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# Complete genome assemblies and antibiograms of 22 *Staphylococcus capitis* isolates

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## Abstract

**Objective** *Staphylococcus capitis* is part of the human microbiome and an opportunistic pathogen known to cause catheter-associated bacteraemia, prosthetic joint infections, skin and wound infections, among others. Detection of *S. capitis* in normally sterile body sites saw an increase over the last decade in England, where a multidrug-resistant clone, NRCS-A, was widely identified in blood samples from infants in neonatal intensive care units. To address a lack of complete genomes and antibiograms of *S. capitis* in public databases, we performed long- and short-read whole-genome sequencing, hybrid genome assembly, and antimicrobial susceptibility testing of 22 diverse isolates.

**Data description** We present complete genome assemblies of two *S. capitis* type strains (subspecies *capitis*: DSM 20326; subspecies *urealyticus*: DSM 6717) and 20 clinical isolates (NRCS-A: 10) from England. Each genome is accompanied by minimum inhibitory concentrations of 13 antimicrobials including vancomycin, teicoplanin, daptomycin, linezolid, and clindamycin. These 22 genomes were 2.4–2.7 Mbp in length and had a GC content of 33%. Plasmids were identified in 20 isolates. Resistance to teicoplanin, daptomycin, gentamicin, fusidic acid, rifampicin, ciprofloxacin, clindamycin, and erythromycin was seen in 1–10 isolates. Our data are a resource for future studies on genomics, evolution, and antimicrobial resistance of *S. capitis*.

**Keywords** *Staphylococcus capitis*, Reference genomes, Hybrid genome assembly, Antimicrobial susceptibility, Antimicrobial resistance, Antibiograms, Bioresource, Genomics, NRCS-A clone, Nanopore MinION sequencing

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## Objective

*Staphylococcus capitis*, consisting of two subspecies *capitis* and *urealyticus* [1, 2], is a coagulase-negative opportunistic pathogen commonly causing late-onset sepsis (LOS) in very-low-birthweight infants in neonatal intensive care units (NICUs) and various infections in adults, such as prosthetic joint infections [3, 4]. A multidrug-resistant clone of *S. capitis* subsp. *urealyticus*, NRCS-A, has emerged as a global concern in neonatal health for its dominance in LOS, reduced susceptibility to vancomycin, enhanced biofilm-forming ability, increased disinfectant and desiccation tolerance, association with neonatal incubators, and persistence in NICUs [5–7]. Between 2020 and 2021, the UK Health Security Agency (UKHSA) convened a nationwide investigation into increased reporting of neonatal *S. capitis* bacteraemia in England [8] and requested voluntary referral of clinical isolates from diagnostic laboratories for whole-genome sequencing (WGS). Genomic epidemiological analysis of the WGS data revealed widespread presence of the NRCS-A clone in neonatal units across the country, highlighting the need to further understand genomics, antimicrobial resistance (AMR), and niche adaptation of this clone in comparison with other *S. capitis* subpopulations [9].

In this report, we describe complete genome assemblies and accompanying antibiograms of 22 *S. capitis* isolates consisting of 20 English clinical isolates and type strains of the two subspecies (*capitis*: DSM 20326; *urealyticus*: DSM 6717). The clinical isolates were selected from UKHSA's culture collection to represent the main *S. capitis* subpopulations previously identified (Figure S1) [9], with 19 of these isolates recovered from normally sterile sites in patients across England. Readers are referred to Table S1 for source information of isolates. Altogether, 10 NRCS-A isolates and 12 non-NRCS-A isolates were sequenced. Our work addresses the lack of finished-grade *S. capitis* reference genomes and antibiograms in the National Center for Biotechnology Information (NCBI) databases, providing a bioresource for future studies on the genomics, AMR, molecular epidemiology, and evolution of *S. capitis*.

