

## Supplementary Information

# Emergence and Genomic Characterization of a *spa* Type t4407 ST6-SCC<sub>mec</sub> Type IVa Methicillin-Resistant *Staphylococcus aureus* Strain Isolated from Al-Karak Hospital, Jordan

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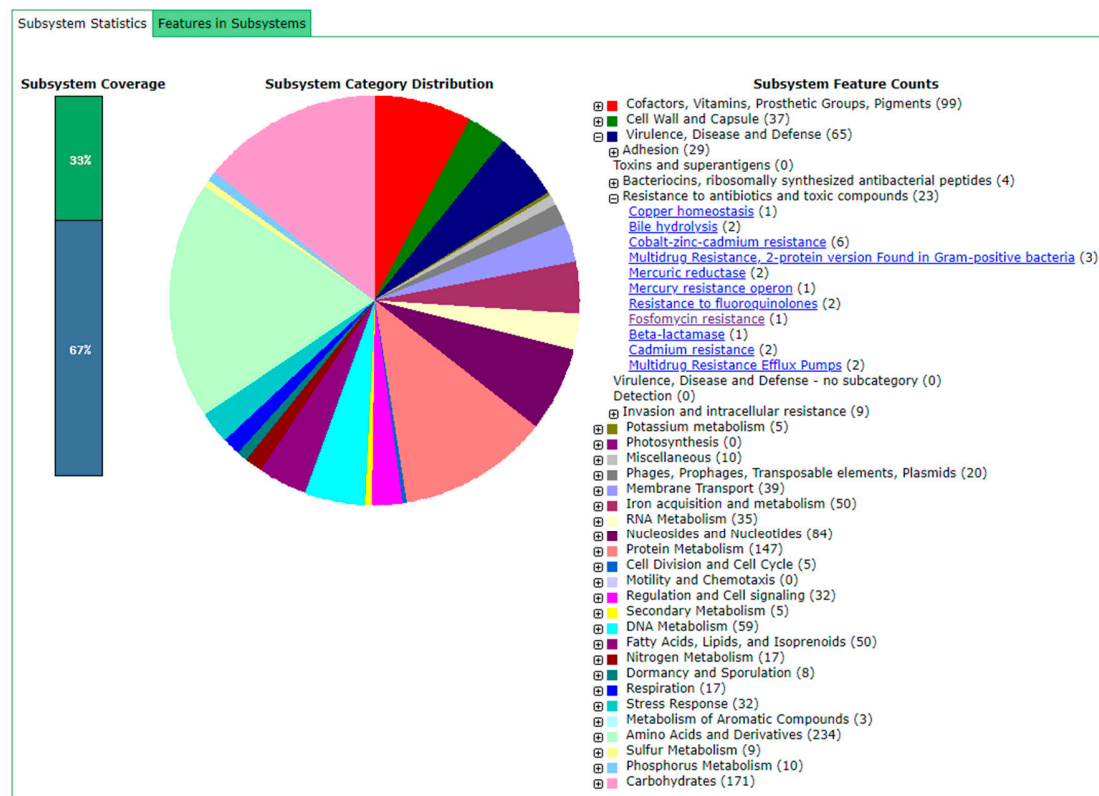
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## Subsystem Information



**Figure S1.** Annotation summary for MRSA strain Karak2019-A29 using RAST subsystem

Table S1 Virulence factors detected in A29 genome in the current study based on Virulence factor tool VirulenceFinder-2.0 Server (last accessed 14/1/2024)

