

Center for Genomic Epidemiology

[Home](#)
[Services](#)
[Instructions](#)
[Output](#)

MLST-2.0 Server - Results

mlst Profile: *ecoli*

Organism: *Escherichia coli*#1

Sequence Type: 278

Locus	Identity	Coverage	Alignment Length	Allele Length	Gaps	Allele
adk	100	100	536	536	0	adk_9
fumC	100	100	469	469	0	fumC_23
gyrB	100	100	460	460	0	gyrB_64
icd	100	100	518	518	0	icd_18
mdh	100	100	452	452	0	mdh_11
purA	100	100	478	478	0	purA_8
recA	100	100	510	510	0	recA_6

[extended output](#)

Input Files: *EC092.fasta*

Please download your results using the buttons below.

[Results as text](#)
[Results tsv](#)
[Hit in genome sequences](#)
[MLST allele sequences](#)

CITATIONS

For publication of results, please cite:

- Multilocus Sequence Typing of Total Genome Sequenced Bacteria. Larsen MV, Cosentino S, Rasmussen S, Friis C, Hasman H, Marvig RL, Jelsbak L, Sicheritz-PontÃ©n T, Ussery DW, Aarestrup FM and Lund O. J. Clin. Microbiol. 2012. 50(4): 1355-1361. PMID: [22238442](#) doi: [10.1128/JCM.06094-11](#)

[Support](#)
[Scientific problems](#)
[Technical problems](#)

Copyright DTU 2011 / All rights reserved
 Center for Genomic Epidemiology, DTU, Kemitorvet, Building 204, 2800 Kgs. Lyngby, Denmark
 Contact: Vibeke Dybdahl Hammer, Telephone: +45 3588 6420, E-mail: vdha@food.dtu.dk
 Funded by: The Danish Council for Strategic Research
 Last modified May 22, 2012 11:08:01 GMT