



Caracterització de paràlegs de la proteïna associada al nucleòide Hha: les proteïnes YdgT, HoIE i YmgB

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Facultat de Biologia
Departament de Microbiologia

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les proteïnes YdgT, HoloE i YmgB**

Programa de Doctorat: Microbiologia Ambiental i Biotecnologia
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Memòria presentada per Laura
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Conformitat dels directors de la
tesi

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**Annex: Resultats anàlisi transcriptòmica en
microxips GeneChip[®] *E. coli* Genome 2.0 Array
(Affymetrix)**

1. Anàlisi transcriptòmica mutant MG1655Y_vs_wt

Taula 1. Gens expressats diferencialment en un mutant *ydgT* (MG1655Y) respecte a la soca salvatge (MG1655) amb un FC>1,5. En diferents intensitats de vermell s'indiquen els gens que es troben induïts respecte a la soca salvatge i en verd els que es troben reprimits.

| Gene.Symbol | Target.Description | FC_Y_vs_WT | adj.P.Val |
|---------------------|---|------------|-----------|
| <i>yghJ</i> | putative endoglucanase | 3,964 | 0,01004 |
| <i>lldP</i> | L-lactate permease | 3,711 | 0,003823 |
| <i>yddB</i> | orf, hypothetical protein | 3,578 | 0,008823 |
| <i>mglA</i> | ATP-binding component of methyl-galactoside transport and galactose taxis | 3,523 | 0,01427 |
| <i>yghJ</i> | orf, hypothetical protein | 3,297 | 0,01046 |
| <i>ndk</i> | nucleoside diphosphate kinase | 3,240 | 0,0119 |
| <i>yddA</i> | putative ATP-binding component of a transport system | 3,059 | 0,03773 |
| <i>mglC</i> | methyl-galactoside transport and galactose taxis | 3,038 | 0,01365 |
| <i>pqqL</i> | putative zinc protease | 3,008 | 0,03614 |
| --- | intergenic region | 2,963 | 0,02582 |
| <i>putA</i> | proline dehydrogenase, P5C dehydrogenase | 2,904 | 0,003894 |
| --- | orf, hypothetical protein | 2,856 | 0,006983 |
| <i>psuG // yeiN</i> | orf, hypothetical protein | 2,608 | 0,002144 |
| <i>stpA</i> | DNA-binding protein; H-NS-like protein; chaperone activity; RNA splicing? | 2,54 | 0,05336 |
| <i>mglB</i> | galactose-binding transport protein; receptor for galactose taxis | 2,415 | 0,01683 |
| <i>putP</i> | major sodiumproline symporter | 2,387 | 0,007968 |
| <i>xylF</i> | xylose binding protein transport system | 2,367 | 0,007406 |
| <i>yqeF</i> | putative acyltransferase | 2,349 | 0,04485 |
| <i>efeO // ycdO</i> | orf, hypothetical protein | 2,305 | 0,02709 |
| <i>borD // borW</i> | putative Bor protein of prophage CP-933X | 2,286 | 0,02689 |
| <i>yihN</i> | putative resistance protein (transport) | 2,272 | 0,04361 |
| <i>efeB // ycdB</i> | orf, hypothetical protein | 2,238 | 0,02657 |
| --- | intergenic region | 2,219 | 0,03752 |
| <i>dadA</i> | D-amino acid dehydrogenase subunit | 2,198 | 0,007104 |
| --- | intergenic region | 2,183 | 0,03737 |
| <i>fiu</i> | putative outer membrane receptor for iron transport | 2,178 | 0,03285 |
| <i>putA</i> | PutA protein | 2,176 | 0,002419 |
| <i>dadX</i> | alanine racemase 2, catabolic | 2,154 | 0,007104 |
| <i>mqo // yojH</i> | hypothetical protein | 2,120 | 0,007104 |
| <i>yiaK</i> | putative dehydrogenase | 2,104 | 0,01136 |
| <i>ppsA</i> | phosphoenolpyruvate synthase | 2,011 | 0,02689 |
| <i>pstC</i> | Phosphate transport system permease protein pstC | 1,978 | 0,02027 |
| --- | intergenic region | 1,978 | 0,03884 |
| <i>araC</i> | transcriptional regulator for ara operon | 1,963 | 0,004336 |
| <i>carB</i> | carbamoyl-phosphate synthase large subunit | 1,947 | 0,02385 |
| --- | intergenic region | 1,940 | 0,01721 |

| | | | |
|---------------------|--|-------|----------|
| <i>dctA</i> | uptake of C4-dicarboxylic acids | 1,897 | 0,01569 |
| <i>psuK // yeiC</i> | putative kinase | 1,887 | 0,02362 |
| <i>rluA // yabO</i> | pseudouridylate synthase | 1,876 | 0,01759 |
| <i>rstA</i> | response transcriptional regulatory protein (RstB sensor) | 1,875 | 0,01115 |
| <i>aldA</i> | aldehyde dehydrogenase, NAD-linked | 1,869 | 0,01721 |
| <i>pstS</i> | high-affinity phosphate-specific transport system; periplasmic phosphate-binding protein | 1,865 | 0,009824 |
| <i>mhpR</i> | transcriptional regulator for mhp operon | 1,862 | 0,0205 |
| <i>ugpA</i> | sn-glycerol 3-phosphate transport system, integral membrane protein | 1,836 | 0,01592 |
| <i>metK</i> | methionine adenosyltransferase 1 (AdoMet synthetase); methyl and propylamine donor, corepressor of met genes | 1,831 | 0,01799 |
| <i>metR</i> | regulator for metE and metH | 1,828 | 0,001453 |
| <i>yhjC</i> | putative transcriptional regulator LYSR-type | 1,821 | 0,02954 |
| <i>ynfO</i> | Unknown protein encoded within prophage | 1,816 | 0,01002 |
| <i>ygfl</i> | partial putative transcriptional regulator LYSR-type | 1,805 | 0,007196 |
| <i>fadA</i> | thiolase I; 3-ketoacyl-CoA thiolase; acetyl-CoA transferase | 1,801 | 0,02951 |
| --- | intergenic region | 1,793 | 0,03439 |
| <i>malX</i> | PTS system, maltose and glucose-specific IIBC component | 1,781 | 0,04142 |
| <i>gntP</i> | gluconate transport system permease 3 | 1,780 | 0,04198 |
| <i>nmpC</i> | outer membrane porin protein; locus of qsr prophage | 1,778 | 0,01258 |
| <i>sdhC</i> | succinate dehydrogenase, cytochrome b556 | 1,777 | 0,01296 |
| <i>yedF</i> | orf, hypothetical protein | 1,776 | 0,02075 |
| <i>dsdC</i> | D-serine dehydratase (deaminase) transcriptional activator | 1,765 | 0,0281 |
| <i>rbsA</i> | ATP-binding component of D-ribose high-affinity transport system | 1,761 | 0,005284 |
| <i>sdhD</i> | succinate dehydrogenase, hydrophobic subunit | 1,746 | 0,007196 |
| <i>entC</i> | isochorismate hydroxymutase 2, enterochelin biosynthesis | 1,744 | 0,04716 |
| <i>entE</i> | 2,3-dihydroxybenzoate-AMP ligase | 1,739 | 0,04677 |
| <i>nrdB</i> | ribonucleoside-diphosphate reductase 1, beta subunit, B2 | 1,730 | 0,007655 |
| <i>ybaE</i> | orf, hypothetical protein | 1,729 | 0,01602 |
| <i>yedE</i> | putative transport system permease protein | 1,718 | 0,03788 |
| ECs1112 | putative minor tail protein | 1,707 | 0,03667 |
| <i>metN</i> | D- and L-methionine transport protein (ABC superfamily, atp_bind) | 1,707 | 0,005387 |
| <i>fecI</i> | probable RNA polymerase sigma factor | 1,707 | 0,04676 |
| <i>lrhA</i> | NADH dehydrogenase transcriptional regulator, LysR family | 1,706 | 0,002419 |
| <i>mltA</i> | Membrane-bound lytic murein transglycosylase A precursor | 1,701 | 0,02776 |
| <i>nmpC</i> | Hypothetical protein | 1,690 | 0,01296 |
| <i>arrD // ybcS</i> | bacteriophage lambda lysozyme homolog | 1,690 | 0,0186 |
| c3192 // c3194 | Hypothetical protein | 1,681 | 0,01958 |
| <i>yncE</i> | putative receptor | 1,667 | 0,02075 |
| --- | intergenic region | 1,655 | 0,03471 |
| <i>sdhA</i> | succinate dehydrogenase, flavoprotein subunit | 1,652 | 0,009813 |
| <i>rnfD // rsxD</i> | electron transport complex protein | 1,649 | 0,03016 |
| <i>livK</i> | high-affinity leucine-specific transport system; periplasmic binding protein | 1,640 | 0,04165 |
| <i>hipA</i> | persistence to inhibition of murein or DNA biosynthesis, DNA-binding regulator | 1,639 | 0,01115 |
| <i>fecE</i> | ATP-binding component of citrate-dependent iron(III) transport protein | 1,629 | 0,01971 |

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|---------------------|---|-------|----------|
| <i>ydhO</i> | putative lipoprotein | 1,628 | 0,005387 |
| <i>lldR</i> | Putative L-lactate dehydrogenase operon Regulatory protein | 1,614 | 0,02785 |
| <i>tnaB</i> | low affinity tryptophan permease | 1,613 | 0,0181 |
| <i>yeaT</i> | putative transcriptional regulator LYSR-type | 1,606 | 0,02256 |
| <i>yegT</i> | putative nucleoside permease protein | 1,589 | 0,0323 |
| <i>sthA // udhA</i> | putative oxidoreductase | 1,588 | 0,006664 |
| <i>lldP</i> | L-lactate permease | 1,583 | 0,03883 |
| <i>ebgA</i> | evolved beta-D-galactosidase, alpha subunit; cryptic gene | 1,583 | 0,003823 |
| <i>yglJ</i> | putative oxidoreductase | 1,582 | 0,007146 |
| c5324 | Hypothetical protein | 1,578 | 0,02315 |
| <i>sdhB</i> | succinate dehydrogenase, iron sulfur protein | 1,575 | 0,03287 |
| <i>cpdB</i> | 2:3-cyclic-nucleotide 2-phosphodiesterase | 1,562 | 0,01845 |
| <i>atoS</i> | sensor protein AtoS for response regulator AtoC | 1,561 | 0,03206 |
| --- | intergenic region | 1,560 | 0,01144 |
| --- | intergenic region | 1,558 | 0,02515 |
| <i>can // yadF</i> | putative carbonic anhydrase (EC 4.2.1.1) | 1,554 | 0,01321 |
| <i>araF</i> | L-arabinose-binding periplasmic protein | 1,554 | 0,009532 |
| ECs1509 | unknown protein encoded by prophage CP-933N | 1,547 | 0,03776 |
| Z5883 | orf; Unknown function | 1,544 | 0,03737 |
| <i>hisP</i> | ATP-binding component of histidine transport | 1,537 | 0,02819 |
| <i>bfd // yheA</i> | hypothetical protein | 1,536 | 0,02776 |
| <i>thiQ</i> | putative ATP-binding component of a transport system | 1,535 | 0,02612 |
| <i>hmpA</i> | dihydropteridine reductase, ferrisiderophore reductase activity | 1,532 | 0,02401 |
| <i>rsxG</i> | hypothetical protein | 1,531 | 0,0187 |
| <i>fumC</i> | fumarase C= fumarate hydratase Class II; isozyme | 1,527 | 0,04016 |
| <i>ebgA</i> | evolved beta-D-galactosidase, alpha subunit; cryptic gene | 1,526 | 0,01622 |
| <i>nrdB</i> | Ribonucleoside-diphosphate reductase 1 beta chain | 1,524 | 0,02167 |
| <i>rsxE // ydgQ</i> | hypothetical protein | 1,522 | 0,02234 |
| <i>yjjM</i> | orf, hypothetical protein | 1,522 | 0,04277 |
| <i>ade // yicP</i> | putative adenine deaminase | 1,517 | 0,0335 |
| c3615 | Unknown in ISEc8 | 1,506 | 0,02167 |
| <i>fucK</i> | L-fuculokinase | 1,505 | 0,008969 |
| <i>uidB</i> | glucuronide permease | 1,504 | 0,04392 |
| <i>yehT</i> | orf, hypothetical protein | 1,503 | 0,02802 |
| <i>intZ</i> | putative prophage integrase | 1,501 | 0,02785 |
| <i>glpD</i> | Aerobic glycerol-3-phosphate dehydrogenase | 1,501 | 0,02496 |
| --- | intergenic region | 1,500 | 0,03471 |
| --- | intergenic region | 1,501 | 0,03192 |
| --- | intergenic region | 1,501 | 0,01038 |
| --- | intergenic region | 1,501 | 0,03964 |
| <i>zntA</i> | zinc-transporting ATPase | 1,507 | 0,009577 |
| Z5814 | orf; Unknown function | 1,507 | 0,01628 |
| --- | intergenic region | 1,507 | 0,00308 |
| <i>yaaX</i> | orf, hypothetical protein | 1,508 | 0,02807 |
| <i>thrL</i> | thr operon leader peptide | 1,508 | 0,04755 |

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|---------------------|---|-------|----------|
| <i>ynfG</i> | putative oxidoreductase Fe-S subunit | 1,510 | 0,0186 |
| --- | intergenic region | 1,510 | 0,01971 |
| <i>talA</i> | transaldolase A | 1,514 | 0,04664 |
| --- | intergenic region | 1,514 | 0,002346 |
| --- | intergenic region | 1,518 | 0,03007 |
| <i>insA</i> | IS1 protein InsA | 1,518 | 0,03058 |
| <i>slyA</i> | transcriptional regulator for cryptic hemolysin | 1,520 | 0,03259 |
| --- | intergenic region | 1,521 | 0,01858 |
| <i>trpE</i> | anthranilate synthase component I (EC 4.1.3.27) | 1,522 | 0,03439 |
| --- | orf, hypothetical protein | 1,523 | 0,01253 |
| --- | intergenic region | 1,525 | 0,03283 |
| --- | intergenic region | 1,525 | 0,01756 |
| <i>ilvG</i> | acetolactate synthase II, valine insensitive, large subunit, silent in K-12 | 1,526 | 0,02115 |
| <i>pinQ // pinR</i> | putative transposon resolvase | 1,526 | 0,00657 |
| --- | intergenic region | 1,530 | 0,01875 |
| <i>adhP</i> | Alcohol dehydrogenase, propanol-preferring | 1,531 | 0,005037 |
| <i>yaiA</i> | orf, hypothetical protein | 1,535 | 0,004237 |
| <i>ydhV</i> | orf, hypothetical protein | 1,535 | 0,04819 |
| <i>yagQ</i> | orf, hypothetical protein | 1,535 | 0,02553 |
| c4007 | Hypothetical protein | 1,538 | 0,0101 |
| --- | intergenic region | 1,539 | 0,01573 |
| ECs4710 | orf, hypothetical protein | 1,541 | 0,04016 |
| --- | intergenic region | 1,542 | 0,01296 |
| --- | intergenic region | 1,545 | 0,03923 |
| <i>ydjJ</i> | hypothetical protein | 1,547 | 0,000853 |
| --- | intergenic region | 1,548 | 0,01258 |
| <i>yobH</i> | orf; Unknown function | 1,548 | 0,006198 |
| <i>ydfV</i> | orf, hypothetical protein | 1,549 | 0,000755 |
| <i>osmF</i> | putative transport system permease protein | 1,551 | 0,04088 |
| --- | intergenic region | 1,551 | 0,01955 |
| --- | intergenic region | 1,552 | 0,02785 |
| <i>galP</i> | galactose-proton symport of transport system | 1,552 | 0,0186 |
| c1126 | Hypothetical protein | 1,553 | 0,01628 |
| <i>fic</i> | induced in stationary phase, recognized by rpoS, affects cell division | 1,553 | 0,02871 |
| c1354 | orf, hypothetical protein | 1,554 | 0,009436 |
| <i>ydcS</i> | putative transport protein | 1,554 | 0,008742 |
| <i>yhhQ</i> | orf, hypothetical protein | 1,555 | 0,02819 |
| --- | intergenic region | 1,556 | 0,03964 |
| <i>hisD</i> | L-histidinal:NAD+ oxidoreductase; L-histidinol:NAD+ oxidoreductase | 1,556 | 0,01117 |
| --- | intergenic region | 1,557 | 0,006664 |
| --- | intergenic region | 1,562 | 0,03911 |
| <i>mltD</i> | cytochrome c552 | 1,563 | 0,01296 |
| <i>fliM</i> | flagellar biosynthesis, component of motor switch and energizing, enabling rotation and determining its direction | 1,565 | 0,0205 |
| c2541 | Hypothetical protein | 1,566 | 0,03392 |
| --- | intergenic region | 1,570 | 0,007655 |

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|---------------------|--|-------|----------|
| c2839 | Hypothetical protein | 1,571 | 0,02193 |
| c1776 | Hypothetical protein | 1,572 | 0,0206 |
| --- | intergenic region | 1,573 | 0,03471 |
| --- | intergenic region | 1,573 | 0,01711 |
| <i>fliD</i> | flagellar biosynthesis; filament capping protein; enables filament assembly | 1,574 | 0,01569 |
| c0182 | Hypothetical protein | 1,575 | 0,01952 |
| Z5852 | orf; Unknown function | 1,576 | 0,02265 |
| <i>ykfG</i> | putative DNA repair protein | 1,578 | 0,002237 |
| <i>rydB</i> | MG1655_rydB_b4430 /SEG=NC_000913:-1762737,1762804 /LEN=67 | 1,579 | 0,03206 |
| --- | intergenic region | 1,581 | 0,003823 |
| <i>yjgI</i> | orf, hypothetical protein | 1,582 | 0,04108 |
| --- | intergenic region | 1,582 | 0,004237 |
| <i>fliZ</i> | orf, hypothetical protein | 1,583 | 0,0206 |
| --- | intergenic region | 1,584 | 0,03185 |
| <i>trpE</i> | anthranilate synthase component I | 1,585 | 0,01496 |
| <i>yebV</i> | orf, hypothetical protein | 1,585 | 0,02819 |
| <i>mcbR</i> | hypothetical protein | 1,586 | 0,02999 |
| --- | intergenic region | 1,589 | 0,005691 |
| <i>ycdY</i> | orf, hypothetical protein | 1,591 | 0,03094 |
| <i>ppdD</i> | prelipin peptidase dependent protein | 1,594 | 0,000755 |
| --- | intergenic region | 1,596 | 0,01665 |
| --- | intergenic region | 1,596 | 0,01296 |
| <i>nikB</i> | transport of nickel, membrane protein | 1,596 | 0,048 |
| --- | intergenic region | 1,601 | 0,002011 |
| <i>ynfF</i> | putative oxidoreductase major subunit | 1,601 | 0,01254 |
| <i>fliA</i> | flagellar biosynthesis; alternative sigma factor 28; regulation of flagellar operons | 1,603 | 0,02807 |
| <i>hybB</i> | probable cytochrome NiFe component of hydrogenase-2 | 1,603 | 0,03887 |
| --- | intergenic region | 1,603 | 0,02315 |
| <i>bhsA // ycfR</i> | orf, hypothetical protein | 1,603 | 0,04165 |
| c0864 | Hypothetical protein | 1,605 | 0,04427 |
| <i>flgA</i> | flagellar biosynthesis; assembly of basal-body periplasmic P ring | 1,607 | 0,004853 |
| --- | intergenic region | 1,608 | 0,02854 |
| --- | intergenic region | 1,609 | 0,002258 |
| --- | intergenic region | 1,610 | 0,03439 |
| <i>phnB // yjdN</i> | orf, hypothetical protein | 1,610 | 0,04391 |
| <i>osmY</i> | hyperosmotically inducible periplasmic protein | 1,611 | 0,01535 |
| --- | intergenic region | 1,618 | 0,003823 |
| c0274 // c1281 | Hypothetical protein | 1,618 | 0,02265 |
| --- | intergenic region | 1,621 | 0,03471 |
| <i>ybgS</i> | putative homeobox protein | 1,621 | 0,04855 |
| <i>flgL</i> | flagellar biosynthesis; hook-filament junction protein | 1,622 | 0,007612 |
| --- | intergenic region | 1,623 | 0,02156 |
| <i>fhlA</i> | formate hydrogen-lyase transcriptional activator for fdhF, hyc and hyp operons | 1,626 | 0,000516 |
| --- | intergenic region | 1,630 | 0,009386 |

| | | | |
|--------------------|---|-------|----------|
| <i>fliF</i> | flagellar biosynthesis; basal-body MS(membrane and supramembrane)-ring and collar protein | 1,631 | 0,03975 |
| --- | intergenic region | 1,632 | 0,01426 |
| <i>yiaA</i> | Hypothetical protein yiaA | 1,634 | 0,0369 |
| --- | intergenic region | 1,635 | 0,001348 |
| Z4613 | orf, hypothetical protein | 1,638 | 0,01759 |
| --- | intergenic region | 1,644 | 0,01218 |
| <i>psrN</i> | MG1655_sraF_b4448 /SEG=NC_000913:+3236015,3236203 /LEN=188 | 1,647 | 0,01789 |
| --- | intergenic region | 1,647 | 0,04819 |
| <i>yaiO</i> | orf, hypothetical protein | 1,652 | 0,03583 |
| --- | intergenic region | 1,654 | 0,008742 |
| c2122 | Hypothetical protein | 1,654 | 0,01648 |
| <i>yejG</i> | orf, hypothetical protein | 1,663 | 0,002015 |
| --- | intergenic region | 1,668 | 0,003823 |
| <i>gltP</i> | glutamate-aspartate symport protein | 1,668 | 0,0323 |
| <i>ybaA</i> | orf, hypothetical protein | 1,669 | 0,01496 |
| --- | intergenic region | 1,674 | 0,04904 |
| <i>yohG</i> | orf, hypothetical protein | 1,676 | 0,02075 |
| <i>ytjA</i> | orf; Unknown function | 1,676 | 0,01375 |
| <i>insJ</i> | IS150 hypothetical protein | 1,677 | 0,02841 |
| <i>ydfK //ynaE</i> | orf, hypothetical protein | 1,678 | 0,02854 |
| --- | intergenic region | 1,678 | 0,009191 |
| <i>ivbL</i> | ilvB operon leader peptide | 1,679 | 0,01723 |
| --- | intergenic region | 1,685 | 0,03614 |
| --- | intergenic region | 1,687 | 0,002258 |
| <i>ybiW</i> | Pyruvate-formate lyase | 1,697 | 0,04031 |
| <i>tktB</i> | transketolase 2 isozyme | 1,698 | 0,02764 |
| --- | intergenic region | 1,698 | 0,009276 |
| --- | intergenic region | 1,701 | 0,01734 |
| <i>blr</i> | beta-lactam resistance protein | 1,704 | 0,003675 |
| --- | intergenic region | 1,705 | 0,007322 |
| <i>phr</i> | deoxyribodipyrimidine photolyase (photoreactivation) | 1,707 | 0,005387 |
| --- | intergenic region | 1,708 | 0,02342 |
| c4645 | Hypothetical protein | 1,709 | 0,01759 |
| c0813 | Hypothetical protein | 1,717 | 0,02673 |
| --- | intergenic region | 1,726 | 0,001745 |
| <i>otsA</i> | trehalose-6-phosphate synthase | 1,729 | 0,04088 |
| --- | phenylalanyl-tRNA synthetase (pheST) operon leader peptide | 1,734 | 0,02967 |
| c2949 | Hypothetical protein | 1,740 | 0,03614 |
| <i>yahO</i> | Hypothetical protein yahO precursor | 1,742 | 0,04144 |
| <i>sugE</i> | suppresses groEL, may be chaperone | 1,743 | 0,03776 |
| <i>yjbJ</i> | orf, hypothetical protein | 1,744 | 0,005055 |
| --- | intergenic region | 1,744 | 0,01513 |
| c2356 | Hypothetical protein | 1,748 | 0,003823 |
| --- | intergenic region | 1,751 | 0,003936 |
| --- | intergenic region | 1,752 | 0,002742 |