Host immunological genes for <i>S. aureus</i> .						
Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
sak	100	492 / 492	CP104989.1 Staphylococcus aureus strain Karak2019-A29 chromosome	2614676..2615167	staphylokinase	BA000017.4
scn	100	351 / 351	CP104989.1 Staphylococcus aureus strain Karak2019-A29 chromosome	2616664..2617014	staphylococcal complement inhibitor	LC032460.1
Exoenzyme genes for <i>S. aureus</i>						
Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
aur	99.87	1530 / 1530	CP104989.1 Staphylococcus aureus strain Karak2019-A29 chromosome	145284..146813	aureolysin	AP014653.1
splA	99.86	708 / 708	CP104989.1 Staphylococcus aureus strain Karak2019-A29 chromosome	1122500..1123207	serine protease splA	AP014942.1
splB	99.72	723 / 723	CP104989.1 Staphylococcus aureus strain Karak2019-A29 chromosome	1123332..1124054	serine protease splB	AP014942.1
splE	100	717 / 717	CP104989.1 Staphylococcus aureus strain Karak2019-A29 chromosome	1125829..1126545	serine protease splE	AP009351.1
Toxin genes for <i>S. aureus</i>						
Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
hlgA	100	930 / 930	CP104989.1 Staphylococcus aureus strain Karak2019-A29 chromosome	1345141..1346070	gamma-hemolysin chain II precursor	AP014942.1
hlgB	99.8	977 / 977	CP104989.1 Staphylococcus aureus strain Karak2019-A29 chromosome	1342648..1343624	gamma-hemolysin component B precursor	BA000033.2
hlgC	99.89	948 / 948	CP104989.1 Staphylococcus aureus strain Karak2019-A29 chromosome	1343626..1344573	gamma-hemolysin component C	AP014653.1
lukD	99.69	983 / 984	CP104989.1 Staphylococcus aureus strain Karak2019-A29 chromosome	1110128..1111110	leukocidin D component	AP014653.1
lukE	99.79	936 / 936	CP104989.1 Staphylococcus aureus strain Karak2019-A29 chromosome	1109191..1110126	leukocidin E component	AP014942.1

sea	100	783 / 783	CP104989.1 Staphylococcus aureus strain Karak2019-A29 chromosome	2612185..2612967	enterotoxin A	AP009324.1
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Table S2 SNP analysis of the A29 genome mapped to the antimicrobial resistance genes in CP047022.1 genome (Danish MRSA isolate)

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome)	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
1	3448	Start	+			cadD	cadmium resistance transporter CadD	STRESS	plus	METAL	CADMIUM	CADMIUM	BLAST P	100	99.51
2	4065	stop	+			cadD	cadmium resistance transporter CadD	STRESS	plus	METAL	CADMIUM	CADMIUM	BLAST P	100	99.51
3	8476	Start	-			blaR1	beta-lactam sensor/signal transducer BlaR1	AMR	core	AMR	BETA-LACTAM	BETA-LACTAM	BLAST P	100	95.56
4	10233	stop	-			blaR1	beta-lactam sensor/signal transducer BlaR1	AMR	core	AMR	BETA-LACTAM	BETA-LACTAM	BLAST P	100	95.56
5	10340	Start	+			blaZ	penicillin-hydrolyzing class A beta-lactamase BlaZ	AMR	core	AMR	BETA-LACTAM	BETA-LACTAM	EXACT P	100	100
6	11185	stop	+			blaZ	penicillin-hydrolyzing class A beta-lactamase BlaZ	AMR	core	AMR	BETA-LACTAM	BETA-LACTAM	EXACT P	100	100

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
7	39653	Start	-			mecA	PBP2a family beta-lactam-resistant peptidoglycan transpeptidase MecA	AMR	core	AMR	BETA-LACTAM	METHICILLIN	EXACT P	100	100
8	41662	stop	-			mecA	PBP2a family beta-lactam-resistant peptidoglycan transpeptidase MecA	AMR	core	AMR	BETA-LACTAM	METHICILLIN	EXACT P	100	100
9	41759	Start	+			mecR1	beta-lactam sensor/signal transducer MecR1	AMR	core	AMR	BETA-LACTAM	METHICILLIN	PARTIAL P	55.56	100
10	42745	stop	+			mecR1	beta-lactam sensor/signal transducer MecR1	AMR	core	AMR	BETA-LACTAM	METHICILLIN	PARTIAL P	55.56	100
11	61423	SNP in A29 genome		C	T										
12	87285	SNP in		C	T										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
		A29 genome													
13	117202	SNP in A29 genome		G	T										
14	122824	Start	+			tet(38)	tetracycline efflux MFS transporter Tet(38)	AMR	core	AMR	TETRACYCLINE	TETRACYCLINE	EXACT P	100	100
15	124176	stop	+			tet(38)	tetracycline efflux MFS transporter Tet(38)	AMR	core	AMR	TETRACYCLINE	TETRACYCLINE	EXACT P	100	100
16	129576	SNP in A29 genome		G	A										
17	195444	SNP in A29 genome		C	T										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
18	20279 2	SNP in A29 genome		T	G										
19	20613 3	SNP in A29 genome		A	C										
20	21999 3	SNP in A29 genome		G	T										
21	26496 4	SNP in A29 genome		A	G										
22	27390 8	SNP in A29 genome		C	T										
23	29716 2	SNP in		G	T										



Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
		A29 genome													
24	351426	Start	+			mepA	multidrug efflux MATE transporter MepA	AMR	plus	AMR	TETRACYCLINE	TIGECYCLINE	BLAST P	100	99.33
25	352781	stop	+			mepA	multidrug efflux MATE transporter MepA	AMR	plus	AMR	TETRACYCLINE	TIGECYCLINE	BLAST P	100	99.33
26	385926	Start	+			selX	staphylococcal enterotoxin-like toxin X	VIRULENCE	plus	VIRULENCE			BLAST P	100	96.06
27	386537	stop	+			selX	staphylococcal enterotoxin-like toxin X	VIRULENCE	plus	VIRULENCE			BLAST P	100	96.06
28	405800	SNP in A29 genome		C	T										
29	433226	SNP in A29 genome		A	T										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
30	459607	SNP in A29 genome		C	T										
31	466745	SNP in A29 genome		A	G										
32	471086	SNP in A29 genome		A	G										
33	478280	SNP in A29 genome		A	G										
34	496834	SNP in A29 genome		T	A										
35	557684	SNP in		A	G										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
		A29 genome													
36	594282	SNP in A29 genome		G	A										
37	596571	SNP in A29 genome		T	C										
38	623798	SNP in A29 genome		G	A										
39	651961	SNP in A29 genome		C	T										
40	788178	SNP in A29		G	T										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
		genome													
41	824558	SNP in A29 genome		A	T										
42	827178	SNP in A29 genome		A	G										
43	847296	SNP in A29 genome		G	A										
44	848111	SNP in A29 genome		A	G										
45	862366	SNP in A29 genome		G	A										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
46	1003956	SNP in A29 genome		A	G										
47	1008726	SNP in A29 genome		T	C										
48	1052634	SNP in A29 genome		A	C										
49	1055966	SNP in A29 genome		C	T										
50	1079677	SNP in A29 genome		A	G										
51	1094915	SNP in		C	T										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
		A29 genome													
52	1096368	SNP in A29 genome		C	A										
53	1100800	SNP in A29 genome		A	G										
54	1169946	SNP in A29 genome		T	C										
55	1265315	SNP in A29 genome		C	T										
56	1304832	SNP in A29		A	G										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
		genome													
57	1313113	SNP in A29 genome		T	C										
58	1337775	SNP in A29 genome		G	A										
59	1348357	SNP in A29 genome		T	A										
60	1358333	SNP in A29 genome		A	G										
61	1363484	SNP in A29 genome		C	T										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
62	1377084	SNP in A29 genome		C	T										
63	1410891	SNP in A29 genome		T	C										
64	1492314	SNP in A29 genome		T	C										
65	1494830	SNP in A29 genome		C	T										
66	1502240	SNP in A29 genome		A	G										
67	1510094	SNP in		C	T										



Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
		A29 genome													
68	1536586	SNP in A29 genome		T	A										
69	1555615	SNP in A29 genome		T	C										
70	1565266	SNP in A29 genome		C	T										
71	1585617	SNP in A29 genome		T	C										
72	1616832	SNP in A29		A	T										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
		genome													
73	1632012	SNP in A29 genome		A	G										
74	1638378	SNP in A29 genome		T	A										
75	1642194	SNP in A29 genome		T	C										
76	1651495	SNP in A29 genome		C	T										
77	1746100	SNP in A29 genome		T	C										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
78	1746407	SNP in A29 genome		G	A										
79	1764608	SNP in A29 genome		A	G										
80	1778611	SNP in A29 genome		A	T										
81	1796127	Start	+			arsB	arsenite efflux transporter membrane subunit ArsB	STRESS	plus	METAL	ARSENIC	ARSENITE	HMM	100	81.82
82	1797419	stop	+			arsB	arsenite efflux transporter membrane subunit ArsB	STRESS	plus	METAL	ARSENIC	ARSENITE	HMM	100	81.82
83	1832210	Start	-			spIE	serine protease SplE	VIRULENCE	plus	VIRULENCE			EXACTP	100	100
84	1832926	stop	-			spIE	serine protease SplE	VIRULENCE	plus	VIRULENCE			EXACTP	100	100

