

STRAND	CDS NUMBER/GENE NAME	PREDICTED FUNCTION	START (nt)	END (nt)	LENGHT (bp)	SIMILAR PROTEIN ACCESSION NUMBER	SIMILAR PROTEIN ORGANISM	% ID	Query coverage
-	CDS 1	phage resistance protein	1	1542	1542	AHE69901	<i>Enterobacter ludwigii</i> P101	100	100
-	<i>spr(yeiV)</i>	membrane protein	1670	2107	438	EUM29602	<i>Enterobacter ludwigii</i> EN-119	100	100
-	CDS 2	membrane protein	2656	3381	726	KIF86397.1	<i>Enterobacter ludwigii</i> EN-119	100	100
-	CDS 3	hypothetical protein	3403	4389	987	KIF86396.1	<i>Enterobacter ludwigii</i> EN-119	99	100
-	CDS 4	D-mannonate oxidoreductase	4513	5979	1467	KIF86395.1	<i>Enterobacter ludwigii</i> EN-119	99	100
+	CDS 5	mannonate dehydratase	6184	7374	1191	EUM09581	<i>Enterobacter</i> sp. BIDMC 30	100	100
-	CDS 6	elongation factor P	7418	7990	573	KIF86393.1	<i>Enterobacter ludwigii</i> EN-119	100	100
-	CDS 7	putative membrane protein/membrane-anchored nucleotide-binding enzyme	8274	9365	1092	KJW84079	<i>Enterobacter cloacae</i> CIDEIMsCOL5	97	100
+	CDS 8	Predicted Fe-S-cluster oxidoreductase containing a putative zinc- or iron-chelating domain	9601	9879	279	KGB13761	<i>Enterobacter cloacae</i> ATCC 13047	86	100
-	CDS 9	hypothetical protein	9882	10475	594	KJC09859	<i>Citrobacter freundii</i> MRSN 11938	97	100
+	CDS 10	hypothetical protein	11057	11623	567	EWD81767	<i>Klebsiella pneumoniae</i> UCI 18	91	77
+	<i>mcsS</i> -like	similar to class IIa microcin S precursor McsS	12368	12730	363	YP_006954535	<i>Escherichia coli</i> G3/10	73	100
+	<i>mcpl</i> -like	similar to microcin immunity protein	12756	12953	198	YP_006954413.1	<i>Escherichia coli</i> EC25	76	93
+	<i>mcsI</i> -like	similar to McsS self-immunity protein	12963	13613	651	YP_006954534	<i>Escherichia coli</i> G3/10	74	100
+	<i>mcsA</i> -like	putative hemolysin secretion protein, HlyD family	13616	14869	1254	YP_006954533	<i>Escherichia coli</i> G3/10	90	100
+	<i>mcsB</i> -like	putative Colicin V secretion ABC transporter ATP-binding protein; bacteriocin/lantibiotic exporters; peptidase C39	14869	17073	2205	YP_006954532	<i>Escherichia coli</i> G3/10	89	98
-	CDS 11	Site-specific serine recombinases, DNA invertase Pin homolog. Partitioning (par)-Resolvase subfamily.	17203	17817	615	KJO38188	<i>Enterobacter asburiae</i> 35009	98	100
+	CDS 12	hypothetical protein	18133	19236	1104	CFQ99063	<i>Yersinia enterocolitica</i> SZ662/97	90	100
+	CDS 13	hypothetical protein	19233	20180	948	CFQ99070	<i>Yersinia enterocolitica</i> SZ662/97	85	100
-	CDS 14	hypothetical protein	20532	21128	597	KJC10670	<i>Citrobacter freundii</i> MRSN 12115	77	100
-	CDS 15	hypothetical protein	21112	21480	369	KGY86150	<i>Citrobacter freundii</i> FDAARGOS_73	88	99
-	CDS 16	hypothetical protein	21470	22324	855	EOD60026	<i>Citrobacter freundii</i> GTC 09629	97	89
-	CDS 17	putative resolvase with a recombinase zinc beta ribbon domain	22494	24410	1917	AKE59181	<i>Citrobacter amalonaticus</i> Y19	98	100
-	CDS 18	putative 4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family	26438	27871	1434	ACR70138	<i>Edwardsiella ictaluri</i> 93-146	60	99
-	CDS 19	hypothetical protein	29211	29711	501	AGZ03780	<i>Serratia marcescens</i> N11-2820	47	92
-	<i>bla<sub>NMC-A</sub></i>	class A beta-lactamase	29756	30634	879	CAA79967	<i>Enterobacter asburiae</i> NOR-1	100	100
+	<i>nmc-R</i>	transcriptional regulator	30776	31663	888	CAA79966	<i>Enterobacter asburiae</i> NOR-1	100	100
+	<i>smvA_2</i> -like	major facilitator superfamily protein, similar to methyl viologen resistance protein SmvA	32458	33966	1509	CNH32633	<i>Yersinia intermedia</i> IP10066	52	95
+	CDS 20	ATP-binding cassette domain of non-transporter proteins; ABC-type Class 2	34232	34969	738	ADG18478	<i>Burkholdera</i> sp. CCGE1002	60	97
-	CDS 21	hypothetical protein	35215	36267	1053	GAB53007	<i>Escherichia hermannii</i> NBRC 105704	50	90
+	CDS 22	Fe-S-cluster oxidoreductase	37355	37552	198	KJN60966	<i>Enterobacter cloacae</i> 35638	92	98
-	CDS 23	sugar efflux transporter B	37549	38730	1182	EUM09584	<i>Enterobacter</i> sp. BIDMC 30	99	100
+	CDS 24	hypothetical protein	38875	39018	144	AHE72828	<i>Enterobacter cloacae</i> P101	100	100
+	CDS 25	PTS fructose transporter subunit IIA	39091	40221	1131	AHE69910	<i>Enterobacter cloacae</i> P101	100	100
+	<i>fruK</i>	1-phosphofructokinase	40221	41159	939	KIF86389.1	<i>Enterobacter ludwigii</i> EN-119	100	100
+	CDS 26	PTS fructose transporter subunit IIBC	41176	42858	1683	KIF86388.1	<i>Enterobacter ludwigii</i> EN-119	100	100
-	CDS 27	endonuclease IV	42906	43763	858	KIF86387	<i>Enterobacter ludwigii</i> EN-119	100	100
-	CDS 28	hypothetical protein	43828	44874	1047	EUM29590	<i>Enterobacter</i> sp. BIDMC 26	100	100

Table S1. List of coding sequences (CDSs) reported in the GenBank record no. KR919803, which includes the EludIMEX-1 element and flanking regions of the *E. ludwigii* AOU-8/14 genome. Similarities of protein products with proteins from non-redundant sequence database, detected using the blastp web tool (<http://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp>) are also reported. Coding sequences present in the EludIMEX-1 element are shaded in grey. Coding sequences are progressively numbered from the beginning of the record, unless a gene name was assigned based on sequence similarity.