| | | | |
|---------------------|---|-------|----------|
| --- | intergenic region | 1,755 | 0,03884 |
| ECs3543 | orf, hypothetical protein | 1,756 | 0,02342 |
| c3935 | Hypothetical protein | 1,757 | 0,03596 |
| --- | intergenic region | 1,761 | 0,002258 |
| <i>rdlB</i> | antisense RNA, trans-acting regulator of <i>ldrB</i> translation | 1,762 | 0,01955 |
| --- | intergenic region | 1,762 | 0,008564 |
| <i>mmnG</i> | glucose-inhibited division; chromosome replication? | 1,767 | 0,00463 |
| --- | intergenic region | 1,777 | 0,000658 |
| <i>viaA // yieM</i> | orf, hypothetical protein | 1,778 | 0,04361 |
| <i>yehB</i> | putative outer membrane protein | 1,781 | 0,01648 |
| <i>fliL</i> | flagellar biosynthesis | 1,782 | 0,02385 |
| c1089 | Hypothetical protein | 1,784 | 0,00316 |
| <i>ygeQ</i> | orf, hypothetical protein | 1,785 | 0,003629 |
| --- | intergenic region | 1,786 | 0,02731 |
| <i>mgtA</i> | Mg ²⁺ transport ATPase, P-type 1 | 1,789 | 0,01798 |
| <i>rpsV // sra</i> | 30S ribosomal subunit protein S22; stationary phase-induced ribosome-associated protein | 1,789 | 0,03884 |
| --- | intergenic region | 1,793 | 0,002141 |
| <i>ecnB</i> | entericidin B | 1,797 | 0,001563 |
| <i>ycaD</i> | putative transport | 1,801 | 0,001474 |
| --- | intergenic region | 1,803 | 0,01166 |
| <i>corA</i> | partial repeat of <i>corA</i> | 1,811 | 0,0369 |
| <i>rdlC</i> | antisense RNA, trans-acting regulator of <i>ldrC</i> translation | 1,811 | 0,0162 |
| <i>ydaG</i> | orf, hypothetical protein | 1,820 | 0,009577 |
| <i>tsgA // yhfC</i> | Hypothetical protein <i>yhfC</i> | 1,822 | 0,04088 |
| --- | intergenic region | 1,822 | 0,01115 |
| c2535 | Hypothetical protein | 1,833 | 0,0205 |
| <i>flu</i> | antigen 43, phase-variable bipartite outer membrane fluffing protein | 1,834 | 0,000853 |
| <i>ldrD</i> | small toxic polypeptide | 1,835 | 0,01648 |
| <i>ydhZ</i> | orf, hypothetical protein | 1,842 | 0,007196 |
| <i>ndh</i> | respiratory NADH dehydrogenase | 1,847 | 0,03151 |
| <i>cysG</i> | uroporphyrinogen III methylase; sirohaeme biosynthesis | 1,851 | 0,004336 |
| --- | intergenic region | 1,853 | 0,007531 |
| --- | intergenic region | 1,857 | 0,006664 |
| c4243 | Hypothetical protein | 1,858 | 0,006163 |
| <i>ycdT</i> | putative ATP-binding component of a transport system | 1,866 | 0,002684 |
| <i>gadY</i> | MG1655_IS183_b4452 /SEG=NC_000913:+3662494,3662598 /LEN=104 | 1,869 | 0,01491 |
| <i>yhfG</i> | orf, hypothetical protein | 1,871 | 0,002801 |
| <i>yeaQ</i> | orf, hypothetical protein | 1,872 | 0,01369 |
| --- | intergenic region | 1,879 | 0,002419 |
| --- | intergenic region | 1,880 | 0,005328 |
| --- | intergenic region | 1,884 | 0,006723 |
| --- | intergenic region | 1,887 | 0,003546 |
| --- | intergenic region | 1,896 | 0,004685 |
| --- | orf, hypothetical protein | 1,902 | 0,01012 |
| <i>yeeS</i> | putative DNA repair protein, RADC family | 1,903 | 0,003713 |

| | | | |
|---------------------|--|-------|----------|
| <i>fliN</i> | flagellar biosynthesis, component of motor switch and energizing, enabling rotation and determining its direction | 1,906 | 0,00308 |
| --- | intergenic region | 1,908 | 0,02496 |
| c3233 | Hypothetical protein | 1,908 | 0,01734 |
| <i>asnA</i> | asparagine synthetase A | 1,911 | 0,02492 |
| --- | intergenic region | 1,915 | 0,00525 |
| <i>yehX</i> | putative ATP-binding component of a transport system | 1,917 | 0,004431 |
| --- | intergenic region | 1,928 | 0,01419 |
| c2371 | Hypothetical protein | 1,937 | 0,0005 |
| --- | intergenic region | 1,948 | 0,00175 |
| <i>nrfD</i> | formate-dependent nitrate reductase complex; transmembrane protein | 1,954 | 0,02752 |
| c4882 | Hypothetical protein | 1,956 | 0,002801 |
| <i>ycjV</i> | putative ATP-binding component of a transport system | 1,956 | 0,0369 |
| <i>yeaG</i> | orf, hypothetical protein | 1,956 | 0,03551 |
| <i>nikC</i> | transport of nickel, membrane protein | 1,964 | 0,00821 |
| --- | intergenic region | 1,967 | 0,001899 |
| <i>yeeR</i> | orf, hypothetical protein | 1,968 | 0,006946 |
| <i>fliQ</i> | flagellar biosynthesis | 1,968 | 0,001899 |
| <i>fliK</i> | flagellar hook-length control protein | 1,968 | 0,005307 |
| c3178 | Hypothetical protein | 1,970 | 0,007026 |
| <i>bcsG // yhjU</i> | orf, hypothetical protein | 1,971 | 0,000874 |
| c3917 | Hypothetical protein | 1,979 | 0,002107 |
| --- | intergenic region | 1,981 | 0,000755 |
| <i>nepl</i> | putative transport protein | 1,985 | 0,002684 |
| <i>deaD</i> | inducible ATP-independent RNA helicase | 1,993 | 0,00179 |
| <i>cspF</i> | CspF | 1,994 | 0,01125 |
| c5458 | Hypothetical protein | 1,994 | 0,003629 |
| <i>fliP</i> | flagellar biosynthesis | 1,998 | 0,000755 |
| --- | Hypothetical protein | 2,021 | 0,001563 |
| --- | intergenic region | 2,021 | 0,00308 |
| <i>fliG</i> | flagellar biosynthesis, component of motor switching and energizing, enabling rotation and determining its direction | 2,031 | 0,003823 |
| <i>fliO</i> | flagellar biosynthesis | 2,032 | 0,002002 |
| <i>flgC</i> | flagellar biosynthesis, cell-proximal portion of basal-body rod | 2,034 | 0,004066 |
| --- | intergenic region | 2,046 | 0,004431 |
| <i>flgB</i> | flagellar biosynthesis, cell-proximal portion of basal-body rod | 2,046 | 0,005642 |
| --- | intergenic region | 2,049 | 0,002041 |
| <i>napG</i> | ferredoxin-type protein: electron transfer | 2,051 | 0,04773 |
| <i>fliI</i> | flagellum-specific ATP synthase | 2,055 | 0,0005 |
| <i>rlmG // ygjO</i> | putative enzyme | 2,056 | 0,001141 |
| <i>yliL</i> | orf, hypothetical protein | 2,059 | 0,005042 |
| <i>frdC</i> | fumarate reductase, anaerobic, membrane anchor polypeptide | 2,062 | 0,02127 |
| <i>yjgX</i> | orf, hypothetical protein | 2,068 | 0,002821 |
| --- | intergenic region | 2,068 | 0,004431 |
| <i>rhIE</i> | putative ATP-dependent RNA helicase | 2,085 | 0,004853 |
| <i>fdhF</i> | selenopolypeptide subunit of formate dehydrogenase H | 2,094 | 0,03737 |

| | | | |
|-------------|---|-------|----------|
| c1624 | Hypothetical protein | 2,099 | 0,0031 |
| <i>yhfL</i> | orf, hypothetical protein | 2,104 | 0,03439 |
| <i>flgJ</i> | flagellar biosynthesis | 2,108 | 0,001453 |
| <i>fliH</i> | Flagellar assembly protein fliH | 2,110 | 0,000871 |
| <i>yeeW</i> | orf, hypothetical protein | 2,126 | 0,01117 |
| <i>isrC</i> | MG1655_IS102_b4435 /SEG=NC_000913:+2069337,2069540 /LEN=203 | 2,129 | 0,000853 |
| <i>fruA</i> | PTS system, fructose-specific transport protein | 2,135 | 0,003823 |
| <i>nikD</i> | ATP-binding protein of nickel transport system | 2,138 | 0,02775 |
| <i>frdD</i> | fumarate reductase, anaerobic, membrane anchor polypeptide | 2,160 | 0,01166 |
| --- | intergenic region | 2,172 | 0,000755 |
| --- | intergenic region | 2,180 | 0,004853 |
| --- | intergenic region | 2,190 | 0,008742 |
| --- | intergenic region | 2,196 | 0,01369 |
| <i>fruK</i> | fructose-1-phosphate kinase | 2,201 | 0,01734 |
| <i>dsrA</i> | anti-sense RNA, silencer of rcsA gene, interacts with rpoS translation | 2,210 | 0,007531 |
| c0902 | Hypothetical protein | 2,211 | 0,00042 |
| --- | Hypothetical protein | 2,215 | 0,0481 |
| --- | intergenic region | 2,219 | 0,001655 |
| --- | intergenic region | 2,224 | 0,003629 |
| c2913 | Hypothetical protein | 2,230 | 0,009618 |
| Z4614 | orf; Unknown function | 2,244 | 0,007157 |
| <i>flgH</i> | flagellar biosynthesis, basal-body outer-membrane L (lipopolysaccharide layer) ring protein | 2,245 | 0,002258 |
| <i>yeaH</i> | Hypothetical protein yeaH | 2,245 | 0,007182 |
| <i>sokB</i> | antisense RNA blocking mokB and hokB translation | 2,283 | 0,0205 |
| <i>cspG</i> | homolog of Salmonella cold shock protein | 2,296 | 0,006792 |
| <i>poxB</i> | pyruvate oxidase | 2,301 | 0,01589 |
| <i>fliJ</i> | flagellar fliJ protein | 2,304 | 0,001021 |
| --- | intergenic region | 2,312 | 0,004573 |
| <i>oxyS</i> | global regulatory RNA OxyS | 2,318 | 0,009733 |
| <i>flgD</i> | flagellar biosynthesis, initiation of hook assembly | 2,331 | 0,00164 |
| <i>rmf</i> | ribosome modulation factor | 2,331 | 0,02082 |
| <i>rybA</i> | MG1655_rybA_b4416 /SEG=NC_000913:-852175,852263 /LEN=88 | 2,336 | 0,004685 |
| <i>flgK</i> | flagellar biosynthesis, hook-filament junction protein 1 | 2,360 | 0,000893 |
| --- | intergenic region | 2,373 | 0,002144 |
| --- | orf; Unknown function | 2,382 | 0,0323 |
| --- | intergenic region | 2,382 | 0,000658 |
| c1714 | Hypothetical protein | 2,385 | 0,007655 |
| --- | intergenic region | 2,402 | 0,00037 |
| <i>sibA</i> | MG1655_ryeC_b4436 /SEG=NC_000913:+2151297,2151445 /LEN=148 | 2,417 | 0,002041 |
| --- | intergenic region | 2,432 | 0,002419 |
| <i>flgF</i> | flagellar biosynthesis, cell-proximal portion of basal-body rod | 2,447 | 0,001745 |
| <i>flgE</i> | flagellar biosynthesis, hook protein | 2,447 | 0,000871 |
| --- | intergenic region | 2,449 | 0,002684 |
| <i>ryhA</i> | MG1655_ryhA_b4450 /SEG=NC_000913:+3348218,3348325 /LEN=107 | 2,450 | 0,00042 |
| --- | intergenic region | 2,459 | 0,003713 |

| | | | |
|---------------------|--|-------|----------|
| <i>ykgL</i> | orf, hypothetical protein | 2,461 | 0,002144 |
| <i>flgG</i> | flagellar biosynthesis, cell-distal portion of basal-body rod | 2,464 | 0,000145 |
| <i>yjaA</i> | orf, hypothetical protein | 2,471 | 0,009706 |
| Z3843 | orf; Unknown function | 2,486 | 0,01314 |
| <i>bssS</i> | orf, hypothetical protein | 2,486 | 0,01648 |
| <i>ycfJ</i> | orf, hypothetical protein | 2,493 | 0,00525 |
| <i>ryeA</i> | MG1655_ryeA_b4432 /SEG=NC_000913:+1921090,1921338 /LEN=248 | 2,546 | 0,01038 |
| <i>flgE</i> | flagellar biosynthesis, hook protein | 2,551 | 0,000532 |
| --- | intergenic region | 2,556 | 0,000263 |
| --- | intergenic region | 2,563 | 0,03007 |
| Z0387 | orf, hypothetical protein | 2,583 | 0,003629 |
| <i>flgI</i> | homolog of Salmonella P-ring of flagella basal body | 2,615 | 0,000755 |
| <i>rybB</i> | MG1655_rybB_b4417 /SEG=NC_000913:-887199,887277 /LEN=78 | 2,635 | 0,001021 |
| <i>glmY</i> | MG1655_tke1_b4441 /SEG=NC_000913:-2689212,2689360 /LEN=148 | 2,645 | 0,01628 |
| <i>cspH</i> | cold shock-like protein | 2,693 | 0,007655 |
| <i>cspl</i> | cold shock-like protein | 2,694 | 0,000853 |
| --- | intergenic region | 2,700 | 0,004237 |
| <i>malQ</i> | 4-alpha-glucanotransferase (amylomaltase) | 2,708 | 0,04485 |
| <i>feoC // yhgG</i> | orf, hypothetical protein | 2,715 | 0,005328 |
| --- | intergenic region | 2,717 | 0,00175 |
| <i>ygaM</i> | orf, hypothetical protein | 2,747 | 0,02035 |
| <i>sibD</i> | MG1655_rygD_b4447 /SEG=NC_000913:-3192767,3192916 /LEN=149 | 2,761 | 0,004066 |
| --- | intergenic region | 2,764 | 0,0009 |
| --- | intergenic region | 2,782 | 0,001703 |
| <i>flgF</i> | Flagellar basal-body rod protein flgF | 2,784 | 0,001348 |
| --- | intergenic region | 2,807 | 9,39E-03 |
| <i>micF</i> | regulatory antisense RNA affecting ompF expression | 2,830 | 0,01628 |
| <i>sibB</i> | MG1655_ryeD_b4437 /SEG=NC_000913:+2151632,2151774 /LEN=142 | 2,832 | 0,001745 |
| <i>yahM</i> | orf; Unknown function | 2,838 | 0,005284 |
| --- | intergenic region | 2,854 | 0,000756 |
| <i>rttR</i> | rtT RNA; may modulate the stringent response | 2,876 | 0,002258 |
| <i>spf</i> | Spot 42 RNA | 2,912 | 0,02553 |
| <i>sibC</i> | MG1655_rygC_b4446 /SEG=NC_000913:+3054835,3054985 /LEN=150 | 2,922 | 0,005387 |
| --- | intergenic region | 2,924 | 0,000893 |
| --- | intergenic region | 2,986 | 0,000451 |
| <i>sokC</i> | antisense RNA blocking mokC (orf69) and hokC (gef) translation | 3,048 | 0,004546 |
| --- | intergenic region | 3,072 | 0,02752 |
| c3379 | Hypothetical protein | 3,132 | 0,00013 |
| c3248 | Hypothetical protein | 3,167 | 0,000657 |
| <i>cspB</i> | CspB | 3,195 | 0,000204 |
| c1036 | Hypothetical protein | 3,213 | 0,02247 |
| <i>hisL</i> | his operon leader peptide | 3,292 | 0,03259 |
| --- | intergenic region | 3,304 | 0,000678 |
| --- | intergenic region | 3,394 | 0,001563 |
| <i>rdID</i> | antisense RNA, trans-acting regulator of ldrD translation | 3,403 | 0,002742 |

| | | | |
|--------------------|---|--------|----------|
| --- | orf, hypothetical protein | 3,413 | 0,0186 |
| <i>hypE</i> | plays structural role in maturation of all 3 hydrogenases | 3,461 | 0,002141 |
| <i>hisL</i> | his operon leader peptide | 3,480 | 0,01296 |
| --- | intergenic region | 3,640 | 9,71E-03 |
| --- | intergenic region | 4,045 | 0,005444 |
| <i>nirC</i> | nitrite reductase activity | 4,078 | 0,01845 |
| --- | intergenic region | 4,332 | 0,0005 |
| --- | intergenic region | 4,386 | 0,00013 |
| <i>nirD</i> | nitrite reductase (NAD(P)H) subunit | 4,408 | 0,04847 |
| <i>nrfC</i> | formate-dependent nitrite reductase; Fe-S centers | 4,519 | 0,0186 |
| <i>dmsB</i> | anaerobic dimethyl sulfoxide reductase subunit B | 4,592 | 0,0186 |
| --- | intergenic region | 4,665 | 0,0369 |
| <i>dmsC</i> | anaerobic dimethyl sulfoxide reductase subunit C | 4,682 | 0,007196 |
| c2318 | MG1655_IS092_b4434 /SEG=NC_000913:-1985862,1986021 /LEN=159 | 7,579 | 0,01294 |
| <i>cnu // ydgT</i> | orf, hypothetical protein | 13,823 | 1,65E-05 |
| --- | intergenic region | 40,224 | 5,26E-08 |

2. Anàlisi transcriptòmica mutant MG1655H_vs_wt

Taula 2. Gens expressats diferencialment en un mutant *hha* (MG1655H) respecte a la soca salvatge (MG1655) amb un FC>1,5. En diferents intensitats de vermell s'indiquen els gens que es troben induïts respecte a la soca salvatge i en verd els que es troben reprimits.

| Gene.Symbol | Target.Description | FC_H_vs_WT | adj.P.Val |
|-------------|--|------------|-----------|
| <i>yhjX</i> | putative resistance protein | 100,845 | 4,65E-03 |
| <i>ibpB</i> | heat shock protein | 75,322 | 0,001034 |
| --- | intergenic region | 49,591 | 4,10E-05 |
| <i>ibpA</i> | heat shock protein | 47,670 | 0,00148 |
| <i>lldP</i> | L-lactate permease | 22,659 | 0,01401 |
| <i>dppB</i> | dipeptide transport system permease protein 1 | 20,865 | 1,50E-02 |
| <i>astD</i> | putative aldehyde dehydrogenase | 20,280 | 0,002313 |
| <i>astA</i> | Arginine N-succinyltransferase | 19,014 | 0,00207 |
| --- | intergenic region | 17,148 | 1,93E-02 |
| --- | Hypothetical protein | 16,564 | 2,37E-02 |
| <i>yjch</i> | orf, hypothetical protein | 15,519 | 0,005475 |
| <i>dppC</i> | dipeptide transport system permease protein 2 | 15,242 | 1,99E-02 |
| <i>dppD</i> | putative ATP-binding component of dipeptide transport system | 14,182 | 7,02E-02 |
| <i>astB</i> | hypothetical protein | 14,113 | 0,000583 |
| <i>acs</i> | acetyl-CoA synthetase | 12,933 | 0,001142 |
| <i>dppF</i> | putative ATP-binding component of dipeptide transport system | 12,623 | 0,000119 |
| <i>actP</i> | acetate permease | 11,448 | 0,003279 |
| --- | intergenic region | 10,928 | 5,25E-04 |

| | | | |
|---------------------|---|--------|----------|
| <i>ylbH</i> | orf, hypothetical protein | 10,666 | 4,48E-04 |
| <i>astE // ydjS</i> | hypothetical protein | 10,260 | 0,000991 |
| <i>rbsA</i> | ATP-binding component of D-ribose high-affinity transport system | 10,042 | 0,001736 |
| <i>rbsC</i> | D-ribose high-affinity transport system | 9,781 | 0,001387 |
| <i>lldR</i> | transcriptional regulator | 9,324 | 0,006268 |
| <i>paaA</i> | hypothetical protein | 9,318 | 0,005336 |
| <i>alsE</i> | putative epimerase | 9,273 | 4,10E-05 |
| <i>argD // astC</i> | acetylornithine delta-aminotransferase | 9,069 | 0,003002 |
| <i>ykgH</i> | orf, hypothetical protein | 9,051 | 4,95E-03 |
| <i>lysA</i> | diaminopimelate decarboxylase | 8,951 | 0,006869 |
| <i>alsA // yjcW</i> | putative ATP-binding component of a transport system | 8,932 | 2,04E-03 |
| <i>ugpA</i> | sn-glycerol 3-phosphate transport system, integral membrane protein | 8,634 | 0,008154 |
| <i>alsK // yjcT</i> | putative NAGC-like transcriptional regulator | 8,491 | 1,65E-05 |
| <i>ydiF</i> | putative enzyme | 8,134 | 1,60E-03 |
| <i>ariR // ymgB</i> | orf, hypothetical protein | 7,879 | 0,000178 |
| <i>cycA</i> | transport of D-alanine, D-serine, and glycine | 7,760 | 0,001612 |
| --- | intergenic region | 7,744 | 0,000451 |
| <i>yjbl</i> | orf, hypothetical protein | 7,511 | 0,000141 |
| <i>yrhA</i> | orf, hypothetical protein | 7,397 | 7,48E-07 |
| <i>iraM</i> | orf, hypothetical protein | 7,377 | 8,59E-02 |
| <i>alsC // yjcV</i> | putative transport system permease protein | 7,377 | 8,03E-04 |
| <i>paaB</i> | hypothetical protein | 7,377 | 0,002602 |
| <i>ycjX</i> | putative EC 2.1 enzymes | 7,326 | 0,002188 |
| <i>paaD</i> | hypothetical protein | 7,185 | 0,000457 |
| <i>ykgI</i> | orf, hypothetical protein | 7,042 | 5,09E-03 |
| <i>ycjF</i> | orf, hypothetical protein | 6,993 | 0,001351 |
| <i>fxsA</i> | hypothetical protein | 6,779 | 0,001669 |
| --- | intergenic region | 6,765 | 0,000395 |
| <i>ybbC</i> | orf, hypothetical protein | 6,676 | 1,57E-03 |
| <i>ymgC</i> | orf, hypothetical protein | 6,580 | 0,000442 |
| --- | intergenic region | 6,548 | 0,000465 |
| <i>paaC</i> | hypothetical protein | 6,503 | 0,001248 |
| <i>paaE</i> | putative oxidoreductase | 6,400 | 0,000624 |
| <i>ycgZ</i> | orf, hypothetical protein | 6,386 | 0,001527 |
| <i>ykgB</i> | orf, hypothetical protein | 6,360 | 1,52E-03 |
| <i>csgF</i> | curli production assembly transport component, 2nd curli operon | 6,264 | 1,96E-02 |
| <i>mhpR</i> | transcriptional regulator for mhp operon | 6,148 | 0,01476 |
| --- | intergenic region | 6,105 | 5,53E-02 |
| --- | intergenic region | 6,038 | 8,58E-02 |
| <i>paaG</i> | hypothetical protein | 6,029 | 0,000572 |
| <i>paaF</i> | hypothetical protein | 6,025 | 0,000486 |
| ECs0245 // Z0275 | orf, hypothetical protein | 6,000 | 1,03E-03 |
| <i>dppA</i> | dipeptide transport protein | 5,984 | 1,07E-03 |
| <i>yagM</i> | orf, hypothetical protein | 5,877 | 1,57E-03 |

| | | | |
|---------------------|---|-------|----------|
| <i>ymgA</i> | orf, hypothetical protein | 5,744 | 0,0024 |
| --- | intergenic region | 5,591 | 0,01195 |
| <i>livM</i> | high-affinity branched-chain amino acid transport | 5,514 | 0,000595 |
| <i>livK</i> | high-affinity leucine-specific transport system; periplasmic binding protein | 5,498 | 0,00136 |
| <i>ytfI</i> | orf, hypothetical protein | 5,464 | 1,63E-02 |
| <i>alsB // yjcX</i> | putative LACI-type transcriptional regulator | 5,460 | 4,76E-04 |
| <i>hslV</i> | heat shock protein hslVU, proteasome-related peptidase subunit | 5,355 | 0,001527 |
| <i>clpB</i> | heat shock protein | 5,300 | 9,84E-03 |
| <i>ugpE</i> | sn-glycerol 3-phosphate transport system, integral membrane protein | 5,238 | 0,0122 |
| <i>paaH</i> | hypothetical protein | 5,137 | 0,000247 |
| <i>yhaC</i> | orf, hypothetical protein | 5,102 | 2,72E-03 |
| <i>evgS</i> | putative sensor for regulator EvgA | 5,028 | 1,94E-06 |
| <i>ybdO</i> | putative transcriptional regulator LYSR-type | 5,000 | 4,23E-02 |
| <i>fadB</i> | 4-enzyme protein: 3-hydroxyacyl-CoA dehydrogenase; 3-hydroxybutyryl-CoA epimerase; delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase; enoyl-CoA hydratase | 5,000 | 0,03644 |
| <i>ugpC</i> | ATP-binding component of sn-glycerol 3-phosphate transport system | 4,966 | 0,002495 |
| --- | intergenic region | 4,833 | 0,01437 |
| <i>putP</i> | major sodiumproline symporter | 4,783 | 0,02733 |
| --- | intergenic region | 4,734 | 0,01525 |
| <i>rbsR</i> | regulator for rbs operon | 4,691 | 0,000871 |
| <i>lldD</i> | L-lactate dehydrogenase | 4,665 | 0,001248 |
| <i>livH</i> | high-affinity branched-chain amino acid transport system; membrane component | 4,649 | 0,001074 |
| <i>rbsD</i> | D-ribose high-affinity transport system; membrane-associated protein | 4,624 | 0,001221 |
| <i>c5008</i> | Hypothetical protein | 4,585 | 4,54E-02 |
| <i>ybgD</i> | putative fimbrial-like protein | 4,579 | 0,0035 |
| <i>ybeD</i> | orf, hypothetical protein | 4,457 | 0,006309 |
| <i>livG</i> | ATP-binding component of high-affinity branched-chain amino acid transport system | 4,448 | 0,003647 |
| <i>mutM</i> | formamidopyrimidine DNA glycosylase | 4,441 | 0,01061 |
| <i>argT</i> | lysine-, arginine-, ornithine-binding periplasmic protein | 4,438 | 0,02148 |
| <i>hslV</i> | heat shock protein hslVU, proteasome-related peptidase subunit | 4,435 | 0,00315 |
| Z0654 | orf, hypothetical protein | 4,408 | 2,72E-03 |
| <i>aldH // puuC</i> | aldehyde dehydrogenase, prefers NADP over NAD | 4,402 | 3,25E-02 |
| <i>yhiD</i> | putative transport ATPase | 4,368 | 0,000119 |
| <i>paal</i> | hypothetical protein | 4,323 | 0,000258 |
| <i>malM</i> | periplasmic protein of mal regulon | 4,320 | 1,56E-03 |
| <i>fimB</i> | recombinase involved in phase variation; regulator for fimA | 4,287 | 1,52E-03 |
| <i>ydcD</i> | hypothetical protein | 4,263 | 2,63E-02 |
| <i>ybbD</i> | orf, hypothetical protein | 4,225 | 0,000389 |
| <i>aceK</i> | isocitrate dehydrogenase kinasephosphatase | 4,170 | 0,003092 |
| <i>dnaJ</i> | chaperone with DnaK; heat shock protein | 4,167 | 0,001124 |
| --- | intergenic region | 4,135 | 0,04837 |
| <i>malQ</i> | 4-alpha-glucanotransferase (amylomaltase) | 4,093 | 8,72E-03 |
| <i>htpG</i> | chaperone Hsp90, heat shock protein C 62.5 | 4,070 | 7,84E-02 |