## Data description

Each isolate was incubated on Columbia agar with horse blood (PB0122A, Thermo Scientific, UK) at 37 °C overnight for DNA extraction and antimicrobial susceptibility testing in 2021 (Batch 1, 19 isolates) or 2023 (Batch 2, three isolates) (Table S2). For Batch 1, genomic DNA of each isolate was extracted using GeneJET Genomic DNA Purification Kits (Thermo Scientific) and aliquoted. Long-read WGS was conducted with Oxford Nanopore Technologies (ONT, UK) MinION R9.4.1 flow-cells (FLO-MIN106D) and Rapid Barcoding Kits (SQK-RBK004). High-accuracy basecalling was performed with guppy (ONT). Short-read sequencing was performed on Illumina HiSeq 2500 systems at UKHSA following an in-house 2 × 101 bp protocol. For Batch 2, genomic DNA was extracted using a Wizard Genomic DNA Purification Kit (Promega, USA) and aliquoted. Long-read WGS was conducted with an ONT MinION R10.4.1 flow-cell (FLO-MIN114) and Rapid Barcoding Kit V14 (SQK-RBK114.24). Super-accuracy basecalling was performed using guppy. Short-read sequencing was performed under a 2 × 251 bp layout on Illumina NovaSeq 6000 systems at MicrobesNG (UK). Susceptibility of isolates to 13 antimicrobials was determined by the UKHSA Antimicrobial Resistance and Healthcare Associated Infections Reference Unit with gradient strips (Liofilchem, Italy, for Batch 1) or broth microdilution (EUSTAPF, Thermo Scientific, for Batch 2) following European Committee on Antimicrobial Susceptibility Testing (EUCAST) breakpoints v13.1. Inducible clindamycin resistance was sought by testing for the antagonism between erythromycin and clindamycin (D-test).

ONT reads were trimmed and filtered with fastp and nanoq [10, 11], respectively, for quality control. Illumina reads were trimmed and filtered with fastp. Hybrid assembly was performed for each genome using an ONT-reads-first strategy with Flye, Raven, and miniasm-minipolish, as implemented in Trycycler [12–15], when quality-processed ONT reads had an estimated depth of ≥ 60 folds and the assemblers produced consistent results; otherwise, Raven was used. When a genome could not be fully assembled from ONT reads, an Illumina-reads-first strategy was applied using Unicycler [16, 17]. All assemblies were polished with ONT reads using medaka (https://github.com/nanoporetech/medaka) followed by Illumina-read polishing using Polypolish and POLCA [18, 19]. Polished assemblies were then reoriented to start from *dnaA* (chromosomes) or *repA* (plasmids) genes using dnaapler [20]. Reoriented assemblies were polished with Illumina reads using Polypolish, assessed using Quast and CheckM2 [21, 22], and annotated with the NCBI Prokaryotic Genome Annotation Pipeline [23].

Twenty-two complete genome assemblies were generated, with the same GC content of 33% and lengths of 2.4–2.7 Mbp (Table S2). One to four plasmids (2.3–69 kbp) were identified in 20 isolates (NRCS-A: 9; non-NRCS-A: 11). The NRCS-A clone exhibited reduced susceptibility to teicoplanin, daptomycin, and gentamicin (Table S3). Resistance to fusidic acid (MICs: 16–32 mg/L), erythromycin (MIC > 256 mg/L), and clindamycin (MIC > 256 mg/L or inducible) was seen in 9/22 (41%), 7/22 (32%), and 5/22 (23%) of isolates, respectively, with no significant frequency difference between NRCS-A and non-NRCS-A isolates ($p$-value = 1, Fisher's

