.2	2,670,427	2,647
<i>Staphylococcus condimenti</i>	DSM 11674	1,493,311	211	32,221	35.8	23.6	2,615,688	2,604
<i>Staphylococcus delphini</i>	NCTC 12225	1,499,070	227	42,122	37.1	52.47	2,751,077	2,716
<i>Staphylococcus devriesei</i>	CCUG 58238	2,004,126	129	49,574	35.6	44.18	2,379,883	2,392
<i>Staphylococcus epidermidis</i>	NCTC 11047	1,852,043	62	55,347	35.8	38.72	2,442,385	2,438
<i>Staphylococcus equorum</i> subsp. <i>equorum</i>	NCTC 12414	1,523,028	93	44,027	33.2	87.8	2,350,071	2,590
<i>Staphylococcus equorum</i> subsp. <i>linens</i>	DSM 15097	1,911,830	101	55,558	34	45.91	2,768,268	2,739
<i>Staphylococcus felis</i>	DSM 7377	1,572,866	244	24,395	36.1	45	2,409,047	2,389
<i>Staphylococcus fleuretii</i>	DSM 13212	1,811,506	156	38,940	31.7	90.36	2,473,007	2,489
<i>Staphylococcus haemolyticus</i>	NCTC 11042	1,975,151	92	55,720	36	35.24	2,472,399	2,466
<i>Staphylococcus hominis</i> subsp. <i>hominis</i>	NCTC 11320	2,793,372	30	144,174	39.1	47.59	2,204,528	2,214
<i>Staphylococcus hominis</i> subsp. <i>novobiosepticus</i>	CCUG 42399	2,349,019	166	35,627	33.4	54.32	2,422,390	2,498
<i>Staphylococcus hyicus</i>	CCUG 6509	2,111,770	134	37,537	37.7	91.88	2,633,558	2,222
<i>Staphylococcus intermedius</i>	NCTC 11048	2,212,778	176	51,566	37.8	41.45	2,801,199	2,797
<i>Staphylococcus kloosii</i>	NCTC 12415	2,000,256	134	36,209	33	74.73	2,607,914	2,642
<i>Staphylococcus lentus</i>	NCTC 12102	3,158,427	79	86,117	32.7	93.32	2,546,437	2,579
<i>Staphylococcus lugdunensis</i>	NCTC 12217	2,272,326	20	94,638	39.8	35.15	2,519,514	2,409
<i>Staphylococcus lutrae</i>	DSM 10244	1,461,603	200	41,148	37.8	42.6	2,429,515	2,354
<i>Staphylococcus massiliensis</i>	CCUG 55927	2,070,218	212	32,379	35	41.69	2,348,540	2,305
<i>Staphylococcus microti</i>	DSM 22147	1,582,916	191	38,659	39.1	53.13	2,409,945	2,429
<i>Staphylococcus muscae</i>	DSM 7068	1,986,642	183	32,200	37.4	63.32	2,049,263	2,075
<i>Staphylococcus nepalensis</i>	DSM 15150	2,186,623	412	13,339	32.9	50.09	2,860,226	2,790
<i>Staphylococcus pasteurii</i>	DSM 10656	1,952,357	233	25,197	31.4	89.61	2,605,275	2,277
<i>Staphylococcus petrasii</i> subsp. <i>croceilyticus</i>	CCUG 62728	1,665,214	147	36,044	34.6	55.76	2,380,571	2,346
<i>Staphylococcus petrasii</i> subsp. <i>jettensis</i>	CCUG 62657	1,923,933	266	23,568	34.7	45.4	2,709,801	2,730
<i>Staphylococcus petrasii</i> subsp. <i>petrasii</i>	CCUG 62727	2,674,384	139	46,072	34.1	58.57	2,486,611	2,508
<i>Staphylococcus petrasii</i> subsp. <i>pragensis</i>	DSM 102853	2,071,432	493	11,863	33	87.81	3,094,570	3,040
<i>Staphylococcus pettenkoferi</i>	CCUG 51270	1,933,064	122	62,580	37.2	46.82	2,455,272	2,399
<i>Staphylococcus piscifermentans</i>	DSM 7373	1,828,752	147	37,718	37	91.44	2,711,458	2,470
<i>Staphylococcus pseudintermedius</i>	CCUG 49543	1,307,526	245	32,222	37.3	33.7	2,507,403	2,482