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|---------------------|---|-------|----------|
| <i>fadA</i> | thiolase I; 3-ketoacyl-CoA thiolase; acetyl-CoA transferase | 4,067 | 0,00756 |
| <i>hslU</i> | heat shock protein hslVU, ATPase subunit, homologous to chaperones | 3,989 | 0,001239 |
| <i>dsdX</i> | D-serine permease | 3,989 | 4,23E-02 |
| --- | intergenic region | 3,986 | 2,88E-02 |
| <i>livF</i> | ATP-binding component of leucine transport | 3,972 | 0,003972 |
| <i>csgE</i> | curli production assemblytransport component, 2nd curli operon | 3,970 | 2,37E-02 |
| <i>frlA</i> | putative amino acidamine transport protein | 3,923 | 4,51E-02 |
| <i>dadX</i> | alanine racemase 2, catabolic | 3,877 | 0,03772 |
| <i>yibA</i> | orf, hypothetical protein | 3,858 | 0,000206 |
| <i>rpiB</i> | ribose 5-phosphate isomerase B | 3,824 | 1,97E-02 |
| --- | intergenic region | 3,821 | 0,000621 |
| --- | intergenic region | 3,803 | 2,11E-02 |
| <i>yncl</i> | orf, hypothetical protein | 3,803 | 2,35E-02 |
| <i>sstT // ygjU</i> | putative transport protein | 3,797 | 8,58E-02 |
| <i>livJ</i> | LeulleVal-binding protein precursor | 3,735 | 0,000626 |
| <i>dadA</i> | D-amino acid dehydrogenase subunit | 3,719 | 0,0425 |
| <i>yjdA</i> | putative vimentin | 3,706 | 1,03E-03 |
| <i>rbsK</i> | ribokinase | 3,701 | 0,000646 |
| <i>malG</i> | part of maltose permease, inner membrane | 3,699 | 5,17E-02 |
| <i>yibG</i> | orf, hypothetical protein | 3,694 | 0,000199 |
| <i>ygjJ</i> | orf, hypothetical protein | 3,688 | 0,00088 |
| <i>ycgH</i> | putative ATP-binding component of a transport system | 3,671 | 2,35E-02 |
| <i>gadA</i> | glutamate decarboxylase isozyme | 3,663 | 0,000527 |
| <i>dnaK</i> | chaperone Hsp70; DNA biosynthesis; autoregulated heat shock proteins | 3,630 | 0,00057 |
| <i>ycdD</i> | orf; Unknown function | 3,625 | 9,88E-03 |
| <i>ilvA</i> | threonine deaminase (dehydratase) | 3,595 | 2,11E-02 |
| <i>yjfK</i> | putative amino acidamine transport protein | 3,570 | 0,001619 |
| <i>fruA</i> | PTS system, fructose-specific transport protein | 3,528 | 0,00256 |
| <i>chbF</i> | phospho-beta-glucosidase; cryptic | 3,494 | 1,97E-02 |
| <i>ugpB</i> | sn-glycerol 3-phosphate transport system; periplasmic binding protein | 3,480 | 0,02767 |
| <i>yhaB</i> | orf, hypothetical protein | 3,480 | 0,000337 |
| <i>fadE</i> | putative acyl-CoA dehydrogenase | 3,465 | 0,005222 |
| <i>rbsB</i> | D-ribose periplasmic binding protein | 3,453 | 0,000116 |
| <i>paaK</i> | hypothetical protein | 3,413 | 0,00318 |
| <i>yjiR</i> | putative regulator | 3,399 | 0,003092 |
| <i>ydiO</i> | Hypothetical protein ydiO | 3,380 | 5,85E-03 |
| <i>yfjI</i> | orf, hypothetical protein | 3,378 | 1,63E-02 |
| <i>puuB</i> | probable oxidoreductase | 3,364 | 0,000102 |
| <i>yjhl</i> | putative regulator | 3,350 | 0,000121 |
| <i>rhsD</i> | rhsD protein in rhs element | 3,340 | 4,23E-02 |
| <i>yhcA</i> | putative chaperone | 3,333 | 0,000124 |
| <i>hisM</i> | histidine transport, membrane protein M | 3,324 | 0,01424 |
| <i>prlC</i> | oligopeptidase A | 3,320 | 0,001806 |
| <i>betA</i> | choline dehydrogenase, a flavoprotein | 3,294 | 0,000613 |

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|-----------------------------|---|-------|----------|
| --- | orf, hypothetical protein | 3,290 | 0,000978 |
| --- | intergenic region | 3,283 | 8,58E-02 |
| <i>ybeF</i> | putative transcriptional regulator LYSR-type | 3,276 | 0,003603 |
| <i>eutS</i> | hypothetical protein | 3,274 | 0,002659 |
| <i>hslR // yrfH</i> | hypothetical protein | 3,272 | 0,008416 |
| <i>fadJ</i> | putative enzyme | 3,240 | 0,000678 |
| --- | intergenic region | 3,236 | 0,000899 |
| <i>yihP</i> | putative permease | 3,229 | 0,00011 |
| <i>puuA</i> | putative glutamine synthetase | 3,191 | 0,0117 |
| <i>yihQ</i> | putative glycosidase | 3,191 | 4,85E-02 |
| c5097 // ECs5584 | orf; Unknown function | 3,173 | 8,48E-03 |
| <i>yafE</i> | putative biotin synthesis protein | 3,171 | 7,50E-02 |
| <i>csgD</i> | putative 2-component transcriptional regulator for 2nd curli operon | 3,169 | 4,23E-02 |
| --- | intergenic region | 3,169 | 0,007197 |
| <i>gdhA</i> | NADP-specific glutamate dehydrogenase | 3,167 | 5,16E-03 |
| <i>yqiH</i> | putative membrane protein | 3,156 | 0,000415 |
| <i>macB // ybjZ</i> | Hypothetical protein | 3,145 | 0,002449 |
| <i>malF</i> | part of maltose permease, periplasmic | 3,132 | 0,000703 |
| <i>ybfL // ydcC // yhhI</i> | H repeat-associated protein of Rhs element | 3,117 | 0,000167 |
| <i>ddpX</i> | hypothetical protein | 3,108 | 0,03177 |
| <i>yjgL</i> | orf, hypothetical protein | 3,099 | 5,77E-02 |
| --- | intergenic region | 3,063 | 0,000348 |
| <i>ydfK // ynaE</i> | orf, hypothetical protein | 3,046 | 3,13E-02 |
| <i>yjcZ</i> | orf, hypothetical protein | 3,044 | 0,000264 |
| --- | intergenic region | 3,042 | 0,001029 |
| <i>gltJ</i> | glutamateaspartate transport system permease | 3,031 | 0,004709 |
| <i>yedV</i> | putative 2-component sensor protein | 3,025 | 0,000449 |
| <i>agaZ // kbaZ</i> | putative tagatose 6-phosphate kinase 2 | 3,025 | 0,000693 |
| <i>ilvD</i> | dihydroxyacid dehydratase | 3,010 | 4,25E-02 |
| <i>yhiL</i> | orf, hypothetical protein | 2,992 | 0,000105 |
| --- | orf, hypothetical protein | 2,990 | 0,006385 |
| --- | intergenic region | 2,981 | 0,000216 |
| <i>xylE</i> | xylose-proton symport | 2,979 | 1,97E-02 |
| --- | intergenic region | 2,979 | 0,000137 |
| <i>hslO</i> | hypothetical protein | 2,977 | 0,01489 |
| <i>lon</i> | DNA-binding, ATP-dependent protease La; heat shock K-protein | 2,967 | 0,002114 |
| --- | intergenic region | 2,963 | 0,001545 |
| <i>uidC</i> | membrane-associated protein | 2,959 | 0,000156 |
| Z0273 | orf; Unknown function | 2,959 | 0,000143 |
| <i>ydeE // ydeF</i> | putative transport protein | 2,957 | 0,007408 |
| <i>psuK // yeiC</i> | putative kinase | 2,953 | 0,000358 |
| <i>ybfd // yhhI</i> | orf; Unknown function | 2,946 | 0,000106 |
| <i>cmtB</i> | PTS system, mannitol-specific enzyme II component, cryptic | 2,936 | 0,000991 |
| <i>hisP</i> | ATP-binding component of histidine transport | 2,932 | 0,01031 |

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|---------------------|--|-------|----------|
| <i>yibJ</i> | orf, hypothetical protein | 2,910 | 0,001646 |
| <i>gcd</i> | glucose dehydrogenase | 2,904 | 0,002515 |
| <i>yibD</i> | putative regulator | 2,900 | 0,000457 |
| <i>hdeB</i> | orf, hypothetical protein | 2,900 | 0,000106 |
| <i>lldD</i> | L-lactate dehydrogenase | 2,890 | 0,008216 |
| c4973 | Hypothetical protein | 2,890 | 0,001499 |
| <i>ddpB</i> | hypothetical protein | 2,880 | 0,001824 |
| <i>yhiQ</i> | orf, hypothetical protein | 2,868 | 0,0279 |
| <i>aldA</i> | aldehyde dehydrogenase, NAD-linked | 2,846 | 0,03727 |
| --- | intergenic region | 2,844 | 8,55E-02 |
| c5324 | Hypothetical protein | 2,838 | 0,04498 |
| <i>ybbN</i> | putative thioredoxin-like protein | 2,826 | 0,001547 |
| <i>rpiR</i> | transcriptional repressor of <i>rpiB</i> expression | 2,799 | 4,29E-02 |
| --- | intergenic region | 2,786 | 2,96E-02 |
| <i>yqeJ</i> | orf, hypothetical protein | 2,784 | 0,001837 |
| --- | intergenic region | 2,782 | 5,73E-02 |
| <i>eutP</i> | orf, hypothetical protein | 2,778 | 0,000356 |
| <i>yhiI</i> | orf, hypothetical protein | 2,766 | 1,92E-02 |
| c4605 | Hypothetical protein | 2,764 | 0,003006 |
| <i>arpA</i> | Arp | 2,763 | 0,001027 |
| <i>malk</i> | ATP-binding component of transport system for maltose | 2,759 | 0,0017 |
| <i>yiaO</i> | putative solute-binding transport protein | 2,753 | 0,000174 |
| <i>yhhZ</i> | orf, hypothetical protein | 2,751 | 5,48E-02 |
| --- | intergenic region | 2,747 | 3,13E-02 |
| <i>yjhH</i> | putative lyasesynthase | 2,730 | 8,72E-03 |
| <i>lar // ralR</i> | restriction alleviation and modification enhancement | 2,730 | 8,72E-03 |
| --- | intergenic region | 2,730 | 0,000595 |
| <i>ygeO</i> | orf, hypothetical protein | 2,719 | 1,93E-02 |
| <i>ycdU</i> | putative transport system permease protein | 2,717 | 0,001489 |
| <i>uidB</i> | glucuronide permease | 2,706 | 0,00028 |
| <i>lyxK</i> | L-xylulose kinase, cryptic | 2,698 | 3,00E-02 |
| --- | intergenic region | 2,694 | 3,56E-02 |
| --- | intergenic region | 2,693 | 5,77E-02 |
| <i>paaJ</i> | putative acyltransferase | 2,691 | 0,001128 |
| <i>mhpA</i> | 3-(3-hydroxyphenyl)propionate hydroxylase | 2,689 | 0,001554 |
| <i>emrK</i> | multidrug resistance protein K | 2,687 | 0,000122 |
| <i>psuG // yeiN</i> | orf, hypothetical protein | 2,668 | 0,000105 |
| <i>emrY</i> | multidrug resistance protein Y | 2,668 | 7,62E-02 |
| <i>ilvB</i> | acetolactate synthase I, valine-sensitive, large subunit | 2,652 | 0,006076 |
| --- | intergenic region | 2,650 | 0,00108 |
| --- | intergenic region | 2,650 | 0,003958 |
| --- | intergenic region | 2,648 | 0,000194 |
| <i>mcbR</i> | hypothetical protein | 2,641 | 0,000336 |
| --- | intergenic region | 2,641 | 0,0146 |
| <i>casA</i> | orf, hypothetical protein | 2,637 | 2,62E-02 |

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|----------------------|--|-------|----------|
| <i>yccE</i> | orf, hypothetical protein | 2,634 | 5,48E-02 |
| <i>alpA</i> | prophage CP4-57 regulatory protein alpA | 2,630 | 2,35E-02 |
| <i>ybeZ</i> | putative ATP-binding protein in pho regulon | 2,626 | 0,001744 |
| <i>yehA</i> | putative type-1 fimbrial protein | 2,621 | 0,000285 |
| <i>puuE</i> | 4-aminobutyrate aminotransferase | 2,621 | 0,000399 |
| <i>fadI</i> | putative acyltransferase | 2,621 | 0,002032 |
| <i>cspB</i> | CspB | 2,612 | 3,57E-05 |
| <i>groES // groS</i> | GroES, 10 Kd chaperone binds to Hsp60 in pres. Mg-ATP, suppressing its ATPase activity | 2,610 | 0,001773 |
| --- | intergenic region | 2,608 | 0,00818 |
| <i>dsdA</i> | D-serine dehydratase (deaminase) | 2,604 | 1,50E-02 |
| c3233 | Hypothetical protein | 2,601 | 0,008885 |
| <i>ycdT</i> | orf, hypothetical protein | 2,595 | 7,53E-02 |
| <i>ysgA</i> | putative enzyme | 2,578 | 5,31E-02 |
| --- | intergenic region | 2,574 | 0,01567 |
| <i>ygiL</i> | putative fimbrial-like protein | 2,569 | 1,76E-02 |
| --- | intergenic region | 2,554 | 0,000207 |
| <i>yigF</i> | orf, hypothetical protein | 2,544 | 0,000254 |
| <i>hisQ</i> | histidine transport system permease protein | 2,544 | 0,02663 |
| --- | intergenic region | 2,540 | 0,000919 |
| <i>gltP</i> | glutamate-aspartate symport protein | 2,539 | 0,000385 |
| <i>gadB</i> | glutamate decarboxylase isozyme | 2,539 | 0,003395 |
| <i>gltK</i> | glutamateaspartate transport system permease | 2,528 | 0,002558 |
| <i>ddpA</i> | putative hemin-binding lipoprotein | 2,523 | 0,017 |
| <i>yigG</i> | orf, hypothetical protein | 2,521 | 0,001563 |
| --- | intergenic region | 2,519 | 0,02448 |
| <i>yhaM</i> | orf, hypothetical protein | 2,511 | 0,000537 |
| <i>ilvE</i> | branched-chain amino-acid aminotransferase | 2,509 | 0,000162 |
| <i>yhdN</i> | orf, hypothetical protein | 2,509 | 0,004049 |
| <i>ygjK</i> | putative isomerase | 2,498 | 0,00028 |
| --- | intergenic region | 2,493 | 0,003227 |
| <i>yghG</i> | orf, hypothetical protein | 2,486 | 0,0378 |
| <i>ilvN</i> | acetolactate synthase I, valine sensitive, small subunit | 2,485 | 0,01213 |
| <i>sthA // udhA</i> | putative oxidoreductase | 2,485 | 0,02064 |
| c3234 // ECs3543 | orf, hypothetical protein | 2,483 | 0,005121 |
| <i>yhaM</i> | orf, hypothetical protein | 2,483 | 0,001333 |
| <i>yjhG</i> | putative dehydratase | 2,481 | 6,51E-02 |
| <i>betB</i> | NAD ⁺ -dependent betaine aldehyde dehydrogenase | 2,481 | 0,01198 |
| <i>zntR</i> | putative transcriptional regulator | 2,479 | 0,003789 |
| <i>lsrR // ydeW</i> | putative transcriptional regulator, sorC family | 2,478 | 0,000194 |
| <i>ybcK</i> | orf, hypothetical protein | 2,474 | 0,000207 |
| <i>lsrB</i> | putative LACI-type transcriptional regulator | 2,471 | 2,25E-02 |
| <i>gspC // yheE</i> | YheE | 2,464 | 0,001027 |
| <i>trpA</i> | tryptophan synthase, alpha protein | 2,462 | 7,02E-02 |
| <i>eutQ</i> | orf, hypothetical protein | 2,462 | 0,000347 |

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|----------------------|--|-------|----------|
| <i>maoC</i> | putative aldehyde dehydrogenase | 2,459 | 0,001027 |
| --- | intergenic region | 2,457 | 9,75E-02 |
| <i>yhhH</i> | orf, hypothetical protein | 2,455 | 0,000127 |
| --- | intergenic region | 2,454 | 5,53E-02 |
| <i>agaV</i> | PTS system, cytoplasmic, N-acetylgalactosamine-specific IIB component 2 (EIIB-AGA) | 2,454 | 0,000457 |
| <i>eutD</i> | ethanolamine utilization; homolog of Salmonella acetylbutyryl P transferase | 2,450 | 0,000157 |
| <i>trpB</i> | tryptophan synthase, beta protein | 2,449 | 0,000118 |
| <i>ybeY</i> | orf, hypothetical protein | 2,449 | 0,001928 |
| c5129 | Hypothetical protein | 2,445 | 0,01145 |
| <i>prlC</i> | Oligopeptidase A | 2,444 | 0,0106 |
| <i>ydfD</i> | orf, hypothetical protein | 2,440 | 0,004485 |
| <i>groEL // groL</i> | GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock protein | 2,405 | 0,001124 |
| <i>insK</i> | IS150 putative transposase | 2,403 | 0,000178 |
| <i>ydeJ</i> | orf, hypothetical protein | 2,400 | 0,001362 |
| --- | intergenic region | 2,392 | 0,001248 |
| <i>yjfl</i> | orf, hypothetical protein | 2,390 | 2,88E-02 |
| <i>casB</i> | orf, hypothetical protein | 2,388 | 1,56E-02 |
| <i>hdeD</i> | orf, hypothetical protein | 2,375 | 0,007867 |
| <i>rlmE // rrmJ</i> | cell division protein | 2,375 | 0,002858 |
| <i>lsrA</i> | putative ATP-binding component of a transport system | 2,373 | 9,43E-02 |
| --- | intergenic region | 2,360 | 0,000295 |
| --- | intergenic region | 2,357 | 0,002611 |
| <i>cspG</i> | homolog of Salmonella cold shock protein | 2,346 | 0,000283 |
| --- | intergenic region | 2,334 | 0,000192 |
| <i>ydaC</i> | orf, hypothetical protein | 2,328 | 5,17E-02 |
| <i>ptsG</i> | PTS system, glucose-specific IIBC component | 2,328 | 0,00067 |
| <i>ycdT</i> | putative ATP-binding component of a transport system | 2,320 | 0,01073 |
| <i>fumC</i> | fumarase C= fumarate hydratase Class II; isozyme | 2,315 | 0,009963 |
| --- | intergenic region | 2,309 | 0,000194 |
| <i>dctR // yhiF</i> | orf, hypothetical protein | 2,307 | 0,000451 |
| <i>acnA</i> | aconitate hydratase 1 | 2,305 | 0,00046 |
| <i>oppB</i> | oligopeptide transport permease protein | 2,305 | 3,54E-02 |
| <i>yiiE</i> | orf, hypothetical protein | 2,302 | 0,001618 |
| --- | intergenic region | 2,299 | 0,01524 |
| <i>evgA</i> | putative positive transcription regulator (sensor EvgS) | 2,296 | 0,000106 |
| <i>yadM</i> | putative fimbrial-like protein | 2,293 | 2,44E-02 |
| <i>yqeH</i> | orf, hypothetical protein | 2,293 | 0,001037 |
| --- | hypothetical protein | 2,293 | 0,000222 |
| <i>frlD</i> | orf, hypothetical protein | 2,283 | 0,000389 |
| <i>aceB</i> | malate synthase A | 2,282 | 0,0226 |
| <i>yqcE</i> | putative transport protein | 2,274 | 0,006154 |
| --- | intergenic region | 2,270 | 0,01587 |
| <i>ugpQ</i> | glycerophosphodiester phosphodiesterase, cytosolic | 2,266 | 0,00112 |
| <i>yjeJ</i> | orf, hypothetical protein | 2,264 | 0,000294 |

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|---------------------|--|-------|----------|
| --- | intergenic region | 2,263 | 0,001162 |
| <i>malP</i> | Maltodextrin phosphorylase | 2,261 | 0,001297 |
| --- | intergenic region | 2,256 | 8,58E-02 |
| <i>yafD</i> | orf, hypothetical protein | 2,250 | 6,86E-02 |
| <i>celB // chbC</i> | PTS system, cellobiose-specific IIC component | 2,249 | 0,001406 |
| <i>gltI // ybeJ</i> | putative periplasmic binding transport protein | 2,247 | 0,002602 |
| <i>lhgO</i> | orf, hypothetical protein | 2,247 | 0,002515 |
| --- | intergenic region | 2,245 | 0,002858 |
| <i>yihT</i> | putative aldolase | 2,244 | 0,000199 |
| <i>ompL</i> | orf, hypothetical protein | 2,242 | 0,003592 |
| --- | orf, hypothetical protein | 2,241 | 0,002616 |
| <i>hdeA</i> | orf, hypothetical protein | 2,239 | 0,000595 |
| <i>yfjH</i> | putative histone | 2,238 | 3,07E-02 |
| <i>yihU</i> | putative dehydrogenase | 2,238 | 5,53E-02 |
| <i>ycdV</i> | Hypothetical ABC transporter permease protein ycdV | 2,230 | 0,000236 |
| <i>yadC</i> | putative fimbrial-like protein | 2,230 | 0,000226 |
| <i>uidC</i> | orf; Unknown function | 2,228 | 0,001049 |
| --- | intergenic region | 2,227 | 0,001353 |
| <i>elaD</i> | putative sulfatase phosphatase | 2,219 | 0,000365 |
| <i>tauA</i> | taurine transport system periplasmic protein | 2,218 | 0,000161 |
| <i>intR</i> | putative transposase | 2,216 | 0,003043 |
| <i>ilvM</i> | acetolactate synthase II, valine insensitive, small subunit | 2,215 | 0,000869 |
| <i>lldP</i> | L-lactate permease | 2,215 | 0,0267 |
| <i>ybfB</i> | orf, hypothetical protein | 2,204 | 0,001353 |
| <i>aceA</i> | isocitrate lyase | 2,201 | 0,000594 |
| <i>yrfF</i> | putative dehydrogenase | 2,199 | 0,02005 |
| <i>dicC</i> | regulator of dicB | 2,192 | 0,002442 |
| <i>ygbK</i> | orf, hypothetical protein | 2,190 | 0,000112 |
| ECs5442 | partial H repeat-associated protein of Rhs element | 2,190 | 0,002378 |
| --- | intergenic region | 2,187 | 0,001382 |
| <i>friC</i> | orf, hypothetical protein | 2,187 | 0,000224 |
| <i>yhfZ</i> | orf, hypothetical protein | 2,176 | 0,04273 |
| <i>yihS</i> | orf, hypothetical protein | 2,175 | 0,000326 |
| <i>betI</i> | probably transcriptional repressor of bet genes | 2,172 | 0,04496 |
| <i>mepA</i> | murein DD-endopeptidase, penicillin-insensitive | 2,172 | 0,001322 |
| <i>kgtP</i> | alpha-ketoglutarate permease | 2,172 | 0,0211 |
| <i>yagE</i> | putative lyasesynthase | 2,169 | 3,08E-02 |
| <i>kdul</i> | homolog of pectin degrading enzyme 5-keto 4-deoxyuronate isomerase | 2,164 | 0,003034 |
| <i>grpE</i> | phage lambda replication; host DNA synthesis; heat shock protein; protein repair | 2,161 | 0,002882 |
| <i>yihR</i> | putative aldose-1-epimerase (EC 5.1.3.3) | 2,161 | 0,000265 |
| <i>ygbJ</i> | putative dehydrogenase | 2,155 | 0,000216 |
| <i>yagL</i> | DNA-binding protein | 2,154 | 0,000178 |
| <i>yihF</i> | putative GTP-binding protein | 2,154 | 0,001049 |
| <i>ilvG</i> | acetolactate synthase II, valine insensitive, large subunit, silent in K-12 | 2,152 | 0,000429 |

| | | | |
|---------------------|--|-------|----------|
| <i>insJ</i> | IS150 hypothetical protein | 2,147 | 0,000218 |
| <i>cstA</i> | carbon starvation protein | 2,145 | 0,003128 |
| <i>kbaY</i> | tagatose-bisphosphate aldolase 2 | 2,144 | 0,001294 |
| --- | intergenic region | 2,144 | 0,002222 |
| --- | intergenic region | 2,142 | 0,004933 |
| <i>menA</i> | 1,4-dihydroxy-2-naphthoate --> dimethylmenaquinone | 2,136 | 0,01864 |
| <i>yliE</i> | orf, hypothetical protein | 2,136 | 0,02043 |
| <i>yggP</i> | orf, hypothetical protein | 2,133 | 0,000178 |
| <i>yjhF</i> | putative transport system permease | 2,132 | 0,000282 |
| <i>friD</i> | kinase (ribokinase family) | 2,130 | 0,000561 |
| <i>yadK</i> | putative fimbrial protein | 2,127 | 0,000117 |
| <i>ynjI</i> | orf; Unknown function | 2,127 | 0,000855 |
| <i>yjiT</i> | orf, hypothetical protein | 2,120 | 0,000116 |
| <i>yceO</i> | orf, hypothetical protein | 2,117 | 0,000494 |
| <i>yagF</i> | putative dehydratase | 2,116 | 0,000337 |
| <i>yjeM</i> | putative transport | 2,116 | 0,004943 |
| --- | intergenic region | 2,114 | 0,000174 |
| <i>uidA</i> | partial beta-D-glucuronidase | 2,111 | 2,35E-02 |
| <i>mlc</i> | putative NAGC-like transcriptional regulator | 2,111 | 0,000431 |
| <i>idnD</i> | L-idonate dehydrogenase | 2,111 | 0,004501 |
| <i>nfuA // yhgl</i> | orf, hypothetical protein | 2,108 | 0,01986 |
| <i>agaW</i> | PTS system N-acetylgalactosamine-specific IIC component 2 | 2,108 | 0,000483 |
| <i>ygaY</i> | putative transport protein | 2,107 | 0,00426 |
| <i>hcaB</i> | 2,3-dihydroxy-2,3-dihydrophenylpropionate dehydrogenase | 2,107 | 0,001547 |
| <i>gltL</i> | ATP-binding protein of glutamateaspartate transport system | 2,098 | 0,00044 |
| --- | intergenic region | 2,097 | 0,0133 |
| <i>lacA</i> | thiogalactoside acetyltransferase | 2,094 | 0,000192 |
| <i>fimZ</i> | fimbrial Z protein; probable signal transducer | 2,088 | 0,001234 |
| <i>ycgF</i> | orf, hypothetical protein | 2,086 | 0,00987 |
| <i>yfcl</i> | orf, hypothetical protein | 2,086 | 0,002747 |
| <i>casC</i> | orf, hypothetical protein | 2,079 | 4,23E-02 |
| <i>lldR</i> | Putative L-lactate dehydrogenase operon Regulatory protein | 2,076 | 0,01951 |
| <i>trpC</i> | N-(5-phosphoribosyl)anthranilate isomerase and indole-3-glycerolphosphate synthetase | 2,075 | 0,001026 |
| <i>gabT</i> | 4-aminobutyrate aminotransferase activity | 2,071 | 0,000167 |
| <i>ycgX</i> | orf, hypothetical protein | 2,068 | 0,00315 |
| <i>eutT</i> | orf, hypothetical protein | 2,068 | 0,000446 |
| <i>ydjJ</i> | putative oxidoreductase | 2,066 | 0,000218 |
| <i>uxuA</i> | mannonate hydrolase | 2,065 | 0,000399 |
| --- | intergenic region | 2,058 | 0,001122 |
| c4168 | Hypothetical protein | 2,049 | 0,03025 |
| <i>yjeN</i> | orf, hypothetical protein | 2,049 | 0,005905 |
| <i>malK</i> | Maltosemaltodextrin transport ATP-binding protein malK | 2,045 | 0,006102 |
| <i>oppC</i> | homolog of Salmonella oligopeptide transport permease protein | 2,045 | 0,000105 |
| <i>ycdS</i> | putative transport protein | 2,042 | 0,03543 |
| <i>trpE</i> | anthranilate synthase component I | 2,041 | 0,000415 |