**Table 1** Overview of datafiles/datasets

| Label | Name of data file/data set | File types (file extension) | Data repository and identifier (DOI or accession number) |
|---|---|---|---|
| Datafile 1 | Figure S1, Genetic relatedness between the 22 selected isolates within the context of 838 *S. capitis* isolates previously analysed | Portable Document Format file (.pdf) | Figshare, https://doi.org/10.6084/m9.figshare.26048464 [25] |
| Datafile 2 | Table S1, sources and data accessions of the 22 *S. capitis* isolates | MS Excel file (.xlsx) | Figshare, https://doi.org/10.6084/m9.figshare.26049013 [26] |
| Datafile 3 | Table S2, methods and summary statistics of 22 hybrid genome assemblies | MS Excel file (.xlsx) | Figshare, https://doi.org/10.6084/m9.figshare.26049070 [27] |
| Datafile 4 | Table S3, antibiograms of the 22 *S. capitis* isolates | MS Excel file (.xlsx) | Figshare, https://doi.org/10.6084/m9.figshare.26049094 [28] |
| Dataset 1 | Illumina and ONT whole-genome sequencing reads of the 22 *S. capitis* isolates | FASTQ (.fastq) | Sequence Read Archive, http://identifiers.org/insdc.sra: SRP483965 [29] |
| Dataset 2 | Genome assembly of isolate DSM20326 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040739495 [30] |
| Dataset 3 | Genome assembly of isolate DSM6717 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040739365 [31] |
| Dataset 4 | Genome assembly of isolate Sc1191092 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040739255 [32] |
| Dataset 5 | Genome assembly of isolate Sc1191106 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040739205 [33] |
| Dataset 6 | Genome assembly of isolate Sc1365665 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040739095 [34] |
| Dataset 7 | Genome assembly of isolate Sc1365666 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040738865 [35] |
| Dataset 8 | Genome assembly of isolate Sc1365669 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040738415 [36] |
| Dataset 9 | Genome assembly of isolate Sc1365670 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040737765 [37] |
| Dataset 10 | Genome assembly of isolate Sc1365673 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040737135 [38] |
| Dataset 11 | Genome assembly of isolate Sc1365674 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040737085 [39] |
| Dataset 12 | Genome assembly of isolate Sc1365682 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040736935 [40] |
| Dataset 13 | Genome assembly of isolate Sc1365688 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040736845 [41] |
| Dataset 14 | Genome assembly of isolate Sc1365695 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040736815 [42] |
| Dataset 15 | Genome assembly of isolate Sc1365701 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040736805 [43] |
| Dataset 16 | Genome assembly of isolate Sc1365706 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040736795 [44] |
| Dataset 17 | Genome assembly of isolate Sc1365750 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040736725 [45] |
| Dataset 18 | Genome assembly of isolate Sc1365753 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040736715 [46] |
| Dataset 19 | Genome assembly of isolate Sc1365754 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040736665 [47] |
| Dataset 20 | Genome assembly of isolate Sc1516939 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040736635 [48] |
| Dataset 21 | Genome assembly of isolate Sc1516941 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040736585 [49] |
| Dataset 22 | Genome assembly of isolate Sc1516943 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040736555 [50] |
| Dataset 23 | Genome assembly of isolate Sc1516945 | FASTA (.fna) | Genome Assembly, http://identifiers.org/insdc.gca: GCA_040736045 [51] |

exact test). One NRCS-A isolate exhibited rifampicin resistance (MIC > 32 mg/L). All isolates were susceptible to vancomycin, linezolid, and quinupristin-dalfopristin, and seven non-NRCS-A isolates, including the two type strains, were susceptible to all 11 antimicrobials having EUCAST breakpoints.

## Limitations

This dataset is limited to a small sample size ($n = 22$), which does not capture all major phenotypic and genetic variations in *S. capitis*. The isolates are limited to England and dominated by invasive isolates ($n = 19$) recovered from normally sterile body sites of humans — eight (42%) invasive isolates were collected from infants of ≤ 90 days of age, one (5%) from an infant between > 90 days and < 1 year of age, two (10%) from children between six and 11 years of age, and eight from adults (≥ 18 years of age). Moreover, antimicrobial susceptibility of all isolates in Batch 1 ($n = 19$) was not determined using the gold-standard method, broth microdilution, owing to technical unavailability. Future work needs to elucidate mechanisms of AMR [24] and include a wider range of isolates, such as those recovered from carriage screening, environments, animals, and other health-related samples from non-clinical settings.

**Abbreviations**

| | |
|---|---|
| AMR | Antimicrobial resistance |
| DHSC | Department of Health and Social Care |
| DSM | Deutsche Sammlung von Mikroorganismen |
| EUCAST | European Committee on Antimicrobial Susceptibility Testing |
| LOS | Late-onset sepsis |
| NCBI | National Center for Biotechnology Information |
| NICU | Neonatal intensive care unit |
| NIHR | National Institute for Health and Care Research |
| ONT | Oxford Nanopore Technologies |
| WGS | Whole-genome sequencing |
| UKHSA | UK Health Security Agency |

## Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12863-025-01303-8.