<i>Staphylococcus pulvereri</i>	DSM 9930	1,085,309	252	21,767	32.8	91.9	2,507,841	2,321
<i>Staphylococcus rostri</i>	DSM 21968	1,857,275	167	39,749	37.6	72.78	2,341,022	2,342
<i>Staphylococcus saccharolyticus</i>	NCTC 11807	1,735,439	93	46,092	34.5	91.58	2,462,952	2,724
<i>Staphylococcus saprophyticus</i> subsp. <i>bovis</i>	CCUG 38042	1,774,718	289	16,602	32.9	48.26	2,709,959	2,757
<i>Staphylococcus saprophyticus</i> subsp. <i>saprophyticus</i>	NCTC 7292	2,626,126	123	46,677	33.3	90.52	2,589,171	2,567
<i>Staphylococcus schleiferi</i> subsp. <i>coagulans</i>	DSM 6628	1,893,687	155	54,157	36.2	41.27	2,443,567	2,378
<i>Staphylococcus schleiferi</i> subsp. <i>scheiferi</i>	NCTC 12218	3,174,090	98	67,466	37.6	90.54	2,896,454	2,368
<i>Staphylococcus schweitzeri</i>	DSM 28300	1,956,713	52	65,148	35.5	37.08	2,743,713	2,725
<i>Staphylococcus sciuri</i> subsp. <i>carnaticus</i>	CCUG 39509	1,454,961	182	40,393	33.6	51.84	2,877,673	2,983
<i>Staphylococcus sciuri</i> subsp. <i>rodentium</i>	CCUG 37923	925,469	82	62,754	36.6	91.96	2,449,200	2,919
<i>Staphylococcus sciuri</i> subsp. <i>sciuri</i>	NCTC 12103	2,205,792	37	123,278	38.7	32.97	2,768,322	2,760
<i>Staphylococcus simiae</i>	CCUG 51256	2,569,797	159	45,657	34.3	77.79	2,598,081	2,523
<i>Staphylococcus simulans</i>	NCTC 11046	1,359,349	99	84,647	37.2	48.33	2,735,408	2,699
<i>Staphylococcus stepanovicii</i>	DSM 26319	1,676,662	140	42,374	35.1	36.62	2,406,018	2,468
<i>Staphylococcus succinus</i> subsp. <i>casei</i>	DSM 15096	1,816,917	169	29,746	34.8	56.18	2,871,374	2,802
<i>Staphylococcus succinus</i> subsp. <i>succinus</i>	DSM 14617	1,805,866	339	18,694	32.2	29.39	2,786,115	2,764
<i>Staphylococcus vitulinus</i>	DSM 15615	1,414,448	259	23,873	32.5	57.23	2,595,808	2,674
<i>Staphylococcus warneri</i>	NCTC 11044	1,997,389	31	115,611	38	35.2	2,401,190	2,353
<i>Staphylococcus xylosus</i>	NCTC 11043	1,802,579	226	25,849	34.4	51.79	2,725,582	2,615

assembled using Velvet 1.2.10 (15) with kmer size and coverage estimated with VelvetOptimiser 2.1.7 (15). To ensure assembly quality, at least 97% of the total assembly was required to be in contigs larger than 1 kb. Draft genome sequences were annotated with Prokka 1.12 (16).

Genome sizes varied between 2.1 million and 3.1 million base pairs across the genus,

with G+C contents ranging from 31.4% to 40.8%. The genome sequences contained a range of 2,075 to 3,040 annotated genes.

**Data availability.** All sequences discussed here have been deposited in GenBank as BioProject number [PRJNA339206](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA339206). Table 1 lists individual accession numbers by taxon. These Sequence Read Archive deposits can be found under the study number [SRP093495](https://www.ncbi.nlm.nih.gov/sra/SRP093495).

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