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|----------------------|---|-------|----------|
| <i>ebgA</i> | evolved beta-D-galactosidase, alpha subunit; cryptic gene | 2,041 | 0,002955 |
| <i>yqiG</i> | putative membrane protein | 2,039 | 0,002154 |
| <i>yhfY</i> | orf, hypothetical protein | 2,038 | 0,01132 |
| <i>friC</i> | orf, hypothetical protein | 2,036 | 0,001547 |
| <i>c3835</i> | Hypothetical protein | 2,035 | 0,02987 |
| <i>fimE</i> | recombinase involved in phase variation; regulator for fimA | 2,031 | 0,000839 |
| <i>yciE</i> | orf, hypothetical protein | 2,028 | 4,51E-02 |
| <i>rhsB</i> | rhsB protein in rhs element | 2,028 | 0,002412 |
| <i>yfdF</i> | orf, hypothetical protein | 2,027 | 0,000263 |
| <i>lamB</i> | phage lambda receptor protein; maltose high-affinity receptor | 2,025 | 4,51E-02 |
| <i>ydjI</i> | putative aldolase | 2,021 | 6,31E-02 |
| <i>murP</i> | putative PTS enzyme II | 2,014 | 0,007787 |
| --- | intergenic region | 2,014 | 0,01024 |
| --- | intergenic region | 2,014 | 0,001652 |
| <i>yjfJ</i> | putative alpha helical protein | 2,013 | 0,001194 |
| <i>hcaA2 // hcaF</i> | small terminal subunit of phenylpropionate dioxygenase | 2,013 | 0,003728 |
| <i>ynaK</i> | orf, hypothetical protein | 2,013 | 0,000404 |
| <i>yhbW</i> | putative enzyme | 2,008 | 0,000486 |
| <i>aroM</i> | protein of aro operon, regulated by aroR | 2,006 | 0,003831 |
| <i>mltA</i> | Membrane-bound lytic murein transglycosylase A precursor | 2,004 | 0,000604 |
| <i>agaC</i> | PTS system N-acetylgalactosamine-specific IIC component 1 | 2,004 | 0,000453 |
| <i>yhiS</i> | orf, hypothetical protein | 2,004 | 0,01715 |
| --- | intergenic region | 2,000 | 0,002101 |
| <i>yael</i> | orf, hypothetical protein | 2,000 | 0,000219 |
| <i>yqel</i> | putative sensory transducer | 1,999 | 0,02828 |
| <i>ydjE</i> | putative transport protein | 1,984 | 0,000595 |
| <i>lhgO // ygaF</i> | Hypothetical protein ygaF | 1,980 | 0,003604 |
| <i>ydjH</i> | putative kinase | 1,977 | 0,000415 |
| <i>ycjM</i> | orf, hypothetical protein | 1,976 | 0,000386 |
| <i>mhpF</i> | acetaldehyde dehydrogenase | 1,976 | 0,000606 |
| <i>yafP</i> | orf, hypothetical protein | 1,976 | 0,000756 |
| <i>ydaY</i> | orf, hypothetical protein | 1,975 | 0,001444 |
| <i>tomB // ybaJ</i> | orf, hypothetical protein | 1,973 | 7,50E-02 |
| --- | orf, hypothetical protein | 1,968 | 0,000264 |
| <i>torY // yecK</i> | putative cytochrome C-type protein | 1,967 | 4,90E-02 |
| --- | intergenic region | 1,966 | 0,000389 |
| <i>ytfQ</i> | putative LACI-type transcriptional regulator | 1,965 | 0,005236 |
| <i>malE</i> | periplasmic maltose-binding protein; substrate recognition for transport and chemotaxis | 1,965 | 8,58E-02 |
| <i>yjgJ /</i> | orf, hypothetical protein | 1,961 | 0,004166 |
| <i>ybeX</i> | putative transport protein | 1,961 | 0,03842 |
| <i>idnO</i> | 5-keto-D-gluconate 5-reductase | 1,961 | 0,003855 |
| <i>ydjO</i> | orf, hypothetical protein | 1,958 | 0,00349 |
| <i>ygeN /</i> | orf, hypothetical protein | 1,958 | 0,014 |
| <i>yiaR</i> | putative 3-hexulose-6-phosphate isomerase | 1,957 | 0,000207 |
| <i>fadh // ygjL</i> | putative NADPH dehydrogenase | 1,956 | 0,01512 |

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|---------------------|---|-------|----------|
| <i>yfcV</i> | putative fimbrial-like protein | 1,955 | 0,002191 |
| --- | intergenic region | 1,955 | 0,002789 |
| --- | intergenic region | 1,952 | 0,001049 |
| <i>agaB</i> | PTS system, cytoplasmic, N-acetylgalactosamine-specific IIB component 1 (EII _B -AGA) | 1,952 | 0,000415 |
| <i>glpG</i> | protein of <i>glp</i> regulon | 1,952 | 0,0405 |
| <i>yihM</i> | orf, hypothetical protein | 1,951 | 0,000367 |
| <i>ygjH</i> | putative tRNA synthetase | 1,948 | 0,000478 |
| <i>mltC</i> | membrane-bound lytic murein transglycosylase C | 1,946 | 0,01015 |
| <i>idnT</i> | L-idonate transporter | 1,944 | 0,004974 |
| --- | intergenic region | 1,943 | 0,02276 |
| <i>proV</i> | ATP-binding component of transport system for glycine, betaine and proline | 1,941 | 0,007197 |
| --- | intergenic region | 1,937 | 0,004991 |
| <i>ycjM</i> | putative polysaccharide hydrolase | 1,937 | 0,000527 |
| <i>aroP</i> | aromatic amino acid transport protein | 1,932 | 0,004071 |
| <i>yffJ</i> | orf, hypothetical protein | 1,930 | 0,002996 |
| <i>yjgJ</i> | orf, hypothetical protein | 1,926 | 0,007806 |
| --- | intergenic region | 1,925 | 0,00029 |
| <i>yrhB</i> | orf, hypothetical protein | 1,919 | 0,002062 |
| <i>ydaG</i> | orf, hypothetical protein | 1,918 | 0,000931 |
| <i>ddpD</i> | putative ATP-binding component of a transport system | 1,917 | 0,003402 |
| <i>topA</i> | DNA topoisomerase type I, omega protein | 1,915 | 0,02189 |
| ECs3713 // Z4178 | orf, hypothetical protein | 1,913 | 0,003239 |
| <i>yhjC</i> | putative transcriptional regulator LYSR-type | 1,913 | 0,01114 |
| <i>cytR</i> | regulator for <i>deo</i> operon, <i>udp</i> , <i>cdd</i> , <i>tsx</i> , <i>nupC</i> , and <i>nupG</i> | 1,912 | 0,003099 |
| --- | intergenic region | 1,911 | 0,01536 |
| <i>yafT</i> | putative aminopeptidase | 1,906 | 0,008216 |
| <i>yjfK</i> | orf, hypothetical protein | 1,906 | 0,001527 |
| --- | intergenic region | 1,905 | 0,000465 |
| <i>ygbL</i> | putative epimerasealdolase | 1,903 | 0,000798 |
| --- | intergenic region | 1,898 | 0,003649 |
| <i>mhpD</i> | 2-keto-4-pentenoate hydratase | 1,898 | 0,008715 |
| --- | intergenic region | 1,897 | 0,001802 |
| <i>csgG</i> | curli production assemblytransport component, 2nd curli operon | 1,896 | 0,000184 |
| <i>yhaO</i> | putative transport system permease protein | 1,896 | 0,000815 |
| <i>ygjI</i> | putative oxidoreductase | 1,895 | 0,000594 |
| <i>gltA</i> | citrate synthase | 1,888 | 0,003649 |
| <i>yjcF</i> | orf, hypothetical protein | 1,887 | 0,01715 |
| <i>tnaB</i> | low affinity tryptophan permease | 1,886 | 0,002113 |
| <i>ycjX</i> | Hypothetical protein <i>ycjX</i> | 1,885 | 0,04792 |
| --- | intergenic region | 1,883 | 0,0032 |
| <i>ftsN</i> | essential cell division protein | 1,883 | 0,002311 |
| <i>aroE // ydiB</i> | putative oxidoreductase | 1,882 | 0,001046 |
| <i>yjiV</i> | orf, hypothetical protein | 1,882 | 0,000248 |
| <i>ycdR</i> | orf, hypothetical protein | 1,882 | 0,000207 |

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|-------------------------------------|---|-------|----------|
| <i>gabD</i> | succinate-semialdehyde dehydrogenase, NADP-dependent activity | 1,881 | 0,000693 |
| <i>dsdC</i> | D-serine dehydratase (deaminase) transcriptional activator | 1,880 | 0,00106 |
| <i>ivbL</i> | ilvB operon leader peptide | 1,877 | 0,01609 |
| <i>intK</i> | orf, hypothetical protein | 1,877 | 0,004695 |
| <i>arnC</i> | putative sugar transferase | 1,876 | 0,000281 |
| <i>hscC // ybeW</i> | DnaK-like protein | 1,874 | 0,001058 |
| <i>yiaL</i> | putative lipase | 1,874 | 0,003572 |
| <i>hcaA1 // hcaE</i> | large terminal subunit of phenylpropionate dioxygenase | 1,874 | 0,0017 |
| --- | intergenic region | 1,873 | 0,001055 |
| c1752 | Hypothetical protein | 1,873 | 0,01193 |
| --- | intergenic region | 1,872 | 0,002853 |
| <i>ydjL</i> | putative oxidoreductase | 1,872 | 0,000473 |
| <i>idnR</i> | L-idonate transcriptional regulator | 1,870 | 0,000493 |
| <i>rhsE</i> | RhsE | 1,870 | 0,000561 |
| <i>yciT /</i> | putative DEOR-type transcriptional regulator | 1,866 | 0,000457 |
| <i>hflX</i> | GTP - binding subunit of protease specific for phage lambda cII repressor | 1,865 | 0,001412 |
| <i>trpE</i> | anthranilate synthase component I (EC 4.1.3.27) | 1,864 | 0,000471 |
| <i>yfeW</i> | putative beta-lactamase | 1,863 | 0,008432 |
| <i>yjhB</i> | putative transport protein | 1,862 | 0,001142 |
| --- | intergenic region | 1,858 | 0,008815 |
| <i>ebgC</i> | evolved beta-D-galactosidase, beta subunit; cryptic gene | 1,858 | 0,003665 |
| ECs075079 | orf, hypothetical protein | 1,854 | 0,00681 |
| <i>yjjJ</i> | orf, hypothetical protein | 1,850 | 0,002033 |
| --- | intergenic region | 1,849 | 0,000814 |
| <i>yjiH</i> | orf, hypothetical protein | 1,849 | 0,001716 |
| <i>uxuB</i> | D-mannonate oxidoreductase | 1,847 | 0,001162 |
| <i>leuB</i> | 3-isopropylmalate dehydrogenase | 1,847 | 0,000502 |
| <i>leuC</i> | 3-isopropylmalate isomerase (dehydratase) subunit | 1,846 | 0,000216 |
| <i>gspE // yheG</i> | YheG | 1,844 | 0,009832 |
| <i>yjgJ</i> | hypothetical protein | 1,843 | 0,0021 |
| <i>yagH</i> | putative beta-xylosidase (EC 3.2.1.37) | 1,842 | 0,000988 |
| <i>yafO</i> | orf, hypothetical protein | 1,841 | 0,000451 |
| --- | intergenic region | 1,840 | 0,000217 |
| <i>kduD</i> | 2-deoxy-D-gluconate 3-dehydrogenase | 1,839 | 0,0049 |
| <i>ulaA</i> | hypothetical protein | 1,839 | 0,006222 |
| <i>oppA</i> | oligopeptide transport; periplasmic binding protein | 1,839 | 3,00E-02 |
| <i>lsrF // yneB</i> | putative aldolase | 1,838 | 0,000253 |
| --- | intergenic region | 1,835 | 0,000248 |
| c2681 | Hypothetical protein | 1,835 | 0,02011 |
| <i>yafF // ybfl // ydcC // yhhI</i> | H repeat-associated protein (ORF-H) | 1,828 | 0,000389 |
| --- | intergenic region | 1,828 | 0,0035 |
| <i>pheA</i> | chorismate mutase-P and prephenate dehydratase | 1,827 | 0,005519 |
| <i>brnQ</i> | branched chain amino acid transport system II carrier protein | 1,826 | 0,000457 |
| <i>yeiS</i> | orf, hypothetical protein | 1,825 | 0,000383 |

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|----------------------------|---|-------|----------|
| <i>lsrG</i> / | orf, hypothetical protein | 1,824 | 6,51E-02 |
| <i>gatR</i> | split galactitol utilization operon repressor, interrupted | 1,823 | 0,000924 |
| <i>yjaH</i> | orf, hypothetical protein | 1,823 | 0,005057 |
| <i>celD</i> // <i>chbR</i> | negative transcriptional regulator of cel operon | 1,822 | 0,002321 |
| <i>yeiR</i> | orf, hypothetical protein | 1,822 | 0,008617 |
| <i>yagG</i> | putative permease | 1,822 | 0,000621 |
| <i>yebB</i> | orf, hypothetical protein | 1,821 | 0,003454 |
| --- | intergenic region | 1,821 | 0,004468 |
| <i>holC</i> | DNA polymerase III, chi subunit | 1,820 | 0,008244 |
| --- | intergenic region | 1,819 | 0,003838 |
| <i>mcrC</i> | component of McrBC 5-methylcytosine restriction system, expands range of sequences restricted | 1,817 | 0,001058 |
| <i>gabP</i> | transport permease protein of gamma-aminobutyrate | 1,816 | 0,00182 |
| <i>nei</i> | endonuclease VIII and DNA N-glycosylase with an AP lyase activity | 1,813 | 0,002763 |
| <i>ycjT</i> | orf, hypothetical protein | 1,810 | 0,001772 |
| --- | orf, hypothetical protein | 1,808 | 0,006523 |
| <i>malQ</i> | 4-alpha-glucanotransferase | 1,806 | 0,004001 |
| <i>yheL</i> | orf, hypothetical protein | 1,806 | 0,0279 |
| --- | intergenic region | 1,806 | 0,006109 |
| <i>yqhG</i> | orf; Unknown function | 1,803 | 0,003742 |
| <i>miaA</i> | delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase | 1,802 | 0,004501 |
| <i>bssS</i> | orf, hypothetical protein | 1,800 | 0,0192 |
| <i>rhaD</i> | rhamnulose-phosphate aldolase | 1,800 | 0,000745 |
| <i>arpB</i> | ankyrin repeat protein | 1,800 | 0,006993 |
| <i>casD</i> | orf, hypothetical protein | 1,800 | 0,001676 |
| <i>yafU</i> | orf, hypothetical protein | 1,800 | 0,001964 |
| <i>cysE</i> | serine acetyltransferase | 1,799 | 0,003114 |
| <i>yeaX</i> | putative diogenase beta subunit | 1,798 | 0,000919 |
| <i>yjfM</i> | Hypothetical protein yjfM | 1,796 | 0,001369 |
| ECs3736 | orf, hypothetical protein | 1,792 | 0,001224 |
| <i>yghS</i> | orf, hypothetical protein | 1,791 | 0,000814 |
| <i>avtA</i> | alanine-alpha-ketoisovalerate (or valine-pyruvate) transaminase, transaminase C | 1,790 | 0,03756 |
| <i>yaaY</i> | orf, hypothetical protein | 1,787 | 0,03228 |
| --- | intergenic region | 1,783 | 0,000839 |
| <i>proW</i> | high-affinity transport system for glycine betaine and proline | 1,782 | 0,01317 |
| <i>yggF</i> | orf, hypothetical protein | 1,780 | 0,000486 |
| <i>ygcG</i> | orf, hypothetical protein | 1,780 | 0,001128 |
| <i>dgoT</i> | D-galactonate transport | 1,773 | 0,000988 |
| <i>intZ</i> | putative prophage integrase | 1,773 | 0,002949 |
| <i>ebgA</i> | evolved beta-D-galactosidase, alpha subunit; cryptic gene | 1,772 | 0,007699 |
| <i>hspQ</i> // <i>yccV</i> | orf, hypothetical protein | 1,771 | 0,01712 |
| <i>pgaC</i> // <i>ycdQ</i> | orf, hypothetical protein | 1,771 | 0,000443 |
| <i>rhaM</i> // <i>yiiL</i> | Hypothetical protein yiiL | 1,769 | 0,003047 |
| <i>celF</i> // <i>chbF</i> | phospho-beta-glucosidase; cryptic | 1,768 | 0,002002 |
| <i>yagN</i> | orf, hypothetical protein | 1,766 | 0,001351 |

| | | | |
|---------------------|--|-------|----------|
| <i>yjfZ</i> | orf, hypothetical protein | 1,766 | 0,000514 |
| <i>clpX</i> | ATP-dependent specificity component of clpP serine protease, chaperone | 1,765 | 0,000395 |
| <i>ygeH</i> | putative invasion protein | 1,762 | 0,00623 |
| <i>yheV</i> | orf; Unknown function | 1,761 | 0,002946 |
| <i>fdoH</i> | formate dehydrogenase-O, iron-sulfur subunit | 1,760 | 0,000863 |
| <i>ytfT</i> | putative transport system permease protein | 1,757 | 0,00182 |
| --- | orf, hypothetical protein | 1,755 | 0,000108 |
| <i>xdhA</i> | hypothetical protein | 1,754 | 0,000244 |
| <i>yiaK</i> | putative dehydrogenase | 1,752 | 0,009446 |
| <i>ycjN</i> | putative transport periplasmic protein | 1,749 | 0,000815 |
| <i>murR</i> | orf, hypothetical protein | 1,745 | 0,003398 |
| --- | orf, hypothetical protein | 1,745 | 0,01203 |
| <i>ycdJ</i> | orf; Unknown function | 1,744 | 0,02268 |
| --- | intergenic region | 1,741 | 0,003383 |
| <i>ybfM</i> | orf, hypothetical protein | 1,740 | 0,005542 |
| --- | intergenic region | 1,734 | 0,02785 |
| <i>dicB</i> | inhibition of cell division | 1,729 | 0,01208 |
| <i>yeaW</i> | orf, hypothetical protein | 1,726 | 0,000479 |
| <i>ygiM</i> | orf, hypothetical protein | 1,725 | 0,006792 |
| <i>yahB</i> | orf; Unknown function | 1,722 | 0,009351 |
| <i>ygbM</i> | orf, hypothetical protein | 1,721 | 0,001162 |
| <i>sucA</i> | 2-oxoglutarate dehydrogenase (decarboxylase component) | 1,719 | 0,001772 |
| c1838 | Hypothetical protein | 1,718 | 0,02064 |
| <i>modF</i> | ATP-binding component of molybdate transport system | 1,717 | 0,01448 |
| --- | intergenic region | 1,716 | 0,01744 |
| <i>xdhD</i> | putative dehydrogenase | 1,715 | 0,003095 |
| <i>bdm</i> | hypothetical protein | 1,710 | 0,000389 |
| <i>htrE</i> | probable outer membrane porin protein involved in fimbrial assembly | 1,708 | 0,003034 |
| <i>ybbO</i> | putative oxidoreductase | 1,707 | 0,000506 |
| <i>ycjN</i> | Putative ABC transporter Periplasmic binding protein <i>ycjN</i> precursor | 1,705 | 0,002236 |
| <i>asnB</i> | asparagine synthetase B | 1,705 | 0,001162 |
| <i>rdoA // yihE</i> | orf, hypothetical protein | 1,705 | 0,01057 |
| <i>yjfL</i> | Hypothetical protein | 1,704 | 0,004166 |
| <i>yjdI</i> | orf, hypothetical protein | 1,703 | 0,02623 |
| <i>yadL</i> | putative fimbrial protein | 1,699 | 0,000319 |
| --- | intergenic region | 1,696 | 0,005121 |
| --- | intergenic region | 1,695 | 0,02608 |
| --- | intergenic region | 1,694 | 0,01233 |
| --- | intergenic region | 1,694 | 0,006176 |
| <i>yhdL</i> | Putative regulator | 1,693 | 0,01636 |
| <i>ykiA</i> | orf, hypothetical protein | 1,690 | 0,002336 |
| <i>yiaS</i> | putative epimerasealdolase | 1,690 | 0,000766 |
| --- | intergenic region | 1,690 | 0,002341 |
| <i>dnaA</i> | DNA biosynthesis; initiation of chromosome replication; can be transcription regulator | 1,689 | 0,0119 |