Supplementary Material 1

Supplementary Material 2

Supplementary Material 3

Supplementary Material 4

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**Author contributions**

Conceptualisation: Y. Wan, B. Pichon; resources: B. Pichon, K. L. Hopkins, J. Coelho, E. Jauneikaite, K. Moganeradj; investigation: Y. Wan, R. Pike, A. Harley, Z. Mumin, I. Potterill, D. Meunier, M. Ganner, M. Getino, K. L. Hopkins; supervision: B. Pichon, K. L. Hopkins, J. Coelho, A. Demirjian, C. S. Brown, A. H. Holmes, E. Jauneikaite, K. Moganeradj; funding acquisition: C. S. Brown, Y. Wan, A. H. Holmes, E. Jauneikaite. Writing, first draft: Y. Wan; editing: Y. Wan, D. Meunier, R. Pike, E. Jauneikaite, A. Demirjian, C. S. Brown, B. Pichon, K. L. Hopkins, K. Moganeradj, M. Ganner; approval of the final manuscript: All.

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**Data availability**

Data generated in this study are listed in Table 1. UK clinical isolates are available at the UKHSA ***Staphylococcus*** and ***Streptococcus*** Reference Service. Type strains DSM 20326 and DSM 6717 are available in the DSMZ-German Collection of Microorganisms and Cell Cultures GmbH, Leibniz Institute (https://www.dsmz.de).

## Declarations

**Ethics approval and consent to participate**

Not applicable.

**Consent for publication**

Not applicable.

**Competing interests**

The authors declare no competing interests.

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**References**

1. Kloos WE, Schleifer KH. Isolation and characterization of Staphylococci from human skin II. Descriptions of four new species: *Staphylococcus warneri*, *Staphylococcus capitis*, *Staphylococcus hominis*, and *Staphylococcus simulans* 1. Int J Syst Evol Microbiol. 1975;25:62–79.
2. Bannerman TL, Kloos WE. *Staphylococcus capitis* subsp. *ureolyticus* subsp. nov. from human skin. Int J Syst Evol Microbiol. 1991;41:144–7.
3. Butin M, Martins-Simões P, Rasigade J-P, Picaud J-C, Laurent F. Worldwide endemicity of a multidrug-resistant *Staphylococcus capitis* clone involved in neonatal sepsis. Emerg Infect Dis. 2017;23:538–9.
4. Tevell S, Baig S, Hellmark B, Martins Simoes P, Wirth T, Butin M, et al. Presence of the neonatal *Staphylococcus capitis* outbreak clone (NRCS-A) in prosthetic joint infections. Sci Rep. 2020;10:22389.
5. Rasigade J-P, Raulin O, Picaud J-C, Tellini C, Bes M, Grando J, et al. Methicillin-resistant *Staphylococcus capitis* with reduced vancomycin susceptibility causes late-onset sepsis in intensive care neonates. PLoS ONE. 2012;7:e31548.
6. Chavignon M, Coignet L, Bonhomme M, Bergot M, Tristan A, Verhoeven P, et al. Environmental persistence of *Staphylococcus capitis* NRCS-A in neonatal intensive care units: role of biofilm formation, desiccation, and disinfectant tolerance. Microbiol Spectr. 2022;10:e04215–22.
7. Moore G, Barry A, Carter J, Ready J, Wan Y, Elsayed M, et al. Detection, survival, and persistence of *Staphylococcus capitis* NRCS-A in neonatal units in England. J Hosp Infect. 2023;140:8–14.
8. Paranthaman K, Wilson A, Verlander N, Rooney G, Macdonald N, Nsonwu O, et al. Trends in coagulase-negative staphylococci (CoNS), England, 2010–2021. Access Microbiol. 2023;5:000491v3.
9. Wan Y, Ganner M, Mumin Z, Ready D, Moore G, Potterill I, et al. Whole-genome sequencing reveals widespread presence of *Staphylococcus capitis* NRCS-A clone in neonatal units across the United Kingdom. J Infect. 2023;87:210–9.
10. Chen S, Zhou Y, Chen Y, Gu J. Fastp: an ultra-fast all-in-one FASTQ preprocessor. Bioinformatics. 2018;34:i884–90.
11. Steinig E, Coin L. Nanoq: ultra-fast quality control for nanopore reads. J Open Source Softw. 2022;7:2991.
12. Kolmogorov M, Yuan J, Lin Y, Pevzner PA. Assembly of long, error-prone reads using repeat graphs. Nat Biotechnol. 2019;37:540–6.
13. Vaser R, Šikić M. Time- and memory-efficient genome assembly with Raven. Nat Comput Sci. 2021;1:332–6.
14. Wick RR, Holt KE. Benchmarking of long-read assemblers for prokaryote whole genome sequencing. F1000Research; 2021.
15. Wick RR, Judd LM, Cerdeira LT, Hawkey J, Méric G, Vezina B, et al. Trycycler: consensus long-read assemblies for bacterial genomes. Genome Biol. 2021;22:266.
16. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, et al. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol. 2012;19:455–77.
17. Wick RR, Judd LM, Gorrie CL, Holt KE. Unicycler: resolving bacterial genome assemblies from short and long sequencing reads. PLoS Comput Biol. 2017;13:e1005595.
18. Wick RR, Holt KE, Polypolish. Short-read polishing of long-read bacterial genome assemblies. PLoS Comput Biol. 2022;18:e1009802.
19. Zimin AV, Salzberg SL. The genome polishing tool POLCA makes fast and accurate corrections in genome assemblies. PLoS Comput Biol. 2020;16:e1007981.
20. Bouras G, Grigson SR, Papudeshi B, Mallawaarachchi V, Roach MJ. Dnaapler: a tool to reorient circular microbial genomes. J Open Source Softw. 2024;9:5968.
21. Gurevich A, Saveliev V, Vyahhi N, Tesler G. QUAST: quality assessment tool for genome assemblies. Bioinformatics. 2013;29:1072–5.
22. Chklovski A, Parks DH, Woodcroft BJ, Tyson GW. CheckM2: a rapid, scalable and accurate tool for assessing microbial genome quality using machine learning. Nat Methods. 2023;20:1203–12.
23. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, et al. NCBI prokaryotic genome annotation pipeline. Nucleic Acids Res. 2016;44:6614–24.