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
85	1834701	Start	-			splB	serine protease SplB	VIRULE NCE	plus	VIRULE NCE			BLAST P	100	99.58
86	1835423	stop	-			splB	serine protease SplB	VIRULE NCE	plus	VIRULE NCE			BLAST P	100	99.58
87	1835548	Start	-			splA	serine protease SplA	VIRULE NCE	plus	VIRULE NCE			EXACT P	100	100
88	1836255	stop	-			splA	serine protease SplA	VIRULE NCE	plus	VIRULE NCE			EXACT P	100	100
89	1848629	Start	-			lukE	bi-component leukocidin LukED subunit E	VIRULE NCE	plus	VIRULE NCE			BLAST P	100	99.68
90	1849564	stop	-			lukE	bi-component leukocidin LukED subunit E	VIRULE NCE	plus	VIRULE NCE			BLAST P	100	99.68
91	1869476	SNP in A29 genome		C	T										
92	1884962	SNP in A29 genome		T	C										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
93	1894879	SNP in A29 genome		A	G										
94	1899804	SNP in A29 genome		T	A										
95	1922068	SNP in A29 genome		C	G										
96	1965750	SNP in A29 genome		G	A										
97	2013482	SNP in A29 genome		G	A										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
98	2019010	Start	-			scn	complement inhibitor SCIN-A	VIRULENCE	plus	VIRULENCE			EXACTP	100	100
99	2019360	stop	-			scn	complement inhibitor SCIN-A	VIRULENCE	plus	VIRULENCE			EXACTP	100	100
100	2020858	Start	-			sak	staphylokinase	VIRULENCE	plus	VIRULENCE			EXACTP	100	100
101	2021349	stop	-			sak	staphylokinase	VIRULENCE	plus	VIRULENCE			EXACTP	100	100
102	2023058	Start	-			sea	staphylococcal enterotoxin type A	VIRULENCE	plus	VIRULENCE			EXACTP	100	100
103	2023831	stop	-			sea	staphylococcal enterotoxin type A	VIRULENCE	plus	VIRULENCE			EXACTP	100	100
104	2028986	SNP in A29 genome		G	A										
105	2077435	Start	-			hld	delta-hemolysin	VIRULENCE	plus	VIRULENCE			EXACTP	100	100
106	2077569	stop	-			hld	delta-hemolysin	VIRULENCE	plus	VIRULENCE			EXACTP	100	100
107	2116396	SNP in		T	C										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
		A29 genome													
108	2154783	SNP in A29 genome		G	T										
109	2156367	SNP in A29 genome		C	T										
110	2167776	SNP in A29 genome		T	C										
111	2194283	SNP in A29 genome		A	G										
112	2215118	SNP in A29		A	G										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
		genome													
113	2227623	Start	-			lmrS	multidrug efflux MFS transporter LmrS	STRESS	plus	BIOCIDE	MACROLIDE/PHENICOL	CHLORAMPHENICOL/ERYTHROMYCIN	BLASTP	100	99.38
114	2229065	stop	-			lmrS	multidrug efflux MFS transporter LmrS	STRESS	plus	BIOCIDE	MACROLIDE/PHENICOL	CHLORAMPHENICOL/ERYTHROMYCIN	BLASTP	100	99.38
115	2244000	SNP in A29 genome		A	G										
116	2259380	SNP in A29 genome		G	A										
117	2265353	SNP in A29 genome		T	G										
118	2306928	SNP in		A	G										



Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
		A29 genome													
119	2309738	SNP in A29 genome		T	C										
120	2318631	SNP in A29 genome		T	C										
121	2323985	SNP in A29 genome		A	G										
122	2326107	SNP in A29 genome		T	C										
123	2328991	SNP in A29		G	A										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
		genome													
124	2370143	SNP in A29 genome		T	C										
125	2371596	Start	+			fosB	FosB1/FosB3 family fosfomycin resistance bacillithiol transferase	AMR	core	AMR	FOSFOMYCIN	FOSFOMYCIN	PARTIALX	74.82	99.04
126	2371907	stop	+			fosB	FosB1/FosB3 family fosfomycin resistance bacillithiol transferase	AMR	core	AMR	FOSFOMYCIN	FOSFOMYCIN	PARTIALX	74.82	99.04
127	2387343	SNP in A29 genome		A	G										
128	2401737	SNP in A29		T	G										

Entry number	Start/Stope/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
		genome													
129	2427776	SNP in A29 genome		A	G										
130	2440156	SNP in A29 genome		A	G										
131	2444821	SNP in A29 genome		C	T										
132	2459283	SNP in A29 genome		A	G										
133	2462440	Start	+			hlgA	bi-component gamma-hemolysin HlgAB subunit A	VIRULENCE	plus	VIRULENCE			EXACT P	100	100

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome)	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
134	24633 69	stop	+			hlgA	bi-component gamma-hemolysin HlgAB subunit A	VIRULE NCE	plu s	VIRULE NCE			EXACT P	100	100
135	24639 37	Start	+			hlgC	bi-component gamma-hemolysin HlgCB subunit C	VIRULE NCE	plu s	VIRULE NCE			BLAST P	100	97.46
136	24648 84	stop	+			hlgC	bi-component gamma-hemolysin HlgCB subunit C	VIRULE NCE	plu s	VIRULE NCE			BLAST P	100	97.46
137	24648 86	Start	+			hlgB	bi-component gamma-hemolysin HlgAB/HlgCB subunit B	VIRULE NCE	plu s	VIRULE NCE			BLAST P	100	97.54
138	24658 63	stop	+			hlgB	bi-component gamma-hemolysin HlgAB/HlgCB subunit B	VIRULE NCE	plu s	VIRULE NCE			BLAST P	100	97.54
139	24674 43	SNP in		C	T										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
		A29 genome													
140	2473513	SNP in A29 genome		T	G										
141	2509534	SNP in A29 genome		T	C										
142	2578503	SNP in A29 genome		C	A										
143	2597962	SNP in A29 genome		T	C										
144	2607734	SNP in A29		C	T										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
		genome													
145	2618918	SNP in A29 genome		C	T										
146	2636282	SNP in A29 genome		A	G										
147	2649108	SNP in A29 genome		G	T										
148	2650162	SNP in A29 genome		A	G										
149	2702407	Start	-			aur	zinc metalloproteinase aureolysin	VIRULENCE	plus	VIRULENCE			BLAST P	100	99.41

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
150	2703936	stop	-			aur	zinc metalloproteinase aureolysin	VIRULENCE	plus	VIRULENCE			BLASTP	100	99.41
151	2703979	SNP in A29 genome		G	A										
152	2743489	SNP in A29 genome		G	A										
153	2747266	Start	+			icaC	polysaccharide intercellular adhesin biosynthesis/export protein IcaC	VIRULENCE	plus	VIRULENCE			EXACTP	100	100
154	2748318	stop	+			icaC	polysaccharide intercellular adhesin biosynthesis/export protein IcaC	VIRULENCE	plus	VIRULENCE			EXACTP	100	100
155	2748508	SNP in		A	C										

Entry number	Start/Stop/SNP ( Numbering according to CP047022.1 , the Danish isolate genome	start/stop	Strand	Danish isolate	SNP detected in A29 genome	Element symbol	Element name	Type	Scope	Subtype	Class	Subclass	Method	% Coverage of reference	% Identity to reference
		A29 genome													
156	2758689	SNP in A29 genome		C	A										
157	2769798	Start	-			cna	collagen adhesin Cna	VIRULE NCE	plus	VIRULE NCE			BLAST P	100	98.22
158	2771818	SNP in A29 genome		A	G										
159	2773349	stop	-			cna	collagen adhesin Cna	VIRULE NCE	plus	VIRULE NCE			BLAST P	100	98.22