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|---------------------|---|-------|----------|
| --- | intergenic region | 1,689 | 0,004695 |
| <i>yfgH</i> | putative outer membrane lipoprotein | 1,688 | 0,02875 |
| <i>arnB // yfbE</i> | putative enzyme | 1,688 | 0,001937 |
| <i>recC</i> | DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ssDNA endonuclease | 1,687 | 0,001124 |
| <i>ftsI</i> | septum formation; penicillin-binding protein 3; peptidoglycan synthetase | 1,686 | 0,000322 |
| --- | intergenic region | 1,685 | 0,00367 |
| <i>yheM</i> | orf, hypothetical protein | 1,685 | 0,007789 |
| <i>manZ</i> | PTS enzyme IID, mannose-specific | 1,683 | 0,001834 |
| --- | intergenic region | 1,681 | 0,02161 |
| <i>ycjS</i> | putative dehydrogenase | 1,680 | 0,001128 |
| --- | intergenic region | 1,680 | 0,004132 |
| <i>aphA</i> | diadenosine tetraphosphatase | 1,678 | 0,001351 |
| <i>malE</i> | Maltose-binding periplasmic protein precursor | 1,675 | 0,008609 |
| <i>ytfM</i> | orf, hypothetical protein | 1,674 | 0,000837 |
| <i>manY</i> | PTS enzyme IIC, mannose-specific | 1,672 | 0,002236 |
| <i>aroC</i> | chorismate synthase | 1,671 | 0,0024 |
| <i>eptB // yhjW</i> | orf, hypothetical protein | 1,670 | 0,002408 |
| <i>symE</i> | orf, hypothetical protein | 1,669 | 0,006222 |
| <i>agaA</i> | putative N-acetylgalactosamine-6-phosphate deacetylase | 1,667 | 0,001177 |
| --- | intergenic region | 1,667 | 0,007582 |
| <i>lsrD // ydeZ</i> | putative transport system permease protein | 1,665 | 0,00224 |
| c5282 | Hypothetical protein | 1,665 | 0,0336 |
| <i>yjeP</i> | putative periplasmic binding protein | 1,664 | 0,01492 |
| <i>secM // yacA</i> | orf, hypothetical protein | 1,664 | 0,001641 |
| <i>yjiD</i> | putative acetyltransferase (EC 2.3.1.18) | 1,660 | 0,000647 |
| <i>ydjG</i> | hypothetical protein | 1,660 | 0,001333 |
| --- | intergenic region | 1,656 | 0,01577 |
| <i>yjhR</i> | putative frameshift suppressor | 1,654 | 0,008223 |
| c0258 | Unknown in ISEc8 | 1,653 | 0,004666 |
| <i>yjcU</i> | D-allulose-6-phosphate 3-epimerase | 1,653 | 0,003552 |
| c0500 | Hypothetical protein | 1,652 | 0,03756 |
| <i>amiB</i> | N-acetylmuramoyl-L-alanine amidase II; a murein hydrolase | 1,651 | 0,008228 |
| <i>hcaC</i> | ferredoxin subunit of phenylpropionate dioxygenase | 1,651 | 0,01633 |
| <i>yffS</i> | orf, hypothetical protein | 1,650 | 0,001049 |
| --- | intergenic region | 1,650 | 0,01831 |
| <i>ftsH</i> | degrades sigma32, integral membrane peptidase, cell division protein | 1,648 | 0,008312 |
| <i>ydbD</i> | orf, hypothetical protein | 1,648 | 0,02928 |
| <i>tesC // ybaW</i> | orf, hypothetical protein | 1,648 | 0,008608 |
| <i>yhaI</i> | putative cytochrome | 1,647 | 0,01341 |
| <i>yihW</i> | putative DEOR-type transcriptional regulator | 1,644 | 0,004063 |
| <i>ybfC</i> | orf, hypothetical protein | 1,644 | 0,0049 |
| --- | intergenic region | 1,644 | 0,03275 |
| <i>ycgH</i> | putative part of putative ATP-binding component of a transport system | 1,642 | 0,002062 |

| | | | |
|---------------------|---|-------|----------|
| <i>arrD // ybcS</i> | bacteriophage lambda lysozyme homolog | 1,641 | 0,02785 |
| <i>rnhB</i> | RNAse HII, degrades RNA of DNA-RNA hybrids | 1,641 | 0,04865 |
| --- | intergenic region | 1,639 | 0,001822 |
| --- | orf, hypothetical protein | 1,638 | 0,008795 |
| <i>yneK</i> | orf, hypothetical protein | 1,636 | 0,04477 |
| <i>pinQ // pinR</i> | putative transposon resolvase | 1,636 | 0,01782 |
| <i>ascB</i> | 6-phospho-beta-glucosidase; cryptic | 1,632 | 0,001489 |
| <i>yheN</i> | orf, hypothetical protein | 1,632 | 0,003047 |
| <i>xdhB // ygeT</i> | putative dehydrogenase | 1,631 | 0,000703 |
| --- | intergenic region | 1,627 | 0,004166 |
| <i>ytjA</i> | orf; Unknown function | 1,626 | 0,0188 |
| <i>yebR</i> | Protein yebR | 1,625 | 0,01872 |
| <i>yfbN</i> | orf, hypothetical protein | 1,625 | 0,01812 |
| <i>yciM</i> | putative heat shock protein | 1,625 | 0,01014 |
| <i>murQ</i> | putative regulator | 1,624 | 0,03304 |
| <i>casE</i> | orf, hypothetical protein | 1,624 | 0,001545 |
| <i>lrp</i> | regulator for leucine (or lrp) regulon and high-affinity branched-chain amino acid transport system | 1,623 | 0,003544 |
| <i>fdoG</i> | formate dehydrogenase-O, major subunit | 1,623 | 0,001799 |
| --- | intergenic region | 1,621 | 0,02321 |
| <i>osmY</i> | hyperosmotically inducible periplasmic protein | 1,620 | 0,006438 |
| <i>gadC // xasA</i> | acid sensitivity protein, putative transporter | 1,619 | 0,03284 |
| <i>yqil</i> | orf, hypothetical protein | 1,617 | 0,01329 |
| --- | intergenic region | 1,616 | 0,03587 |
| <i>yegZ</i> | orf, hypothetical protein | 1,615 | 0,002002 |
| <i>yjcS</i> | orf, hypothetical protein | 1,614 | 0,01782 |
| <i>mtlA</i> | PTS system, mannitol-specific IIBC component | 1,614 | 0,001969 |
| --- | intergenic region | 1,610 | 0,00683 |
| <i>mfd</i> | transcription-repair coupling factor; mutation frequency decline | 1,608 | 0,03571 |
| --- | intergenic region | 1,607 | 0,00349 |
| <i>clpP</i> | ATP-dependent proteolytic subunit of clpA-clpP serine protease, heat shock protein F21.5 | 1,607 | 0,00093 |
| <i>ybfM</i> | orf; Unknown function | 1,607 | 0,001248 |
| <i>yahB</i> | putative transcriptional regulator LYSR-type | 1,607 | 0,002399 |
| <i>proX</i> | high-affinity transport system for glycine betaine and proline | 1,606 | 0,000457 |
| <i>ykgD</i> | putative ARAC-type regulatory protein | 1,606 | 0,001468 |
| <i>argE</i> | acetylornithine deacetylase | 1,605 | 0,004626 |
| <i>ampH // yaiH</i> | Penicillin-binding protein ampH | 1,604 | 0,04351 |
| --- | intergenic region | 1,601 | 0,02149 |
| --- | intergenic region | 1,600 | 0,04486 |
| <i>cspA</i> | cold shock protein 7.4, transcriptional activator of hns | 1,600 | 0,001547 |
| <i>frwB</i> | PTS system fructose-like IIBC component 1 | 1,600 | 0,00556 |
| <i>lsrK // ydeV</i> | putative kinase | 1,600 | 0,002826 |
| <i>ydbA</i> | orf, hypothetical protein | 1,599 | 0,001231 |
| <i>ygcE</i> | putative kinase | 1,598 | 0,01848 |
| <i>ygaV</i> | orf, hypothetical protein | 1,597 | 0,002975 |

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|---------------------|---|-------|----------|
| <i>rimN // yrdC</i> | orf, hypothetical protein | 1,594 | 0,01763 |
| <i>fdol</i> | formate dehydrogenase, cytochrome B556 (FDO) subunit | 1,593 | 0,000815 |
| <i>oppD</i> | homolog of Salmonella ATP-binding protein of oligopeptide ABC transport system | 1,591 | 0,002102 |
| --- | intergenic region | 1,591 | 0,01763 |
| <i>mukF</i> | mukF protein (killing factor KICB) | 1,591 | 0,003972 |
| <i>ftsL</i> | cell division protein; ingrowth of wall at septum | 1,590 | 0,000814 |
| <i>ynbD</i> | putative enzymes | 1,589 | 0,00555 |
| <i>ydfJ</i> | putative transport protein | 1,589 | 0,008008 |
| <i>yihO</i> | putative permease | 1,589 | 0,02432 |
| <i>recC</i> | DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ssDNA endonuclease | 1,587 | 0,003095 |
| <i>hcaD</i> | ferredoxin reductase subunit of phenylpropionate dioxygenase | 1,587 | 0,003647 |
| <i>yhjJ</i> | orf, hypothetical protein | 1,586 | 0,005425 |
| <i>fsr</i> | fosmidomycin resistance protein | 1,586 | 0,001676 |
| <i>yjgI</i> | putative oxidoreductase | 1,586 | 0,01072 |
| <i>insG</i> | Putative conserved protein | 1,584 | 0,005813 |
| <i>dtd // yihZ</i> | hypothetical protein | 1,583 | 0,001107 |
| <i>hfIK</i> | protease specific for phage lambda cII repressor | 1,583 | 0,001928 |
| <i>betA</i> | Choline dehydrogenase | 1,583 | 0,005213 |
| <i>tnaA</i> | tryptophanase | 1,582 | 0,001268 |
| <i>yijE</i> | orf, hypothetical protein | 1,582 | 0,005044 |
| --- | intergenic region | 1,581 | 0,02215 |
| c0497 | Hypothetical protein | 1,581 | 0,02148 |
| <i>glpX</i> | unknown function in glycerol metabolism | 1,580 | 0,01823 |
| <i>ydfX</i> | orf, hypothetical protein | 1,577 | 0,01189 |
| <i>yhjE</i> | putative transport protein | 1,576 | 0,002659 |
| <i>glpF</i> | facilitated diffusion of glycerol | 1,575 | 0,01683 |
| --- | intergenic region | 1,575 | 0,004063 |
| <i>yeiL</i> | stationary phase nitrogen starvation regulator | 1,574 | 0,004001 |
| <i>yihL</i> | putative transcriptional regulator | 1,573 | 0,007582 |
| <i>ycjZ</i> | putative transcriptional regulator LYSR-type | 1,572 | 0,006222 |
| --- | intergenic region | 1,572 | 0,01478 |
| ECs3459 | orf, hypothetical protein | 1,569 | 0,04888 |
| --- | intergenic region | 1,569 | 0,002532 |
| <i>yiaN</i> | putative membrane protein | 1,568 | 0,01364 |
| <i>ybaQ</i> | orf, hypothetical protein | 1,568 | 0,01256 |
| <i>smf</i> | orf, fragment 1 | 1,567 | 0,003092 |
| <i>sgaB // ulaB</i> | orf, hypothetical protein | 1,567 | 0,006072 |
| <i>yagU</i> | orf, hypothetical protein | 1,567 | 0,04616 |
| <i>yjeE</i> | orf, hypothetical protein | 1,566 | 0,008154 |
| ECs5432 | orf; Unknown function | 1,565 | 0,001925 |
| --- | intergenic region | 1,565 | 0,02652 |
| <i>ycjO</i> | putative binding-protein dependent transport protein | 1,563 | 0,03608 |
| <i>ydfI</i> | Hypothetical oxidoreductase ydfI | 1,559 | 0,004615 |
| <i>arnA</i> | putative transformylase | 1,559 | 0,02189 |

| | | | |
|---------------------|---|-------|----------|
| <i>trkG</i> | trk system potassium uptake | 1,559 | 0,001878 |
| <i>yjcE</i> | orf, hypothetical protein | 1,558 | 0,03499 |
| --- | intergenic region | 1,556 | 0,03284 |
| <i>gspD</i> | YheF | 1,555 | 0,02339 |
| <i>intD</i> | prophage DLP12 integrase | 1,555 | 0,003923 |
| <i>gpsA</i> | glycerol-3-phosphate dehydrogenase (NAD+) | 1,553 | 0,001075 |
| <i>nlpA</i> | lipoprotein-28 | 1,553 | 0,007568 |
| <i>yjiY</i> | putative carbon starvation protein | 1,551 | 0,02623 |
| <i>ilvG</i> | acetolactate synthase II, large subunit, cryptic, interrupted | 1,548 | 0,001948 |
| <i>secB</i> | protein export; molecular chaperone; may bind to signal sequence | 1,547 | 0,000495 |
| <i>rmuC // yigN</i> | Hypothetical protein | 1,547 | 0,001641 |
| --- | glycolate oxidase iron-sulfur subunit | 1,546 | 0,00136 |
| --- | intergenic region | 1,545 | 0,0274 |
| --- | intergenic region | 1,545 | 0,01479 |
| c4813 | Hypothetical protein | 1,545 | 0,0032 |
| <i>purU</i> | formyltetrahydrofolate deformylase; for purT-dependent FGAR synthesis | 1,543 | 0,01601 |
| <i>yhdW</i> | putative periplasmic binding transport protein | 1,541 | 0,001685 |
| <i>pgaA</i> | putative outer membrane protein | 1,541 | 0,005635 |
| <i>yggP</i> | putative oxidoreductase | 1,540 | 0,003002 |
| <i>lpxB</i> | tetraacyldisaccharide-1-P; lipid A biosynthesis, penultimate step | 1,539 | 0,03429 |
| --- | intergenic region | 1,539 | 0,001685 |
| <i>ytfN</i> | orf, hypothetical protein | 1,538 | 0,001387 |
| <i>mhpE</i> | 4-hydroxy-2-ketovalerate aldolase | 1,538 | 0,007789 |
| <i>friB</i> | putative transport protein | 1,534 | 0,005754 |
| <i>bisZ // torZ</i> | biotin sulfoxide reductase 2 | 1,533 | 0,000766 |
| <i>ykgA</i> | putative ARAC-type regulatory protein | 1,532 | 0,003769 |
| --- | intergenic region | 1,530 | 0,008941 |
| <i>ycjP</i> | putative transport system permease protein | 1,530 | 0,03036 |
| <i>yebA</i> | orf, hypothetical protein | 1,529 | 0,04607 |
| <i>serB</i> | Phosphoserine phosphatase | 1,527 | 0,006402 |
| <i>mhpC</i> | 2-hydroxy-6-ketono-2,4-dienedioic acid hydrolase | 1,527 | 0,02074 |
| c5075 | Hypothetical protein | 1,527 | 0,008124 |
| <i>ygeF</i> | orf, hypothetical protein | 1,525 | 0,02244 |
| <i>gppA</i> | guanosine pentaphosphatase; exopolyphosphatase | 1,524 | 0,01844 |
| <i>yihN</i> | putative resistance protein (transport) | 1,523 | 0,006457 |
| <i>ribE // ribH</i> | riboflavin synthase, beta chain | 1,522 | 0,0266 |
| <i>yeeL</i> | orf, hypothetical protein | 1,520 | 0,02603 |
| <i>flxA</i> | orf, hypothetical protein | 1,519 | 0,01689 |
| <i>ygbF</i> | orf, hypothetical protein | 1,519 | 0,001812 |
| <i>recE</i> | exonuclease VIII, ds DNA exonuclease, 5 --> 3 specific | 1,517 | 0,02339 |
| <i>yiaG</i> | orf, hypothetical protein | 1,514 | 0,04732 |
| <i>ybgL</i> | putative lactam utilization protein | 1,514 | 0,002408 |
| --- | intergenic region | 1,514 | 0,04097 |
| <i>yjeP</i> | putative periplasmic binding protein | 1,513 | 0,0226 |
| <i>murE</i> | UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate | 1,512 | 0,003817 |

| | ligase | | |
|---------------------|---|-------|----------|
| <i>yiiG</i> | orf, hypothetical protein | 1,510 | 0,008314 |
| --- | intergenic region | 1,510 | 0,01409 |
| <i>chiA</i> | hypothetical protein | 1,510 | 0,006229 |
| <i>rmuC // yigN</i> | putative alpha helix chain | 1,508 | 0,002918 |
| <i>yheO</i> | orf, hypothetical protein | 1,508 | 0,003647 |
| <i>leuD</i> | isopropylmalate isomerase subunit | 1,507 | 0,002969 |
| c3178 | Hypothetical protein | 1,506 | 0,04406 |
| --- | intergenic region | 1,503 | 0,0275 |
| <i>fdhE</i> | affects formate dehydrogenase-N | 1,502 | 0,001616 |
| <i>caiC</i> | probable crotonobetainecarnitine-CoA ligase | 1,501 | 0,003971 |
| <i>ycdQ</i> | Hypothetical protein | 1,503 | 0,003592 |
| <i>yebF</i> | orf, hypothetical protein | 1,504 | 0,008583 |
| <i>artI</i> | arginine 3rd transport system periplasmic binding protein | 1,504 | 0,02826 |
| <i>mrr</i> | restriction of methylated adenine | 1,505 | 0,0146 |
| --- | intergenic region | 1,506 | 0,003588 |
| --- | intergenic region | 1,506 | 0,01975 |
| <i>alkB</i> | DNA repair system specific for alkylated DNA | 1,508 | 0,004713 |
| <i>ybiS</i> | orf, hypothetical protein | 1,508 | 0,03151 |
| <i>fimG</i> | fimbrial morphology | 1,509 | 0,01094 |
| <i>rfc</i> | O-antigen polymerase | 1,512 | 0,006594 |
| c4571 | Hypothetical protein yfjX | 1,513 | 0,004727 |
| <i>yfjM</i> | orf, hypothetical protein | 1,515 | 0,02404 |
| <i>trmA</i> | tRNA (uracil-5-)-methyltransferase | 1,515 | 0,04442 |
| <i>mscL</i> | mechanosensitive channel | 1,515 | 0,04442 |
| --- | intergenic region | 1,516 | 0,004219 |
| <i>mnmA</i> | hypothetical protein | 1,517 | 0,01752 |
| --- | intergenic region | 1,518 | 0,006102 |
| <i>ryfA</i> | Hypothetical protein | 1,518 | 0,01075 |
| <i>rplL</i> | 50S ribosomal subunit protein L7L12 | 1,519 | 0,001224 |
| <i>truB</i> | tRNA pseudouridine 5S synthase | 1,519 | 0,002408 |
| <i>yliL</i> | orf, hypothetical protein | 1,521 | 0,04623 |
| <i>ypdA</i> | putative sensor protein | 1,522 | 0,04273 |
| <i>rybA</i> | MG1655_rybA_b4416 /SEG=NC_000913:-852175,852263 /LEN=88 | 1,524 | 0,03389 |
| --- | intergenic region | 1,525 | 0,03036 |
| <i>gcvB</i> | regulatory RNA | 1,525 | 0,00802 |
| --- | intergenic region | 1,526 | 0,02608 |
| --- | intergenic region | 1,527 | 0,02909 |
| <i>rplT</i> | 50S ribosomal subunit protein L20, and regulator | 1,528 | 0,01089 |
| <i>mgrB // yobG</i> | orf, hypothetical protein | 1,529 | 0,02353 |
| --- | intergenic region | 1,530 | 0,03567 |
| <i>ldrB</i> | small toxic polypeptide | 1,530 | 0,03947 |
| --- | intergenic region | 1,531 | 0,02198 |
| --- | intergenic region | 1,531 | 0,01986 |
| --- | intergenic region | 1,531 | 0,01977 |

| | | | |
|---------------------|---|-------|----------|
| <i>mug // ygfF</i> | orf, hypothetical protein | 1,532 | 0,0379 |
| <i>pitA</i> | low-affinity phosphate transport | 1,533 | 0,01362 |
| <i>yciH</i> | Protein yciH | 1,534 | 0,04947 |
| ECs3891 | orf, hypothetical protein | 1,535 | 0,03391 |
| --- | intergenic region | 1,536 | 0,03036 |
| <i>cmk</i> | cytidylate kinase | 1,539 | 0,01296 |
| <i>secY</i> | putative ATPase subunit of translocase | 1,541 | 0,001799 |
| <i>rlmG // ygjO</i> | putative enzyme | 1,542 | 0,03567 |
| --- | intergenic region | 1,543 | 0,01753 |
| --- | Bacteriophage P1 gene repA | 1,545 | 0,005519 |
| <i>cheW</i> | positive regulator of CheA protein activity | 1,546 | 0,007804 |
| <i>yeyK</i> | protein present in spermidine nucleoids | 1,546 | 0,004727 |
| --- | intergenic region | 1,548 | 0,02189 |
| c4645 | Hypothetical protein | 1,548 | 0,01609 |
| --- | intergenic region | 1,551 | 0,0319 |
| <i>ansP</i> | L-asparagine permease | 1,554 | 0,04049 |
| <i>yccS</i> | orf, hypothetical protein | 1,557 | 0,03299 |
| --- | intergenic region | 1,557 | 0,02909 |
| --- | intergenic region | 1,560 | 0,0208 |
| --- | intergenic region | 1,564 | 0,02192 |
| <i>yehE</i> | orf, hypothetical protein | 1,566 | 0,03166 |
| <i>yjiN</i> | putative oxidoreductase | 1,568 | 0,01476 |
| <i>menC</i> | o-succinylbenzoyl-CoA synthase; conversion of chorismate to 2-o-succinylbenzoyl-CoA | 1,568 | 0,02109 |
| <i>yeiW</i> | Hypothetical protein | 1,570 | 0,02643 |
| <i>stfP</i> | hypothetical protein | 1,571 | 0,01617 |
| <i>rpiA</i> | ribosephosphate isomerase, constitutive | 1,577 | 0,001527 |
| <i>yghB</i> | orf, hypothetical protein | 1,581 | 0,02707 |
| <i>rplM</i> | 50S ribosomal subunit protein L13 | 1,581 | 0,003972 |
| --- | intergenic region | 1,582 | 0,01095 |
| --- | intergenic region | 1,583 | 0,006853 |
| <i>ccmH</i> | possible subunit of heme lyase | 1,583 | 0,01975 |
| Z5852 | orf; Unknown function | 1,585 | 0,0453 |
| <i>ribA</i> | GTP cyclohydrolase II | 1,586 | 0,007071 |
| --- | intergenic region | 1,586 | 0,006222 |
| <i>yeaN</i> | putative amino acidamine transport protein | 1,586 | 0,002131 |
| --- | intergenic region | 1,586 | 0,01886 |
| --- | intergenic region | 1,589 | 0,008585 |
| <i>slyX</i> | host factor for lysis of phiX174 infection | 1,591 | 0,002232 |
| <i>glyA</i> | serine hydroxymethyltransferase | 1,593 | 0,005308 |
| <i>yfhL</i> | orf, hypothetical protein | 1,593 | 0,008558 |
| <i>yefM</i> | orf, hypothetical protein | 1,595 | 0,007172 |
| <i>ycaR</i> | orf, hypothetical protein | 1,595 | 0,01031 |
| <i>tadA // yfhC</i> | tRNA-specific adenosine deaminase | 1,597 | 0,000811 |
| <i>maf // yceF</i> | orf, hypothetical protein | 1,598 | 0,002373 |
| <i>yoeB</i> | Hypothetical protein | 1,599 | 0,007658 |

| | | | |
|---------------------|---|-------|----------|
| --- | intergenic region | 1,600 | 0,01191 |
| <i>kdpB</i> | ATPase of high-affinity potassium transport system, B chain | 1,604 | 0,01218 |
| c4090 | Hypothetical protein | 1,605 | 0,0345 |
| <i>kdsA</i> | 2-dehydro-3-deoxyphosphooctulonate aldolase | 1,606 | 0,00076 |
| c4074 | Hypothetical protein | 1,608 | 0,01652 |
| <i>yeaD</i> | orf, hypothetical protein | 1,609 | 0,01424 |
| --- | intergenic region | 1,609 | 0,01438 |
| <i>yljJ</i> | putative transferase | 1,610 | 0,0115 |
| --- | intergenic region | 1,611 | 0,004142 |
| <i>ydiH</i> | orf, hypothetical protein | 1,612 | 0,01399 |
| --- | intergenic region | 1,614 | 0,006938 |
| <i>yebG</i> | orf, hypothetical protein | 1,615 | 0,01812 |
| Z1987 | orf; Unknown function | 1,616 | 0,03238 |
| <i>miaB // yleA</i> | orf, hypothetical protein | 1,616 | 0,02351 |
| <i>pta</i> | Phosphate acetyltransferase | 1,617 | 0,01534 |
| <i>insH</i> | IS5 transposase | 1,617 | 0,02244 |
| c1103 | Hypothetical protein | 1,618 | 0,00349 |
| --- | Hypothetical protein | 1,618 | 0,002216 |
| --- | intergenic region | 1,623 | 0,003454 |
| <i>cfa</i> | cyclopropane fatty acyl phospholipid synthase | 1,627 | 0,02473 |
| <i>rpmD</i> | 50S ribosomal subunit protein L30 | 1,627 | 0,000858 |
| c4195 | Hypothetical protein | 1,632 | 0,0285 |
| <i>purA</i> | adenylosuccinate synthetase | 1,632 | 0,001353 |
| <i>dkgB</i> | 2,5-diketo-D-gluconate reductase B | 1,632 | 0,000389 |
| <i>rsxG</i> | hypothetical protein | 1,633 | 0,02817 |
| <i>purN /</i> | phosphoribosylglycinamide formyltransferase 1 | 1,634 | 0,002201 |
| <i>speE</i> | spermidine synthase = putrescine aminopropyltransferase | 1,634 | 0,003796 |
| <i>yegE</i> | putative sensor-type protein | 1,635 | 0,002236 |
| --- | intergenic region | 1,638 | 0,04543 |
| <i>cydD</i> | ATP-binding component of cytochrome-related transport, Zn sensitive | 1,638 | 0,003498 |
| <i>speD</i> | S-adenosylmethionine decarboxylase | 1,639 | 0,02608 |
| --- | intergenic region | 1,641 | 0,01153 |
| <i>ccmG // dsbE</i> | disulfide oxidoreductase | 1,643 | 0,01512 |
| c4088 | Hypothetical protein | 1,644 | 0,03859 |
| <i>ygiQ</i> | orf, hypothetical protein | 1,645 | 0,01825 |
| --- | intergenic region | 1,645 | 0,0258 |
| <i>yibO</i> | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase | 1,648 | 0,04792 |
| <i>spf</i> | Spot 42 RNA | 1,648 | 0,000573 |
| --- | intergenic region | 1,649 | 0,003789 |
| <i>argD</i> | acetylornithine delta-aminotransferase | 1,650 | 0,000951 |
| c2806 | Hypothetical protein | 1,650 | 0,01364 |
| --- | intergenic region | 1,650 | 0,003112 |
| <i>lysP</i> | lysine-specific permease | 1,650 | 0,02075 |
| c0205 | Hypothetical protein | 1,651 | 0,003034 |
| c4078 | Hypothetical protein | 1,652 | 0,04271 |