24. Chindelevitch L, van Dongen M, Graz H, Pedrotta A, Suresh A, Uplekar S, et al. Ten simple rules for the sharing of bacterial genotype—phenotype data on antimicrobial resistance. PLoS Comput Biol. 2023;19:e1011129.
25. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D, et al. Figure S1, genetic relatedness between the 22 selected isolates within the context of 838 *S. capitis* isolates previously analysed. Figshare. 2024. https://doi.org/10.6084/m9.figshare.26048464
26. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D, et al. Table S1, sources and data accessions of the 22 *S. capitis* isolates. Figshare. 2024. https://doi.org/10.6084/m9.figshare.26049013
27. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D, et al. Table S2, methods and summary statistics of 22 hybrid genome assemblies. Figshare. 2024. https://doi.org/10.6084/m9.figshare.26049070
28. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D, et al. Table S3, antibiograms of the 22 *S. capitis* isolates. Figshare. 2024. https://doi.org/10.6084/m9.figshare.26049094
29. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Whole-genome sequencing reads of the 22 *S. capitis* isolates. Seq Read Archive. 2024. http://identifiers.org/insdc.sra:SRP483965
30. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate DSM20326. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040739495
31. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate DSM6717. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040739365
32. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1191092. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040739255
33. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1191106. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040739205
34. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1365665. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040739095
35. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1365666. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040738865
36. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1365669. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040738415
37. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1365670. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040737765
38. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1365673. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040737135
39. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1365674. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040737085
40. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1365682. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040736935
41. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1365688. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040736845
42. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1365695. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040736815
43. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1365701. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040736805
44. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1365706. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040736795
45. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1365750. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040736725
46. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1365753. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040736715
47. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1365754. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040736665
48. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1516939. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040736635
49. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1516941. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040736585
50. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1516943. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040736555
51. Wan Y, Pike R, Harley A, Mumin Z, Potterill I, Meunier D et al. Genome assembly of *Staphylococcus capitis* isolate Sc1516945. Genome Assembly. 2024. http://identifiers.org/insdc.gca:GCA_040736045


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