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|---------------------|---|-------|----------|
| <i>flgL</i> | flagellar biosynthesis; hook-filament junction protein | 1,653 | 0,000527 |
| <i>yqcC</i> | orf, hypothetical protein | 1,654 | 0,02005 |
| c3354 | Hypothetical protein | 1,656 | 0,00182 |
| <i>truC // yqcB</i> | orf, hypothetical protein | 1,656 | 0,01636 |
| --- | intergenic region | 1,657 | 0,01277 |
| c0746 | Hypothetical protein | 1,659 | 0,04117 |
| <i>nupC</i> | permease of transport system for 3 nucleosides | 1,659 | 0,01079 |
| <i>ybhB</i> | orf, hypothetical protein | 1,660 | 0,002118 |
| <i>ybhT</i> | orf, hypothetical protein | 1,660 | 0,003968 |
| <i>ybiJ</i> | orf, hypothetical protein | 1,664 | 0,01735 |
| <i>flgG</i> | flagellar biosynthesis, cell-distal portion of basal-body rod | 1,668 | 0,000606 |
| --- | intergenic region | 1,670 | 0,01225 |
| <i>gltS</i> | glutamate transport | 1,670 | 0,001085 |
| <i>sibC</i> | MG1655_rygC_b4446 /SEG=NC_000913:+3054835,3054985 /LEN=150 | 1,670 | 0,006295 |
| <i>marA</i> | multiple antibiotic resistance; transcriptional activator of defense systems | 1,671 | 0,004537 |
| <i>yccK</i> | putative sulfite reductase (EC 1.8.-.-) | 1,672 | 0,002016 |
| --- | intergenic region | 1,673 | 0,01852 |
| <i>nth</i> | endonuclease III; specific for apurinic and/or apyrimidinic sites | 1,677 | 0,02993 |
| <i>yjE</i> | orf, hypothetical protein | 1,678 | 0,00991 |
| <i>ychE</i> | putative channel protein | 1,679 | 0,00057 |
| <i>menB</i> | dihydroxynaphthoic acid synthetase | 1,681 | 0,01248 |
| <i>rplC</i> | 50S ribosomal subunit protein L3 | 1,682 | 0,000227 |
| <i>yedF</i> | orf, hypothetical protein | 1,683 | 0,02454 |
| --- | intergenic region | 1,684 | 0,00349 |
| <i>rpsS</i> | 30S ribosomal subunit protein S19 | 1,684 | 0,000142 |
| <i>yacl</i> | orf, hypothetical protein | 1,684 | 0,03525 |
| <i>ymbA</i> | orf, hypothetical protein | 1,686 | 0,000499 |
| <i>purR</i> | transcriptional repressor for pur regulon, glyA, glnB, prsA, speA | 1,689 | 0,005824 |
| <i>marB</i> | multiple antibiotic resistance protein | 1,689 | 0,008154 |
| <i>folD</i> | 5,10-methylene-tetrahydrofolate dehydrogenase; 5,10-methylene-tetrahydrofolate cyclohydrolase | 1,690 | 0,001584 |
| <i>kdsB</i> | CTP:CMP-3-deoxy-D-manno-octulosonate transferase | 1,692 | 0,002928 |
| <i>pgsA</i> | phosphatidylglycerophosphate synthetase = CDP-1,2-diacyl-sn-glycerol-3-phosphate phosphatidyl transferase | 1,692 | 0,000915 |
| --- | intergenic region | 1,693 | 0,0205 |
| <i>pnuC</i> | required for NMN transport | 1,694 | 0,01731 |
| <i>rph</i> | RNase PH | 1,695 | 0,006076 |
| <i>ccmH</i> | Cytochrome c-type biogenesis protein ccmH precursor | 1,696 | 0,000855 |
| <i>sohB</i> | putative protease | 1,697 | 0,01459 |
| <i>trmD</i> | tRNA methyltransferase; tRNA (guanine-7-)-methyltransferase | 1,697 | 0,000136 |
| <i>rsxE // ydgQ</i> | hypothetical protein | 1,702 | 0,008956 |
| <i>rplY</i> | 50S ribosomal subunit protein L25 | 1,702 | 0,006527 |
| <i>ypfH</i> | orf, hypothetical protein | 1,704 | 0,005336 |
| <i>adhE</i> | CoA-linked acetaldehyde dehydrogenase and iron-dependent alcohol dehydrogenase; pyruvate-formate-lyase deactivase | 1,706 | 0,04792 |
| --- | hypothetical protein | 1,706 | 0,03322 |

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|---------------------|--|-------|----------|
| <i>prfC</i> | peptide chain release factor RF-3 | 1,706 | 0,01978 |
| <i>aat</i> | leucyl, phenylalanyl-tRNA-protein transferase | 1,706 | 0,001552 |
| <i>aceE</i> | pyruvate dehydrogenase (decarboxylase component) | 1,709 | 0,001452 |
| <i>rpsO</i> | 30S ribosomal subunit protein S15 | 1,709 | 0,005315 |
| <i>flgE</i> | flagellar biosynthesis, hook protein | 1,714 | 0,001062 |
| <i>rplV</i> | 50S ribosomal subunit protein L22 | 1,714 | 0,000741 |
| <i>ybaA</i> | orf, hypothetical protein | 1,714 | 0,02772 |
| <i>yfeH</i> | putative cytochrome oxidase | 1,715 | 0,00334 |
| <i>ybhA</i> | putative phosphatase | 1,718 | 0,004311 |
| <i>cyaR</i> | MG1655_ryeE_b4438 /SEG=NC_000913:+2165134,2165219 /LEN=85 | 1,720 | 0,003095 |
| <i>mscS // yggB</i> | putative transport protein | 1,720 | 0,000982 |
| c2913 | Hypothetical protein | 1,723 | 0,01731 |
| c3379 | Hypothetical protein | 1,724 | 0,02003 |
| <i>codA</i> | cytosine deaminase | 1,729 | 0,002191 |
| <i>yggL</i> | orf, hypothetical protein | 1,730 | 0,000232 |
| <i>mtfA // yeel</i> | orf, hypothetical protein | 1,730 | 0,03602 |
| --- | intergenic region | 1,731 | 0,001412 |
| <i>pqqL</i> | putative zinc protease | 1,731 | 0,004142 |
| --- | intergenic region | 1,731 | 0,01169 |
| <i>sad // ynel</i> | putative aldehyde dehydrogenase | 1,732 | 0,005772 |
| <i>yajQ</i> | orf, hypothetical protein | 1,735 | 0,000561 |
| <i>yegE</i> | partial putative sensor kinase | 1,735 | 0,000899 |
| <i>flgE</i> | flagellar biosynthesis, hook protein | 1,736 | 0,001652 |
| --- | intergenic region | 1,737 | 0,00802 |
| --- | intergenic region | 1,738 | 0,01014 |
| <i>plsX</i> | glycerolphosphate auxotrophy in plsB background | 1,744 | 0,000595 |
| --- | intergenic region | 1,746 | 0,02108 |
| --- | putative RNA | 1,748 | 0,03402 |
| <i>rplK</i> | 50S ribosomal subunit protein L11 | 1,748 | 5,73E-02 |
| <i>rplP</i> | 50S ribosomal subunit protein L16 | 1,751 | 0,00076 |
| --- | intergenic region | 1,755 | 0,002101 |
| --- | intergenic region | 1,755 | 0,03019 |
| <i>thiD</i> | phosphomethylpyrimidine kinase | 1,755 | 0,002002 |
| <i>potB</i> | spermidineputrescine transport system permease | 1,759 | 0,0285 |
| <i>hycl</i> | Hydrogenase 3 maturation protease | 1,761 | 0,002753 |
| --- | intergenic region | 1,761 | 0,003239 |
| <i>ccmF</i> | cytochrome c-type biogenesis protein | 1,764 | 0,04759 |
| <i>yqgC</i> | orf, hypothetical protein | 1,770 | 0,00987 |
| <i>typA // yihK</i> | putative GTP-binding factor | 1,771 | 0,000758 |
| <i>yneE</i> | orf, hypothetical protein | 1,774 | 0,009426 |
| <i>yfaE</i> | orf, hypothetical protein | 1,776 | 0,002928 |
| --- | intergenic region | 1,776 | 0,02652 |
| --- | intergenic region | 1,776 | 0,004222 |
| <i>yfaZ</i> | orf, hypothetical protein | 1,776 | 0,01437 |
| <i>aceF</i> | pyruvate dehydrogenase (dihydrolipoyltransacetylase component) | 1,777 | 0,007582 |

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|---------------------------|---|-------|----------|
| Z0115 | orf, hypothetical protein | 1,779 | 0,01136 |
| <i>ybiN</i> | orf, hypothetical protein | 1,779 | 0,00318 |
| --- | intergenic region | 1,783 | 0,01429 |
| --- | intergenic region | 1,784 | 0,01628 |
| <i>ycfD</i> | orf, hypothetical protein | 1,784 | 0,002222 |
| c5290 | Hypothetical protein | 1,785 | 0,00722 |
| <i>rdIA</i> | antisense RNA, trans-acting regulator of <i>ldrA</i> translation | 1,789 | 0,000439 |
| <i>rpsC</i> | 30S ribosomal subunit protein S3 | 1,789 | 0,000703 |
| <i>guaA</i> | GMP synthase (glutamine-hydrolyzing) | 1,794 | 0,000991 |
| c4300 | Hypothetical protein | 1,794 | 0,01824 |
| <i>ymfM</i> | hypothetical protein | 1,797 | 0,001799 |
| <i>yejG</i> | orf, hypothetical protein | 1,797 | 0,02074 |
| <i>nupC</i> | Nucleoside permease <i>nupC</i> | 1,802 | 0,000837 |
| <i>ftnB // yecl</i> | ferritin-like protein | 1,806 | 0,04368 |
| <i>yodB</i> | cytochrome b561 homolog 1 | 1,811 | 0,003555 |
| <i>guaB</i> | IMP dehydrogenase | 1,811 | 0,008435 |
| <i>nrdB</i> | Ribonucleoside-diphosphate reductase 1 beta chain | 1,815 | 0,000499 |
| <i>rlmI // yccW 9</i> | putative oxidoreductase | 1,816 | 0,01144 |
| <i>mgtA</i> | Mg ²⁺ transport ATPase, P-type 1 | 1,817 | 0,011 |
| <i>ycbC</i> | orf, hypothetical protein | 1,817 | 0,001498 |
| c0274 | Hypothetical protein | 1,819 | 0,01382 |
| <i>ydgl</i> | putative arginineornithine antiporter | 1,821 | 0,005513 |
| <i>rpsF</i> | 30S ribosomal subunit protein S6 | 1,822 | 0,001333 |
| <i>rpsJ</i> | 30S ribosomal subunit protein S10 | 1,823 | 0,000374 |
| <i>corA</i> | Mg ²⁺ transport, system I | 1,823 | 0,00677 |
| <i>psiE // yjbA</i> | orf, hypothetical protein | 1,824 | 0,002747 |
| <i>rsmF // yebU</i> | putative nucleolar proteins | 1,826 | 0,008314 |
| <i>bhsA // ycfR</i> | orf, hypothetical protein | 1,831 | 0,01208 |
| <i>dinI</i> | damage-inducible protein I | 1,833 | 0,006851 |
| <i>flgA</i> | flagellar biosynthesis; assembly of basal-body periplasmic P ring | 1,839 | 0,003047 |
| <i>cmr</i> | proton motive force efflux pump | 1,840 | 0,01067 |
| <i>ybcY</i> | orf, hypothetical protein | 1,843 | 0,002143 |
| <i>rplW</i> | 50S ribosomal subunit protein L23 | 1,843 | 4,32E-02 |
| c4889 | Hypothetical protein | 1,846 | 0,03897 |
| --- | intergenic region | 1,846 | 0,01507 |
| c0754 | Hypothetical protein | 1,852 | 0,01524 |
| <i>potC</i> | spermidineputrescine transport system permease | 1,855 | 0,005952 |
| <i>focA_2</i> | intergenic region | 1,856 | 0,00182 |
| <i>nrdB</i> | ribonucleoside-diphosphate reductase 1, beta subunit, B2 | 1,861 | 0,000635 |
| --- | intergenic region | 1,865 | 0,01858 |
| <i>folA</i> | dihydrofolate reductase type I; trimethoprim resistance | 1,866 | 0,01412 |
| <i>yfdY</i> | orf, hypothetical protein | 1,870 | 0,02093 |
| <i>ghrA // ycdW</i> | putative dehydrogenase | 1,871 | 0,000534 |
| c1294 | Hypothetical protein | 1,872 | 0,008328 |
| c5447 | Hypothetical protein | 1,876 | 0,000628 |

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|---------------------|--|-------|----------|
| c0869 | Hypothetical protein | 1,878 | 0,02244 |
| <i>tfaE</i> | hypothetical protein | 1,879 | 0,000322 |
| c0385 | Hypothetical protein | 1,879 | 0,04351 |
| <i>yccF</i> | orf, hypothetical protein | 1,886 | 0,000766 |
| <i>focA</i> | probable formate transporter (formate channel 1) | 1,888 | 0,02533 |
| <i>htrB // lpxL</i> | heat shock protein | 1,890 | 0,001641 |
| <i>moeB</i> | molybdopterin biosynthesis | 1,895 | 0,03875 |
| <i>rimM /</i> | hypothetical protein | 1,896 | 5,28E-02 |
| <i>rpsR</i> | 30S ribosomal subunit protein S18 | 1,896 | 0,000415 |
| --- | intergenic region | 1,897 | 0,01891 |
| <i>yraQ</i> | orf, hypothetical protein | 1,901 | 0,000919 |
| <i>metK</i> | methionine adenosyltransferase 1 (AdoMet synthetase); methyl and propylamine donor, corepressor of met genes | 1,904 | 0,00855 |
| <i>cydC</i> | ATP-binding component of cytochrome-related transport | 1,904 | 0,00027 |
| c2541 | Hypothetical protein | 1,905 | 0,01069 |
| <i>flg</i> | Flagellar basal-body rod protein flgF | 1,906 | 0,00134 |
| <i>rplA</i> | 50S ribosomal subunit protein L1, regulates synthesis of L1 and L11 | 1,906 | 4,23E-02 |
| <i>rydB</i> | MG1655_rydB_b4430 /SEG=NC_000913:-1762737,1762804 /LEN=67 | 1,908 | 0,009446 |
| <i>znuC</i> | putative ATP-binding component of a transport system | 1,912 | 0,002647 |
| <i>priB</i> | primosomal replication protein N | 1,916 | 0,000228 |
| <i>nrdG</i> | anaerobic ribonucleotide reductase activating protein | 1,917 | 0,002154 |
| --- | intergenic region | 1,921 | 0,001162 |
| --- | intergenic region | 1,926 | 0,02479 |
| <i>obgE // obgE</i> | putative GTP-binding factor | 1,927 | 0,000389 |
| <i>thiM</i> | hydroxyethylthiazole kinase | 1,927 | 0,001203 |
| <i>ybhL</i> | orf, hypothetical protein | 1,934 | 0,01293 |
| --- | intergenic region | 1,935 | 0,001461 |
| --- | intergenic region | 1,938 | 0,0146 |
| <i>rpsP</i> | 30S ribosomal subunit protein S16 | 1,946 | 5,95E-02 |
| --- | intergenic region | 1,957 | 0,03656 |
| <i>ycfJ</i> | orf, hypothetical protein | 1,957 | 0,003121 |
| --- | intergenic region | 1,966 | 0,00722 |
| <i>nagB</i> | glucosamine-6-phosphate deaminase | 1,968 | 0,04108 |
| <i>csrB</i> | CsrB regulatory RNA | 1,969 | 0,01712 |
| <i>yedR</i> | Hypothetical protein yedR | 1,970 | 0,00802 |
| <i>speB</i> | agmatinase | 1,971 | 0,001468 |
| <i>pspA</i> | phage shock protein, inner membrane protein | 1,972 | 0,000167 |
| <i>dusB // yhdG</i> | putative dehydrogenase | 1,972 | 0,000395 |
| <i>rplB</i> | 50S ribosomal subunit protein L2 | 1,972 | 4,90E-02 |
| <i>yeiP</i> | putative elongation factor | 1,983 | 0,000415 |
| <i>cspF</i> | CspF | 1,983 | 0,003034 |
| <i>menG // rraA</i> | menaquinone biosynthesis, unknown | 2,003 | 0,02593 |
| <i>hokB</i> | small toxic membrane polypeptide | 2,014 | 0,01091 |
| <i>ppsA</i> | phosphoenolpyruvate synthase | 2,020 | 0,04665 |
| <i>nrdD</i> | anaerobic ribonucleoside-triphosphate reductase | 2,022 | 0,005105 |
| ECs4539 | unknown protein encoded within prophage CP-933L | 2,025 | 0,00102 |

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|---------------------|--|-------|----------|
| <i>rpmC</i> | 50S ribosomal subunit protein L29 | 2,035 | 0,000351 |
| <i>rpsI</i> | 30S ribosomal subunit protein S9 | 2,035 | 0,000534 |
| --- | orf, hypothetical protein | 2,035 | 0,001128 |
| <i>ybgC</i> | orf, hypothetical protein | 2,038 | 0,002573 |
| <i>flgC</i> | flagellar biosynthesis, cell-proximal portion of basal-body rod | 2,061 | 0,000494 |
| --- | intergenic region | 2,061 | 0,04406 |
| <i>rplD</i> | 50S ribosomal subunit protein L4, regulates expression of S10 operon | 2,062 | 1,96E-02 |
| <i>yccU</i> | orf; Unknown function | 2,071 | 0,003316 |
| <i>yegD</i> | putative heat shock protein | 2,073 | 0,000527 |
| <i>deaD</i> | inducible ATP-independent RNA helicase | 2,075 | 0,000241 |
| ECs5426 | Hypothetical protein | 2,076 | 0,007696 |
| <i>flgF</i> | flagellar biosynthesis, cell-proximal portion of basal-body rod | 2,076 | 0,001928 |
| <i>pflA</i> | pyruvate formate lyase activating enzyme 1 | 2,076 | 0,01781 |
| <i>fis</i> | site-specific DNA inversion stimulation factor; DNA-binding protein; a trans activator for transcription | 2,083 | 0,004244 |
| <i>pyrD</i> | Dihydroorotate dehydrogenase | 2,083 | 6,43E-02 |
| <i>ccrB</i> | orf, hypothetical protein | 2,086 | 0,000457 |
| <i>rmf</i> | ribosome modulation factor | 2,094 | 0,01215 |
| <i>rplQ</i> | 50S ribosomal subunit protein L17 | 2,097 | 7,99E-02 |
| c2612 | intergenic region | 2,108 | 0,01492 |
| <i>flgD</i> | flagellar biosynthesis, initiation of hook assembly | 2,113 | 0,000457 |
| <i>ffs</i> | 4.5S RNA; component of ribonucleoprotein particle | 2,114 | 0,0118 |
| <i>ygiQ</i> | orf, hypothetical protein | 2,117 | 0,000751 |
| <i>yifE</i> | orf, hypothetical protein | 2,117 | 0,000164 |
| ECs5328 | Hypothetical protein | 2,121 | 0,004001 |
| <i>sotB // ydeA</i> | sugar efflux transporter; L-arabinose and isopropyl-b-D-thiogalactopyranoside exporter protein | 2,123 | 0,000142 |
| <i>ogrK</i> | prophage P2 ogr protein | 2,124 | 0,0017 |
| <i>mokB</i> | regulatory peptide whose translation enables hokB expression | 2,126 | 0,02422 |
| <i>pyrH</i> | uridylyate kinase | 2,127 | 0,000359 |
| <i>flgB</i> | flagellar biosynthesis, cell-proximal portion of basal-body rod | 2,129 | 0,001032 |
| <i>rplS</i> | 50S ribosomal subunit protein L19 | 2,138 | 1,50E-02 |
| ECs2049 | orf, hypothetical protein | 2,142 | 0,000588 |
| c3248 | Hypothetical protein | 2,149 | 0,009245 |
| <i>yjcB</i> | orf, hypothetical protein | 2,155 | 0,00708 |
| --- | intergenic region | 2,158 | 0,01436 |
| <i>ybjE</i> | putative surface protein | 2,169 | 0,005735 |
| c5343 | Hypothetical protein | 2,198 | 0,001327 |
| <i>rimO // yliG</i> | orf, hypothetical protein | 2,204 | 0,01248 |
| --- | intergenic region | 2,205 | 0,002483 |
| <i>rhIE</i> | putative ATP-dependent RNA helicase | 2,213 | 0,001316 |
| --- | Hypothetical protein | 2,244 | 0,001964 |
| <i>purE</i> | phosphoribosylaminoimidazole carboxylase = AIR carboxylase, catalytic subunit | 2,247 | 0,000771 |
| <i>cdaR // yaeG</i> | hypothetical protein | 2,283 | 0,000326 |
| <i>yoeA</i> | orf, hypothetical protein | 2,288 | 0,001852 |
| <i>rpsQ</i> | 30S ribosomal subunit protein S17 | 2,309 | 4,96E-02 |

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|---------------------|---|-------|----------|
| <i>guaC</i> | GMP reductase | 2,310 | 5,05E-02 |
| <i>sokC</i> | antisense RNA blocking mokC (orf69) and hokC (gef) translation | 2,315 | 0,009736 |
| <i>rpmE</i> | 50S ribosomal subunit protein L31 | 2,317 | 4,23E-02 |
| <i>glmY</i> | MG1655_tke1_b4441 /SEG=NC_000913:-2689212,2689360 /LEN=148 | 2,318 | 0,006721 |
| <i>sokB</i> | antisense RNA blocking mokB and hokB translation | 2,325 | 0,001294 |
| <i>ydeN</i> | putative sulfatase | 2,333 | 0,04426 |
| --- | intergenic region | 2,341 | 0,000346 |
| <i>ycaO</i> | orf, hypothetical protein | 2,342 | 0,001316 |
| <i>ychH</i> | orf, hypothetical protein | 2,349 | 0,02268 |
| --- | intergenic region | 2,365 | 0,004222 |
| <i>phoA</i> | alkaline phosphatase | 2,365 | 8,08E-03 |
| --- | intergenic region | 2,369 | 0,004579 |
| <i>yciX</i> | orf; Unknown function | 2,375 | 0,00559 |
| <i>ymiA</i> | orf; Unknown function | 2,380 | 0,006051 |
| <i>uspG // ybdQ</i> | orf, hypothetical protein | 2,388 | 0,02101 |
| --- | intergenic region | 2,405 | 0,0178 |
| <i>prsA</i> | phosphoribosylpyrophosphate synthetase | 2,420 | 0,000619 |
| --- | intergenic region | 2,433 | 0,004501 |
| <i>ydiA</i> | orf, hypothetical protein | 2,447 | 0,000409 |
| <i>cueO</i> | hypothetical protein | 2,471 | 0,009636 |
| <i>erpA // yadR</i> | orf, hypothetical protein | 2,488 | 0,009668 |
| <i>ycaK</i> | orf, hypothetical protein | 2,495 | 1,13E-02 |
| <i>ydiY</i> | orf, hypothetical protein | 2,507 | 0,003034 |
| --- | intergenic region | 2,540 | 0,001581 |
| <i>yahM</i> | orf; Unknown function | 2,546 | 0,02161 |
| <i>melA</i> | alpha-galactosidase | 2,565 | 0,0226 |
| <i>speC</i> | ornithine decarboxylase isozyme | 2,565 | 0,000106 |
| <i>potD</i> | spermidineputrescine periplasmic transport protein | 2,604 | 1,76E-02 |
| <i>purP</i> | putative membrane transport protein | 2,606 | 0,001277 |
| <i>ycaC</i> | orf, hypothetical protein | 2,645 | 0,002573 |
| <i>yegQ</i> | orf, hypothetical protein | 2,650 | 0,003358 |
| <i>rplI</i> | 50S ribosomal subunit protein L9 | 2,654 | 7,50E-02 |
| <i>purP // yieG</i> | putative membrane transport protein | 2,657 | 0,001124 |
| <i>purB</i> | adenylosuccinate lyase | 2,687 | 5,40E-02 |
| c0273 | putative DNA repair protein, RAD51 family | 2,693 | 4,51E-02 |
| c3554 | Hypothetical protein | 2,693 | 0,000252 |
| <i>gpt</i> | guanine-hypoxanthine phosphoribosyltransferase | 2,709 | 0,000258 |
| <i>ychM</i> | putative sulfate transporter | 2,730 | 0,000199 |
| <i>fepA</i> | outer membrane receptor for ferric enterobactin (enterochelin) and colicins B and D | 2,763 | 0,006102 |
| --- | intergenic region | 2,772 | 0,000244 |
| --- | hypothetical protein | 2,772 | 1,93E-02 |
| <i>yfbM</i> | orf, hypothetical protein | 2,813 | 0,001362 |
| --- | intergenic region | 2,819 | 0,000415 |
| <i>purK</i> | phosphoribosylaminoimidazole carboxylase = AIR carboxylase, CO(2)-fixing subunit | 2,842 | 0,000457 |

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|---------------------|--|-------|----------|
| <i>cydA</i> | cytochrome d terminal oxidase, polypeptide subunit I | 2,844 | 0,01778 |
| --- | orf, hypothetical protein | 2,890 | 0,02438 |
| --- | intergenic region | 2,910 | 0,005513 |
| <i>carB</i> | carbamoyl-phosphate synthase large subunit | 2,936 | 0,000359 |
| c5293 | Hypothetical protein | 2,969 | 0,005177 |
| <i>yohK</i> | putative serotonin transporter | 2,990 | 0,00432 |
| <i>gudD // ygcX</i> | Glucarate dehydratase | 3,004 | 6,86E-02 |
| <i>isrC</i> | MG1655_IS102_b4435 /SEG=NC_000913:+2069337,2069540 /LEN=203 | 3,036 | 8,72E-03 |
| <i>cydB</i> | cytochrome d terminal oxidase polypeptide subunit II | 3,044 | 0,01574 |
| <i>rluB // yciL</i> | orf, hypothetical protein | 3,074 | 2,55E-02 |
| --- | intergenic region | 3,093 | 0,002888 |
| <i>cvpA</i> | membrane protein required for colicin V production | 3,097 | 4,65E-03 |
| <i>purL</i> | phosphoribosylformyl-glycineamide synthetase = FGAM synthetase | 3,184 | 2,87E-02 |
| --- | orf; Unknown function | 3,224 | 0,001124 |
| <i>purC</i> | phosphoribosylaminoimidazole-succinocarboxamide synthetase = SAICAR synthetase | 3,301 | 0,000119 |
| <i>pyrC</i> | dihydro-orotase | 3,378 | 7,74E-02 |
| --- | intergenic region | 3,389 | 0,000667 |
| <i>purF</i> | amidophosphoribosyltransferase = PRPP amidotransferase | 3,418 | 1,69E-02 |
| <i>ybgE</i> | orf, hypothetical protein | 3,432 | 0,009044 |
| <i>copA</i> | putative ATPase | 3,451 | 0,00708 |
| <i>fiu</i> | putative outer membrane receptor for iron transport | 3,461 | 0,0427 |
| <i>ybgT</i> | hypothetical protein | 3,465 | 0,00622 |
| <i>ndh</i> | respiratory NADH dehydrogenase | 3,509 | 0,008832 |
| <i>flu</i> | antigen 43, phase-variable bipartite outer membrane fluffing protein | 3,526 | 5,28E-02 |
| --- | intergenic region | 3,550 | 0,000152 |
| --- | intergenic region | 3,648 | 0,000896 |
| <i>entH // ybdb</i> | orf, hypothetical protein | 3,691 | 0,003052 |
| <i>yeeF</i> | putative amino acidamine transport protein | 3,691 | 0,00054 |
| <i>ybfA</i> | orf, hypothetical protein | 3,776 | 0,000483 |
| <i>borD // borW</i> | putative Bor protein of prophage CP-933X | 3,816 | 0,002152 |
| <i>rtrR</i> | rtT RNA; may modulate the stringent response | 3,824 | 0,000389 |
| <i>entA</i> | 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase, enterochelin biosynthesis | 3,848 | 0,002602 |
| --- | intergenic region | 3,874 | 0,000527 |
| --- | intergenic region | 3,883 | 0,00027 |
| <i>carA</i> | carbamoyl-phosphate synthetase, glutamine (small) subunit | 3,907 | 5,48E-02 |
| <i>cspH</i> | cold shock-like protein | 4,000 | 0,000595 |
| c0813 | Hypothetical protein | 4,011 | 0,007886 |
| <i>ycaD</i> | putative transport | 4,093 | 0,000294 |
| <i>iraP // yaiB</i> | orf, hypothetical protein | 4,104 | 0,002048 |
| <i>ygaW</i> | orf, hypothetical protein | 4,158 | 0,004139 |
| <i>yeeR</i> | orf, hypothetical protein | 4,320 | 9,07E-07 |
| <i>entB</i> | 2,3-dihydro-2,3-dihydroxybenzoate synthetase, isochroismatase | 4,326 | 0,003647 |
| <i>codB</i> | cytosine permeasetransport | 4,329 | 5,03E-03 |
| c0039 | Hypothetical protein | 4,371 | 1,56E-02 |

| | | | |
|---------------------|--|--------|----------|
| <i>yjcD</i> | Hypothetical protein yjcD | 4,395 | 0,000106 |
| <i>pyrD</i> | dihydro-orotate dehydrogenase | 4,503 | 4,30E-05 |
| <i>purH</i> | phosphoribosylaminoimidazolecarboxamideformyltransferase | 4,519 | 2,35E-02 |
| <i>pyrL</i> | pyrBI operon leader peptide | 4,522 | 2,16E-03 |
| <i>upp</i> | uracil phosphoribosyltransferase | 4,554 | 8,40E-06 |
| <i>purL</i> | phosphoribosylformyl-glycineamide synthetase = FGAM synthetase | 4,787 | 4,29E-02 |
| <i>c1602</i> | Hypothetical protein | 5,039 | 1,03E-03 |
| <i>xanP // yicE</i> | putative transport protein | 5,162 | 5,09E-02 |
| <i>purD</i> | phosphoribosylglycinamide synthetase = GAR synthetase | 5,173 | 7,50E-02 |
| <i>gudX // ygcY</i> | putative (D)-glucarate dehydratase 2 | 5,205 | 5,85E-03 |
| <i>garD // yhaG</i> | (D)-galactarate dehydrogenase | 5,227 | 0,00802 |
| <i>c5055</i> | Hypothetical protein | 5,242 | 2,79E-02 |
| --- | intergenic region | 5,359 | 0,004727 |
| <i>intE</i> | prophage e14 integrase | 5,378 | 4,74E-04 |
| <i>ymfJ</i> | hypothetical protein | 5,676 | 8,40E-06 |
| <i>purM</i> | phosphoribosylaminoimidazole synthetase = AIR synthetase | 5,700 | 1,56E-02 |
| <i>suhB</i> | inositol-1-monophosphatase | 5,852 | 6,06E-02 |
| <i>yohJ</i> | orf, hypothetical protein | 6,173 | 0,002993 |
| <i>garR</i> | tartronate semialdehyde reductase (TSAR) | 6,199 | 5,95E-02 |
| <i>guaB</i> | IMP dehydrogenase | 6,741 | 1,63E-02 |
| <i>purT</i> | phosphoribosylglycinamide formyltransferase 2 | 6,984 | 1,69E-02 |
| <i>garP // yhaU</i> | putative transport protein | 6,993 | 0,00101 |
| <i>uraA</i> | uracil transport | 7,037 | 3,07E-02 |
| <i>garK // yhaD</i> | glycerate kinase I | 7,062 | 1,95E-03 |
| <i>garL // yhaF</i> | alpha-dehydro-beta-deoxy-D-glucarate aldolase | 8,317 | 0,000264 |
| <i>c2318</i> | MG1655_IS092_b4434 /SEG=NC_000913:-1985862,1986021 /LEN=159 | 8,604 | 0,002573 |
| <i>xisE</i> | hypothetical protein | 8,712 | 5,25E-04 |
| --- | intergenic region | 9,396 | 0,000327 |
| <i>mcrA</i> | restriction of DNA at 5-methylcytosine residues; at locus of e14 element | 9,606 | 1,97E-02 |
| <i>pyrI</i> | aspartate carbamoyltransferase, regulatory subunit | 10,629 | 4,23E-02 |
| <i>gudP</i> | putative D-glucarate permease (MFS family) | 10,860 | 1,50E-02 |
| <i>pyrB</i> | aspartate carbamoyltransferase, catalytic subunit | 16,518 | 4,23E-02 |
| <i>c1036</i> | Hypothetical protein | 17,172 | 0,00011 |
| <i>ymfD</i> | orf, hypothetical protein | 18,909 | 1,01E-08 |
| <i>ymfE</i> | orf, hypothetical protein | 32,424 | 4,45E-06 |
| <i>lit</i> | phage T4 late gene expression; at locus of e14 element | 44,140 | 1,11E-04 |
| <i>cohE</i> | putative phage repressor | 45,506 | 4,10E-05 |
| <i>ymfI</i> | hypothetical protein | 85,272 | 3,85E-07 |

3. Anàlisi transcriptòmica mutant MG1655HY_vs_wt

Taula 3. Gens expressats diferencialment en un doble mutant *hha ydgT* (MG1655HY) respecte a la soca salvatge (MG1655) amb un FC>1,5. En diferents intensitats de vermell s'indiquen els gens que es troben induïts respecte a la soca salvatge i en verd els que es troben reprimits.

| Gene.Symbol | Target.Description | FC_HY_vs_WT | Adj.P.Val |
|---------------------|--|-------------|-----------|
| --- | intergenic region | 98,56 | 8,64E-05 |
| <i>yIbH</i> | orf, hypothetical protein | 87,73 | 7,15E-07 |
| --- | intergenic region | 77,65 | 6,92E-06 |
| --- | intergenic region | 61,01 | 2,00E-06 |
| <i>ytfl</i> | orf, hypothetical protein | 58,28 | 2,29E-06 |
| <i>yibG</i> | orf, hypothetical protein | 55,52 | 5,57E-06 |
| Z0654 | orf, hypothetical protein | 53,63 | 5,62E-07 |
| ECs0245 | orf, hypothetical protein | 50,49 | 7,15E-07 |
| <i>yncl</i> | orf, hypothetical protein | 49,04 | 1,17E-06 |
| <i>yhiD</i> | putative transport ATPase | 46,46 | 1,11E-05 |
| <i>ybcK</i> | orf, hypothetical protein | 44,48 | 1,17E-06 |
| <i>ybfD // yhhI</i> | orf; Unknown function | 44,20 | 1,49E-06 |
| --- | intergenic region | 43,68 | 7,39e-09 |
| <i>ydiF</i> | putative enzyme | 43,20 | 2,00E-06 |
| <i>ybbD</i> | orf, hypothetical protein | 41,56 | 4,63E-05 |
| <i>ybfB</i> | orf, hypothetical protein | 39,97 | 2,80E-06 |
| <i>intR</i> | putative transposase | 39,37 | 7,40E-06 |
| <i>yrhA</i> | orf, hypothetical protein | 39,12 | 1,17E-06 |
| <i>ybfL // ydcC</i> | H repeat-associated protein of Rhs element | 38,51 | 3,36E-06 |
| <i>psiF</i> | induced by phosphate starvation | 35,60 | 1,02E-06 |
| --- | orf, hypothetical protein | 34,37 | 4,91E-05 |
| <i>ycgH</i> | putative ATP-binding component of a transport system | 34,13 | 1,72E-06 |
| <i>ydaC</i> | orf, hypothetical protein | 33,80 | 5,62E-07 |
| <i>phoA</i> | alkaline phosphatase | 33,50 | 9,78E-08 |
| <i>ykgB</i> | orf, hypothetical protein | 33,41 | 1,34E-06 |
| --- | intergenic region | 33,31 | 1,03E-05 |
| <i>yagM</i> | orf, hypothetical protein | 32,47 | 1,17E-06 |
| --- | intergenic region | 32,40 | 1,17E-06 |
| <i>yafT</i> | putative aminopeptidase | 30,82 | 1,01E-05 |
| <i>lar // ralR</i> | restriction alleviation and modification enhancement | 30,44 | 4,36E-07 |
| <i>ydaQ</i> | putative lambdoid prophage Rac excisionase | 29,88 | 2,92E-06 |
| <i>ybcL</i> | orf, hypothetical protein | 29,80 | 2,00E-06 |
| <i>yfcV</i> | putative fimbrial-like protein | 29,14 | 2,92E-06 |
| ECs5442 | partial H repeat-associated protein of Rhs element | 28,84 | 9,76E-06 |
| <i>yhhH</i> | orf, hypothetical protein | 28,74 | 1,17E-06 |
| <i>ykgI</i> | orf, hypothetical protein | 28,42 | 7,01e-09 |
| --- | intergenic region | 28,34 | 1,17E-06 |

| | | | |
|---------------------|--|-------|----------|
| <i>yhcA</i> | putative chaperone | 27,88 | 7,40E-06 |
| --- | intergenic region | 27,86 | 1,62E-05 |
| <i>yhiF</i> | orf, hypothetical protein | 27,28 | 2,55E-06 |
| --- | intergenic region | 27,15 | 1,26E-06 |
| --- | intergenic region | 26,35 | 2,79E-05 |
| --- | intergenic region | 26,28 | 1,51E-05 |
| --- | intergenic region | 26,10 | 6,73E-06 |
| --- | intergenic region | 24,99 | 1,49E-04 |
| ECs4472 | hypothetical protein | 24,56 | 3,36E-06 |
| --- | intergenic region | 24,00 | 2,55E-06 |
| <i>yhaC</i> | orf, hypothetical protein | 23,85 | 1,98E-06 |
| <i>yibJ</i> | orf, hypothetical protein | 23,22 | 1,11E-04 |
| --- | intergenic region | 22,72 | 2,44E-05 |
| <i>yjbM</i> | orf, hypothetical protein | 22,56 | 1,26E-05 |
| <i>ygeF</i> | orf, hypothetical protein | 22,47 | 3,86E-06 |
| <i>ybbC</i> | orf, hypothetical protein | 22,46 | 3,36E-06 |
| <i>yagL</i> | DNA-binding protein | 22,10 | 1,17E-06 |
| --- | intergenic region | 21,77 | 1,17E-06 |
| <i>ycdD</i> | hypothetical protein | 20,85 | 1,01E-05 |
| --- | orf, hypothetical protein | 20,39 | 3,06E-05 |
| <i>ompL</i> | orf, hypothetical protein | 20,38 | 4,88E-05 |
| --- | orf, hypothetical protein | 20,32 | 1,47E-05 |
| --- | intergenic region | 20,08 | 1,68E-05 |
| --- | intergenic region | 19,96 | 4,94E-05 |
| <i>ycgX</i> | orf, hypothetical protein | 19,85 | 1,89E-05 |
| --- | intergenic region | 19,75 | 9,31E-06 |
| --- | intergenic region | 19,64 | 1,11E-08 |
| --- | intergenic region | 19,47 | 4,98E-06 |
| <i>ybdO</i> | putative transcriptional regulator LYSR-type | 19,27 | 4,86E-05 |
| --- | intergenic region | 19,23 | 1,17E-06 |
| <i>ydfK // ynaE</i> | orf, hypothetical protein | 19,21 | 2,55E-06 |
| --- | intergenic region | 18,97 | 5,25E-06 |
| --- | intergenic region | 18,91 | 7,79E-08 |
| <i>csgF</i> | curli production assemblytransport component, 2nd curli operon | 18,71 | 5,31E-05 |
| <i>ydiO</i> | Hypothetical protein ydiO | 18,70 | 1,17E-06 |
| <i>yqeJ</i> | orf, hypothetical protein | 18,60 | 1,64E-04 |
| <i>ydjO</i> | orf, hypothetical protein | 18,48 | 1,39E-05 |
| <i>chbF</i> | phospho-beta-glucosidase; cryptic | 18,15 | 3,36E-06 |
| <i>yccE</i> | orf, hypothetical protein | 18,10 | 2,00E-06 |
| --- | intergenic region | 17,99 | 2,17E-04 |
| <i>yhiL</i> | orf, hypothetical protein | 17,94 | 8,95E-06 |
| <i>ygiL</i> | putative fimbrial-like protein | 17,93 | 1,02E-06 |
| --- | intergenic region | 17,75 | 1,03E-05 |
| <i>ibpB</i> | heat shock protein | 17,11 | 0,006606 |
| <i>rhsB</i> | rhsB protein in rhs element | 16,94 | 1,62E-05 |

| | | | |
|-----------------------------|--|-------|-----------|
| <i>ydcD</i> | orf; Unknown function | 16,45 | 2,80E-06 |
| Z0655 | orf; Unknown function | 16,18 | 9,80E-06 |
| <i>yhhZ</i> | orf, hypothetical protein | 15,88 | 3,36E-06 |
| <i>csgE</i> | curli production assemblytransport component, 2nd curli operon | 15,88 | 1,19E-05 |
| --- | intergenic region | 15,80 | 3,68E-06 |
| --- | intergenic region | 15,77 | 1,16e-08 |
| <i>ycdT</i> | orf, hypothetical protein | 15,77 | 3,36E-06 |
| <i>ybcM</i> | putative ARAC-type regulatory protein | 15,44 | 1,85E-06 |
| Z0273 | orf; Unknown function | 15,23 | 1,78E-05 |
| <i>yhaB</i> | orf, hypothetical protein | 15,23 | 1,47E-04 |
| <i>yfjl</i> | orf, hypothetical protein | 14,99 | 3,36E-06 |
| <i>ybfO</i> | orf, hypothetical protein | 14,79 | 1,66E-04 |
| <i>fimZ</i> | fimbrial Z protein; probable signal transducer | 14,66 | 1,32E-05 |
| <i>yafU</i> | orf, hypothetical protein | 14,54 | 4,82E-06 |
| --- | intergenic region | 14,41 | 2,39e-06 |
| <i>yhiI</i> | orf, hypothetical protein | 14,13 | 1,72E-06 |
| <i>yafF // ybfl // ydcC</i> | H repeat-associated protein (ORF-H) | 13,96 | 1,25E-06 |
| --- | intergenic region | 13,90 | 8,86E-03 |
| <i>yhaI</i> | putative cytochrome | 13,79 | 2,20E-05 |
| <i>ybfD</i> | putative DNA ligase | 13,78 | 7,40E-06 |
| <i>ybfC</i> | orf, hypothetical protein | 13,78 | 5,25E-06 |
| <i>yagK</i> | orf, hypothetical protein | 13,65 | 1,17E-06 |
| <i>ygeH</i> | putative invasion protein | 13,50 | 2,04E-05 |
| <i>yigG</i> | orf, hypothetical protein | 13,49 | 1,47E-04 |
| <i>ydaY</i> | orf, hypothetical protein | 13,46 | 1,16E-05 |
| --- | intergenic region | 13,34 | 4,93E-05 |
| --- | intergenic region | 13,32 | 3,74E-05 |
| <i>psuK // yeiC</i> | putative kinase | 13,27 | 7,79e-08 |
| <i>ynaK</i> | orf, hypothetical protein | 13,22 | 3,36E-06 |
| --- | intergenic region | 13,20 | 2,28E-05 |
| --- | intergenic region | 13,14 | 8,53E-04 |
| <i>ibpA</i> | heat shock protein | 13,03 | 0,008755 |
| --- | intergenic region | 13,00 | 4,32E-04 |
| --- | intergenic region | 12,99 | 6,51E-06 |
| <i>cspl</i> | cold shock-like protein | 12,92 | 1,90E-03 |
| <i>yqiH</i> | putative membrane protein | 12,92 | 1,65E-04 |
| --- | intergenic region | 12,88 | 1,47E-04 |
| <i>yehA</i> | putative type-1 fimbrial protein | 12,85 | 2,58E-05 |
| <i>rhcC</i> | orf, hypothetical protein | 12,73 | 2,28E-05 |
| --- | intergenic region | 12,61 | 1,37e-06 |
| --- | hypothetical protein | 12,50 | 6,92E-06 |
| --- | intergenic region | 12,02 | 0,0005087 |
| <i>alsE</i> | putative epimerase | 11,93 | 2,00E-06 |
| <i>yedN</i> | orf, hypothetical protein | 11,88 | 1,00E-05 |
| <i>ygeG</i> | orf, hypothetical protein | 11,51 | 1,32E-04 |

| | | | |
|---------------------|---|-------|-----------|
| <i>gadE // yhiE</i> | orf, hypothetical protein | 11,41 | 0,0003352 |
| <i>rhsD</i> | rhsD protein in rhs element | 11,36 | 2,29E-05 |
| <i>casA</i> | orf, hypothetical protein | 11,26 | 2,92E-06 |
| <i>alsA // yjcW</i> | putative ATP-binding component of a transport system | 11,22 | 9,11e-08 |
| --- | intergenic region | 11,17 | 3,81E-04 |
| --- | intergenic region | 11,13 | 4,63E-05 |
| --- | intergenic region | 11,12 | 1,32E-04 |
| <i>pinQ // pinR</i> | putative transposon resolvase | 11,07 | 6,13E-05 |
| <i>yaiV</i> | orf, hypothetical protein | 11,03 | 0,00039 |
| <i>ydaG</i> | orf, hypothetical protein | 11,03 | 9,07E-06 |
| <i>yfjJ</i> | orf, hypothetical protein | 10,97 | 4,57E-05 |
| <i>arpA</i> | Arp | 10,96 | 3,51E-04 |
| --- | intergenic region | 10,94 | 7,40E-06 |
| <i>alsK // yjcT</i> | putative NAGC-like transcriptional regulator | 10,91 | 1,17E-06 |
| <i>appY</i> | regulatory protein affecting appA and other genes | 10,82 | 1,35E-02 |
| <i>yibD</i> | putative regulator | 10,81 | 1,86E-04 |
| --- | intergenic region | 10,81 | 6,72E-05 |
| <i>iraM</i> | orf, hypothetical protein | 10,66 | 5,29E-03 |
| <i>cspB</i> | CspB | 10,65 | 4,32E-06 |
| --- | intergenic region | 10,61 | 9,88E-05 |
| <i>alpA</i> | prophage CP4-57 regulatory protein alpA | 10,59 | 2,95E-06 |
| <i>allB // ybbX</i> | orf; Unknown function | 10,59 | 2,83E-06 |
| <i>yjbL</i> | orf, hypothetical protein | 10,53 | 5,31E-03 |
| <i>emrY</i> | multidrug resistance protein Y | 10,53 | 1,23E-05 |
| <i>yliE</i> | orf, hypothetical protein | 10,53 | 3,78E-03 |
| --- | intergenic region | 10,51 | 1,19E-04 |
| <i>casB</i> | orf, hypothetical protein | 10,49 | 1,17E-06 |
| <i>yhiS</i> | orf, hypothetical protein | 10,40 | 1,34E-03 |
| <i>recE</i> | exonuclease VIII, ds DNA exonuclease, 5 --> 3 specific | 10,34 | 3,29E-05 |
| <i>c4305</i> | Hypothetical protein | 10,25 | 1,26E-04 |
| <i>evgS</i> | putative sensor for regulator EvgA | 10,24 | 1,03E-05 |
| <i>yjgL</i> | orf, hypothetical protein | 10,07 | 3,24E-05 |
| <i>yadC</i> | putative fimbrial-like protein | 10,00 | 1,06E-05 |
| <i>ydeQ</i> | putative adhesin; similar to FimH protein | 10,00 | 2,41E-02 |
| --- | intergenic region | 9,99 | 1,17E-06 |
| --- | intergenic region | 9,93 | 3,36E-06 |
| --- | intergenic region | 9,86 | 1,20E-04 |
| <i>ycgH</i> | putative part of putative ATP-binding component of a transport system | 9,76 | 4,82E-06 |
| --- | intergenic region | 9,67 | 4,88E-05 |
| --- | intergenic region | 9,54 | 2,27E-05 |
| <i>psuG // yeiN</i> | orf, hypothetical protein | 9,52 | 2,44E-05 |
| --- | intergenic region | 9,50 | 2,55E-04 |
| <i>yigF</i> | orf, hypothetical protein | 9,49 | 4,86E-05 |
| <i>yjhR</i> | putative frameshift suppressor | 9,49 | 3,74E-05 |
| --- | orf, hypothetical protein | 9,43 | 1,82E-02 |

| | | | |
|---------------------|--|------|-----------|
| c3178 | Hypothetical protein | 9,40 | 1,32E-04 |
| <i>yqiG</i> | putative membrane protein | 9,39 | 9,51E-05 |
| --- | intergenic region | 9,36 | 3,41E-03 |
| <i>ykgH</i> | orf, hypothetical protein | 9,31 | 4,38E-04 |
| <i>alsC // yjcV</i> | putative transport system permease protein | 9,31 | 2,44E-05 |
| --- | orf, hypothetical protein | 9,29 | 4,81E-06 |
| ECs3713 | orf, hypothetical protein | 9,26 | 8,47E-05 |
| <i>csgD</i> | putative 2-component transcriptional regulator for 2nd curli operon | 9,25 | 3,17E-05 |
| --- | intergenic region | 9,16 | 0,0008067 |
| <i>yadK</i> | putative fimbrial protein | 9,15 | 4,67E-06 |
| --- | intergenic region | 9,13 | 1,40E-04 |
| <i>rhsE</i> | RhsE | 9,10 | 6,92E-06 |
| --- | intergenic region | 9,09 | 7,36e-07 |
| <i>cspG</i> | homolog of Salmonella cold shock protein | 9,03 | 3,15E-05 |
| <i>yiiE</i> | orf, hypothetical protein | 9,01 | 2,60E-04 |
| <i>ydaE</i> | hypothetical protein | 9,01 | 7,29E-05 |
| --- | intergenic region | 8,99 | 2,91E-05 |
| <i>ybgD</i> | putative fimbrial-like protein | 8,96 | 0,0001376 |
| <i>yfdE</i> | putative enzyme | 8,88 | 4,20E-03 |
| <i>kil // kilR</i> | hypothetical protein | 8,74 | 2,44E-05 |
| <i>ygeO</i> | orf, hypothetical protein | 8,74 | 5,17E-06 |
| --- | intergenic region | 8,73 | 1,64E-04 |
| --- | intergenic region | 8,71 | 7,19E-04 |
| --- | intergenic region | 8,70 | 0,0001129 |
| <i>gadB</i> | glutamate decarboxylase isozyme | 8,68 | 2,46E-03 |
| --- | intergenic region | 8,65 | 6,99e-09 |
| <i>yedV</i> | putative 2-component sensor protein | 8,59 | 6,00E-04 |
| <i>casC</i> | orf, hypothetical protein | 8,59 | 1,80E-06 |
| --- | intergenic region | 8,56 | 1,64E-04 |
| <i>ygeN</i> | orf, hypothetical protein | 8,46 | 1,54E-03 |
| --- | intergenic region | 8,32 | 0,0003554 |
| <i>cmtB</i> | PTS system, mannitol-specific enzyme II component, cryptic | 8,31 | 1,66e-06 |
| <i>yfgH</i> | putative outer membrane lipoprotein | 8,21 | 7,69E-04 |
| --- | intergenic region | 8,17 | 1,65E-04 |
| --- | intergenic region | 8,09 | 0,0004172 |
| <i>yedN</i> | orf, hypothetical protein | 8,06 | 4,12E-05 |
| <i>hdeB</i> | orf, hypothetical protein | 8,01 | 9,26E-05 |
| <i>ariR // ymgB</i> | orf, hypothetical protein | 8,00 | 4,77E-02 |
| --- | orf, hypothetical protein | 7,96 | 1,88E-04 |
| <i>yqil</i> | orf, hypothetical protein | 7,92 | 1,06E-04 |
| <i>yfdF</i> | orf, hypothetical protein | 7,89 | 1,09E-05 |
| <i>yggP</i> | orf, hypothetical protein | 7,82 | 1,19E-05 |
| <i>yjeN</i> | orf, hypothetical protein | 7,78 | 9,25E-04 |
| c0500 | Hypothetical protein | 7,77 | 1,16E-03 |
| <i>mcrA</i> | restriction of DNA at 5-methylcytosine residues; at locus of e14 element | 7,74 | 7,16E-03 |

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|---------------------|---|------|-----------|
| <i>yjfK</i> | orf, hypothetical protein | 7,74 | 5,27E-05 |
| <i>yjfL</i> | Hypothetical protein | 7,71 | 4,89e-08 |
| <i>yadN</i> | putative fimbrial-like protein | 7,71 | 1,77E-04 |
| --- | intergenic region | 7,67 | 3,07e-08 |
| <i>gadA</i> | glutamate decarboxylase isozyme | 7,67 | 4,99E-03 |
| --- | intergenic region | 7,66 | 1,57E-02 |
| <i>ydeS</i> | putative fimbrial-like protein | 7,65 | 0,0009319 |
| <i>ydeR</i> | putative fimbrial-like protein | 7,65 | 0,0003007 |
| <i>yjdA</i> | putative vimentin | 7,62 | 3,18E-06 |
| <i>ydbD</i> | orf, hypothetical protein | 7,59 | 7,36e-07 |
| --- | intergenic region | 7,57 | 3,79E-05 |
| --- | intergenic region | 7,55 | 2,09E-04 |
| <i>yfdE</i> | orf, hypothetical protein | 7,55 | 1,45E-02 |
| --- | intergenic region | 7,51 | 6,17e-06 |
| <i>gadX // yhiX</i> | putative ARAC-type regulatory protein | 7,50 | 7,66E-02 |
| --- | intergenic region | 7,46 | 1,95E-06 |
| <i>ygeK</i> | orf, hypothetical protein | 7,41 | 2,03E-04 |
| --- | orf, hypothetical protein | 7,40 | 1,75E-04 |
| --- | intergenic region | 7,37 | 7,96E-03 |
| --- | intergenic region | 7,37 | 3,48E-04 |
| --- | intergenic region | 7,34 | 1,97E-04 |
| <i>yfdR</i> | orf, hypothetical protein | 7,32 | 9,08E-03 |
| <i>yfdV</i> | putative receptor protein | 7,30 | 8,91E-04 |
| <i>aroE // ydiB</i> | putative oxidoreductase | 7,25 | 3,55E-05 |
| <i>allB // ybbX</i> | putative hydrolase | 7,25 | 9,26E-05 |
| <i>casD</i> | orf, hypothetical protein | 7,23 | 3,84e-08 |
| <i>yjhF</i> | putative transport system permease | 7,19 | 2,91E-05 |
| --- | intergenic region | 7,19 | 1,38E-04 |
| <i>dppF</i> | putative ATP-binding component of dipeptide transport system | 7,16 | 0,0002428 |
| <i>arpB</i> | ankyrin repeat protein | 7,16 | 1,91E-03 |
| --- | intergenic region | 7,16 | 1,73E-04 |
| <i>gspA // yheD</i> | putative export protein A for general secretion pathway (GSP) | 7,14 | 9,00E-08 |
| <i>ymfD</i> | orf, hypothetical protein | 7,12 | 1,76E-05 |
| --- | intergenic region | 7,09 | 1,65E-04 |
| <i>recT</i> | recombinase, DNA renaturation | 7,06 | 5,97E-06 |
| <i>yadM</i> | putative fimbrial-like protein | 7,05 | 3,86E-06 |
| --- | intergenic region | 7,03 | 4,94E-05 |
| <i>ECs3736</i> | orf, hypothetical protein | 7,03 | 2,58E-05 |
| --- | intergenic region | 6,99 | 1,19E-04 |
| --- | intergenic region | 6,98 | 1,13E-03 |
| <i>celF // chbF</i> | phospho-beta-glucosidase; cryptic | 6,94 | 4,63E-05 |
| <i>ybcV</i> | putative an envelop protein | 6,90 | 1,78E-03 |
| --- | intergenic region | 6,88 | 6,53E-04 |
| <i>ynch</i> | orf, hypothetical protein | 6,86 | 3,13E-03 |
| <i>ydfJ</i> | putative transport protein | 6,86 | 6,31E-05 |

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|---------------------|---|------|-----------|
| <i>casE</i> | orf, hypothetical protein | 6,80 | 1,01E-05 |
| --- | intergenic region | 6,78 | 9,06E-05 |
| <i>mcbR</i> | hypothetical protein | 6,77 | 3,48E-04 |
| --- | intergenic region | 6,76 | 1,77E-05 |
| <i>matA // ykgK</i> | putative regulator | 6,76 | 0,0001131 |
| <i>yjfM</i> | Hypothetical protein yjfM | 6,76 | 3,74E-05 |
| <i>ymgC</i> | orf, hypothetical protein | 6,69 | 0,0001468 |
| --- | intergenic region | 6,68 | 2,57E-04 |
| <i>yahE</i> | orf, hypothetical protein | 6,67 | 1,28E-04 |
| <i>ygeQ</i> | orf, hypothetical protein | 6,65 | 1,13E-05 |
| --- | intergenic region | 6,64 | 1,20E-03 |
| <i>emrK</i> | multidrug resistance protein K | 6,62 | 1,32E-04 |
| --- | intergenic region | 6,57 | 2,52E-04 |
| <i>yqeK</i> | orf, hypothetical protein | 6,54 | 2,75E-05 |
| <i>ydeT</i> | putative outer membrane protein | 6,54 | 0,0009913 |
| <i>ygel</i> | orf, hypothetical protein | 6,51 | 1,32E-04 |
| <i>yjeM</i> | putative transport | 6,51 | 2,31E-03 |
| c2481 | Hypothetical protein | 6,46 | 5,35E-03 |
| --- | intergenic region | 6,42 | 3,50E-06 |
| <i>ydhZ</i> | orf, hypothetical protein | 6,41 | 5,41E-05 |
| <i>yddA</i> | putative ATP-binding component of a transport system | 6,39 | 0,0006699 |
| <i>celD // chbR</i> | negative transcriptional regulator of cel operon | 6,38 | 1,22E-04 |
| <i>ybeR</i> | orf, hypothetical protein | 6,36 | 2,50E-04 |
| --- | intergenic region | 6,32 | 4,42E-04 |
| ECs3519 | putative enzyme | 6,32 | 5,59E-04 |
| c4302 | orf; Unknown function | 6,31 | 5,05E-05 |
| c1929 | orf, hypothetical protein | 6,31 | 1,49E-04 |
| Z2263 | unknown protein associated with Rhs element | 6,31 | 2,43E-03 |
| <i>ydeP</i> | putative oxidoreductase, major subunit | 6,30 | 7,29E-05 |
| <i>ydhY</i> | putative oxidoreductase, Fe-S subunit | 6,25 | 0,002962 |
| <i>racC</i> | RacC protein | 6,25 | 4,10E-04 |
| <i>dppD</i> | putative ATP-binding component of dipeptide transport system | 6,23 | 0,0003328 |
| <i>yjeI</i> | orf, hypothetical protein | 6,21 | 1,07E-04 |
| --- | intergenic region | 6,20 | 0,0001227 |
| --- | intergenic region | 6,19 | 6,14E-04 |
| <i>yibA</i> | orf, hypothetical protein | 6,18 | 4,91E-03 |
| --- | intergenic region | 6,17 | 0,0002206 |
| <i>htrE</i> | probable outer membrane porin protein involved in fimbrial assembly | 6,15 | 8,28E-05 |
| --- | intergenic region | 6,11 | 4,83E-04 |
| <i>yqel</i> | putative sensory transducer | 6,11 | 2,99E-05 |
| <i>yfdX</i> | orf, hypothetical protein | 6,10 | 3,07E-04 |
| <i>yjfl</i> | orf, hypothetical protein | 6,08 | 1,16E-08 |
| <i>yjhS</i> | orf, hypothetical protein | 6,01 | 0,0002188 |
| --- | intergenic region | 6,01 | 4,96E-04 |
| <i>alsB // yjcX</i> | putative LACI-type transcriptional regulator | 5,99 | 2,09E-05 |

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|---------------------|--|------|-----------|
| --- | intergenic region | 5,99 | 1,80E-02 |
| <i>yahF</i> | putative oxidoreductase subunit | 5,97 | 3,97e-06 |
| <i>ydaF</i> | hypothetical protein | 5,96 | 1,90E-04 |
| <i>yrhB</i> | orf, hypothetical protein | 5,81 | 3,10E-04 |
| --- | intergenic region | 5,80 | 5,27E-05 |
| <i>yjiC</i> | orf, hypothetical protein | 5,79 | 9,31E-04 |
| <i>yhaB</i> | Hypothetical protein | 5,78 | 9,30E-03 |
| --- | intergenic region | 5,74 | 2,59E-02 |
| --- | intergenic region | 5,74 | 5,13E-03 |
| --- | intergenic region | 5,72 | 3,90E-05 |
| --- | intergenic region | 5,69 | 3,04E-04 |
| <i>hlyE</i> | Putative conserved protein | 5,65 | 8,12E-02 |
| --- | intergenic region | 5,63 | 0,0004717 |
| <i>ymgA</i> | orf, hypothetical protein | 5,63 | 0,001302 |
| --- | intergenic region | 5,62 | 4,03E-02 |
| --- | intergenic region | 5,62 | 4,93E-05 |
| ECs3712 | putative 2-component transcriptional regulator | 5,61 | 1,07E-03 |
| --- | intergenic region | 5,58 | 4,99E-05 |
| <i>psuT</i> | putative transport system permease protein | 5,57 | 2,95E-05 |
| <i>yjfZ</i> | orf, hypothetical protein | 5,56 | 2,03E-05 |
| <i>wcaD</i> | putative colanic acid polymerase | 5,55 | 4,52e-06 |
| <i>pinH</i> | orf, hypothetical protein | 5,54 | 6,59E-04 |
| --- | intergenic region | 5,54 | 9,18e-08 |
| <i>pbl</i> | orf, hypothetical protein | 5,53 | 3,72E-03 |
| <i>ycgZ</i> | orf, hypothetical protein | 5,53 | 0,001219 |
| <i>hdeD</i> | orf, hypothetical protein | 5,53 | 3,43E-02 |
| <i>ybhM</i> | orf, hypothetical protein | 5,49 | 3,56E-05 |
| <i>ybeF</i> | putative transcriptional regulator LYSR-type | 5,49 | 0,0001478 |
| <i>yjfJ</i> | putative alpha helical protein | 5,49 | 3,37E-04 |
| <i>arpB</i> | Hypothetical protein | 5,46 | 0,0001095 |
| <i>gmd</i> | GDP-D-mannose dehydratase | 5,46 | 5,36E-05 |
| --- | intergenic region | 5,46 | 2,32E-04 |
| <i>yjcF</i> | orf, hypothetical protein | 5,45 | 9,68E-03 |
| --- | intergenic region | 5,43 | 1,5e-07 |
| --- | intergenic region | 5,40 | 4,05E-04 |
| --- | intergenic region | 5,40 | 1,11E-04 |
| <i>yfdS</i> | orf, hypothetical protein | 5,38 | 1,12E-02 |
| <i>hdeA</i> | orf, hypothetical protein | 5,34 | 5,09E-04 |
| --- | intergenic region | 5,33 | 5,96E-04 |
| c2320 | Hypothetical protein | 5,33 | 0,003392 |
| --- | intergenic region | 5,32 | 4,59e-06 |
| <i>gspC // yheE</i> | YheE | 5,31 | 2,89E-03 |
| --- | intergenic region | 5,26 | 1,40E-04 |
| <i>insK</i> | IS150 putative transposase | 5,26 | 2,15E-04 |
| --- | intergenic region | 5,25 | 0,0001239 |

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|---------------------|---|------|-----------|
| --- | intergenic region | 5,25 | 1,63e-05 |
| <i>ycbR</i> | putative chaperone | 5,23 | 1,64E-04 |
| <i>lldR</i> | transcriptional regulator | 5,23 | 0,01863 |
| <i>yliF</i> | orf, hypothetical protein | 5,22 | 0,0001169 |
| <i>c1611</i> | Hypothetical protein | 5,21 | 8,64E-05 |
| ECs0371 | hypothetical protein | 5,17 | 2,05E-05 |
| --- | intergenic region | 5,16 | 1,27E-04 |
| <i>yjhl</i> | putative regulator | 5,16 | 2,48E-03 |
| --- | intergenic region | 5,15 | 3,66E-04 |
| <i>yjhH</i> | putative lyasesynthase | 5,11 | 1,83E-05 |
| --- | intergenic region | 5,09 | 4,29E-04 |
| --- | intergenic region | 5,09 | 6,80E-04 |
| <i>arrD // ybcS</i> | bacteriophage lambda lysozyme homolog | 5,08 | 4,25E-03 |
| <i>wcaG</i> | putative nucleotide di-P-sugar epimerase or dehydratase | 5,08 | 2,11E-04 |
| --- | intergenic region | 5,06 | 1,73E-03 |
| <i>yjcZ</i> | orf, hypothetical protein | 5,06 | 3,59E-03 |
| <i>yjhB</i> | putative transport protein | 5,04 | 1,79e-07 |
| <i>yjhG</i> | putative dehydratase | 5,03 | 1,16E-04 |
| --- | intergenic region | 5,01 | 5,10E-04 |
| c0408 | Hypothetical protein | 5,01 | 9,54E-05 |
| --- | intergenic region | 5,01 | 4,86E-03 |
| Z5814 | orf; Unknown function | 5,00 | 6,95E-04 |
| <i>yadL</i> | putative fimbrial protein | 4,99 | 1,03E-05 |
| <i>yfbN</i> | orf, hypothetical protein | 4,98 | 1,74e-06 |
| --- | intergenic region | 4,98 | 4,47E-04 |
| --- | intergenic region | 4,97 | 5,13E-03 |
| <i>yihP</i> | putative permease | 4,96 | 2,07E-03 |
| <i>ydeO</i> | putative ARAC-type regulatory protein | 4,94 | 2,26E-04 |
| --- | intergenic region | 4,93 | 0,000242 |
| <i>nanC // yjhA</i> | orf, hypothetical protein | 4,93 | 0,0001172 |
| <i>wcaF</i> | putative transferase | 4,92 | 9,18e-08 |
| <i>yeeL</i> | orf, hypothetical protein | 4,92 | 1,03e-06 |
| c5129 | Hypothetical protein | 4,92 | 0,0001403 |
| --- | intergenic region | 4,92 | 1,96E-03 |
| <i>ydjE</i> | putative transport protein | 4,91 | 1,94E-04 |
| --- | intergenic region | 4,91 | 0,001001 |
| --- | intergenic region | 4,88 | 0,0003881 |
| --- | intergenic region | 4,86 | 3,95E-03 |
| <i>yihQ</i> | putative glycosidase | 4,83 | 7,30E-04 |
| <i>yiaB</i> | orf, hypothetical protein | 4,83 | 4,21E-03 |
| --- | intergenic region | 4,82 | 7,12E-02 |
| <i>ydbA</i> | orf, hypothetical protein | 4,81 | 2,58E-05 |
| <i>yebB</i> | orf, hypothetical protein | 4,81 | 8,78E-04 |
| <i>yeal</i> | orf, hypothetical protein | 4,79 | 0,01514 |
| <i>yhfl</i> | orf, hypothetical protein | 4,78 | 0,0006057 |

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|---------------------|--|------|-----------|
| --- | intergenic region | 4,78 | 0,002256 |
| --- | intergenic region | 4,78 | 9,08E-03 |
| --- | intergenic region | 4,77 | 0,0002824 |
| --- | intergenic region | 4,77 | 6,38E-03 |
| <i>eutS</i> | hypothetical protein | 4,76 | 0,0001928 |
| --- | intergenic region | 4,75 | 1,95E-04 |
| <i>yral</i> | putative chaperone | 4,74 | 1,47E-03 |
| <i>ydfD</i> | orf, hypothetical protein | 4,72 | 4,29e-05 |
| <i>ycgV</i> | putative adhesion and penetration protein | 4,71 | 4,18E-03 |
| <i>ycgV</i> | partial putative adhesion protein | 4,71 | 4,14E-02 |
| <i>tomB // ybaJ</i> | orf, hypothetical protein | 4,71 | 1,83E-05 |
| <i>tfaX // ylcE</i> | orf, hypothetical protein | 4,70 | 6,83E-04 |
| <i>ytfA</i> | orf, hypothetical protein | 4,70 | 1,33e-05 |
| --- | intergenic region | 4,69 | 2,64e-07 |
| <i>torY // yecK</i> | putative cytochrome C-type protein | 4,69 | 1,08E-05 |
| --- | intergenic region | 4,67 | 1,00E-02 |
| --- | intergenic region | 4,67 | 2,44E-05 |
| <i>yfgl</i> | putative membrane protein | 4,66 | 1,55E-02 |
| <i>gatR</i> | split galactitol utilization operon repressor, interrupted | 4,64 | 1,54E-04 |
| <i>ydbA</i> | orf, hypothetical protein | 4,63 | 4,39E-05 |
| --- | intergenic region | 4,59 | 3,27E-04 |
| --- | intergenic region | 4,59 | 2,58E-05 |
| --- | intergenic region | 4,59 | 9,85E-05 |
| <i>emrE</i> | methylviologen resistance | 4,59 | 3,21E-03 |
| c1752 | Hypothetical protein | 4,58 | 1,18E-02 |
| <i>oxc</i> | hypothetical protein | 4,58 | 1,84E-04 |
| --- | intergenic region | 4,58 | 0,0008067 |
| <i>arpB</i> | ankyrin repeat protein | 4,58 | 2,9e-06 |
| <i>cspF /</i> | CspF | 4,58 | 2,99e-06 |
| --- | intergenic region | 4,55 | 9,09E-04 |
| <i>wcaE</i> | putative colanic acid biosynthesis glycosyl transferase | 4,54 | 1,27E-03 |
| <i>yghG</i> | orf, hypothetical protein | 4,52 | 0,001524 |
| --- | orf, hypothetical protein | 4,51 | 1,01E-03 |
| --- | intergenic region | 4,50 | 3,26E-03 |
| <i>gip // hyi</i> | glyoxylate-induced protein | 4,48 | 2,15E-04 |
| <i>yneK /</i> | orf, hypothetical protein | 4,47 | 2,05E-02 |
| <i>insJ</i> | IS150 hypothetical protein | 4,47 | 2,09E-04 |
| --- | intergenic region | 4,46 | 5,18E-04 |
| <i>ynbA</i> | hypothetical protein | 4,43 | 1,30E-04 |
| <i>gadW // yhiW</i> | putative ARAC-type regulatory protein | 4,42 | 0,0001296 |
| --- | intergenic region | 4,41 | 9,02E-03 |
| <i>ydfR</i> | orf, hypothetical protein | 4,41 | 1,64E-04 |
| --- | intergenic region | 4,41 | 5,39E-04 |
| <i>sfa // ymcE</i> | suppresses fabA and ts growth mutation | 4,40 | 2,22E-04 |
| --- | intergenic region | 4,39 | 1,86E-03 |

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|---------------------|--|------|-----------|
| --- | intergenic region | 4,39 | 2,32E-02 |
| --- | intergenic region | 4,38 | 0,0001697 |
| --- | intergenic region | 4,37 | 0,0002371 |
| --- | intergenic region | 4,34 | 9,25E-04 |
| --- | intergenic region | 4,33 | 1,45E-03 |
| --- | intergenic region | 4,32 | 4,74e-07 |
| <i>yjhC</i> | putative dehydrogenase | 4,31 | 8,51E-05 |
| <i>ycbS</i> | putative outer membrane protein | 4,30 | 6,42E-05 |
| <i>yeiS</i> | orf, hypothetical protein | 4,30 | 7,35E-05 |
| <i>blr</i> | beta-lactam resistance protein | 4,30 | 1,09E-02 |
| c1441 | Hypothetical protein | 4,30 | 6,82E-03 |
| <i>yciE</i> | orf, hypothetical protein | 4,29 | 2,21E-05 |
| <i>bglG</i> | positive regulation of bgl operon | 4,27 | 5,55E-03 |
| <i>lyxK</i> | L-xylulose kinase, cryptic | 4,26 | 1,99E-04 |
| <i>yihF</i> | putative GTP-binding protein | 4,26 | 2,52E-03 |
| <i>ynbB</i> | putative phosphatidate cytidiltransferase | 4,25 | 1,15E-04 |
| <i>yceO</i> | orf, hypothetical protein | 4,23 | 7,69E-04 |
| --- | intergenic region | 4,23 | 2,64E-04 |
| <i>chbG</i> | orf, hypothetical protein | 4,21 | 2,17E-04 |
| <i>yiaO</i> | putative solute-binding transport protein | 4,21 | 2,52E-03 |
| <i>ygbT</i> | orf, hypothetical protein | 4,21 | 8,64E-05 |
| <i>yggP</i> | putative oxidoreductase | 4,18 | 9,67E-05 |
| --- | intergenic region | 4,18 | 4,91E-03 |
| <i>ydeJ</i> | orf, hypothetical protein | 4,17 | 1,30E-02 |
| <i>ykiA</i> | orf, hypothetical protein | 4,17 | 3,51E-04 |
| <i>ydiV</i> | orf, hypothetical protein | 4,15 | 3,13E-03 |
| --- | intergenic region | 4,15 | 9,06E-05 |
| <i>yfcl</i> | orf, hypothetical protein | 4,14 | 8,57E-03 |
| --- | intergenic region | 4,14 | 6,22E-03 |
| <i>yafO</i> | orf, hypothetical protein | 4,13 | 1,32E-04 |
| <i>intQ</i> | integrase fragment, cryptic prophage CP-933P | 4,13 | 2,10E-03 |
| --- | intergenic region | 4,12 | 1,64E-03 |
| <i>yafP</i> | orf, hypothetical protein | 4,12 | 6,95E-04 |
| <i>cmtA</i> | PTS system, mannitol-specific enzyme II component, cryptic | 4,11 | 2,26E-04 |
| <i>dppB</i> | dipeptide transport system permease protein 1 | 4,10 | 0,0008587 |
| <i>dppC</i> | dipeptide transport system permease protein 2 | 4,10 | 0,00061 |
| <i>yqiI</i> | putative oxidoreductase | 4,09 | 2,74E-02 |
| --- | intergenic region | 4,08 | 0,0002631 |
| <i>nanM // yjhT</i> | orf, hypothetical protein | 4,08 | 0,0001105 |
| <i>yhcD</i> | putative outer membrane protein | 4,06 | 5,09E-04 |
| <i>celB // chbC</i> | PTS system, cellobiose-specific IIC component | 4,05 | 8,43E-03 |
| <i>trkG</i> | trk system potassium uptake | 4,05 | 7,75E-05 |
| <i>ypdI</i> | orf, hypothetical protein | 4,04 | 2,96E-03 |
| <i>intG</i> | orf, hypothetical protein | 4,04 | 6,17E-03 |
| --- | intergenic region | 4,04 | 6,14E-03 |

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|---------------------|--|------|-----------|
| <i>ymfE</i> | orf, hypothetical protein | 4,03 | 4,38E-04 |
| <i>ydel</i> | orf, hypothetical protein | 4,03 | 1,04E-03 |
| <i>yggF</i> | orf, hypothetical protein | 4,03 | 1,11E-04 |
| <i>ydhV</i> | orf, hypothetical protein | 4,02 | 0,0008744 |
| --- | intergenic region | 4,00 | 5,02E-03 |
| <i>mdtE // yhiU</i> | putative membrane protein | 3,99 | 0,001732 |
| --- | intergenic region | 3,99 | 2,00E-03 |
| --- | intergenic region | 3,98 | 6,89E-03 |
| --- | intergenic region | 3,95 | 7,57E-02 |
| --- | intergenic region | 3,95 | 1,28E-03 |
| --- | intergenic region | 3,94 | 4,66e-05 |
| --- | intergenic region | 3,89 | 3,20E-02 |
| <i>ycbS</i> | partial fimbrial usher protein | 3,87 | 2,15E-04 |
| --- | intergenic region | 3,85 | 2,77E-02 |
| --- | intergenic region | 3,84 | 6,17E-02 |
| <i>yjeO</i> | orf, hypothetical protein | 3,83 | 2,38E-03 |
| <i>yahA</i> | orf, hypothetical protein | 3,83 | 0,00068 |
| <i>yahG</i> | orf, hypothetical protein | 3,83 | 3,59E-04 |
| <i>gspB // pinO</i> | calcium-binding protein required for initiation of chromosome replication | 3,82 | 9,28E-03 |
| <i>ecpD</i> | probable pilin chaperone similar to PapD | 3,80 | 6,23E-03 |
| <i>dnaJ</i> | chaperone with DnaK; heat shock protein | 3,80 | 0,0007785 |
| --- | intergenic region | 3,79 | 0,01904 |
| --- | intergenic region | 3,79 | 4,45E-03 |
| --- | intergenic region | 3,79 | 0,000367 |
| <i>ycdU</i> | orf, hypothetical protein | 3,78 | 3,98E-02 |
| --- | intergenic region | 3,78 | 6,07E-05 |
| --- | intergenic region | 3,78 | 4,21E-03 |
| <i>yeeL</i> | orf, hypothetical protein | 3,77 | 2,70E-02 |
| --- | intergenic region | 3,76 | 4,42E-04 |
| --- | intergenic region | 3,76 | 0,0001033 |
| --- | intergenic region | 3,75 | 1,09E-02 |
| --- | intergenic region | 3,75 | 6,44E-02 |
| --- | intergenic region | 3,75 | 4,42E-04 |
| --- | intergenic region | 3,74 | 0,001724 |
| <i>ygaQ</i> | orf, hypothetical protein | 3,72 | 4,06E-02 |
| <i>celC // chbA</i> | PEP-dependent phosphotransferase enzyme III for cellobiose, arbutin, and salicin | 3,72 | 5,26E-02 |
| --- | intergenic region | 3,72 | 8,64E-03 |
| <i>fimB</i> | recombinase involved in phase variation; regulator for fimA | 3,71 | 3,03E-04 |
| <i>glcA // yghK</i> | putative permease | 3,70 | 2,19E-02 |
| --- | intergenic region | 3,70 | 8,75E-03 |
| --- | intergenic region | 3,69 | 7,96E-03 |
| --- | intergenic region | 3,68 | 3,48E-04 |
| <i>htrL // yibB</i> | involved in lipopolysaccharide biosynthesis | 3,67 | 2,02e-07 |
| <i>ydgK</i> | orf, hypothetical protein | 3,66 | 6,83E-04 |

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|---------------------|---|------|-----------|
| --- | intergenic region | 3,66 | 3,02E-02 |
| --- | intergenic region | 3,65 | 5,53E-02 |
| --- | intergenic region | 3,65 | 1,24E-02 |
| <i>yddB</i> | orf, hypothetical protein | 3,65 | 2,95E-03 |
| --- | intergenic region | 3,64 | 0,000894 |
| <i>eutP</i> | orf, hypothetical protein | 3,63 | 1,73E-02 |
| <i>citA // dpiB</i> | putative sensor-type protein | 3,63 | 4,21E-04 |
| <i>elaD</i> | putative sulfatase phosphatase | 3,63 | 2,22E-03 |
| --- | intergenic region | 3,62 | 0,001324 |
| --- | intergenic region | 3,61 | 2,7e-05 |
| --- | intergenic region | 3,61 | 0,001447 |
| <i>ygfJ // ygfJ</i> | orf, hypothetical protein | 3,60 | 0,002624 |
| <i>ypjC</i> | orf, hypothetical protein | 3,60 | 1,9e-05 |
| <i>csgG</i> | curli production assemblytransport component, 2nd curli operon | 3,58 | 1,47E-04 |
| <i>yjgN</i> | orf, hypothetical protein | 3,58 | 1,41E-04 |
| <i>mdtF // yhiV</i> | putative transport system permease protein | 3,58 | 3,84E-02 |
| <i>fxsA</i> | hypothetical protein | 3,56 | 0,009856 |
| --- | orf, hypothetical protein | 3,56 | 3,40E-04 |
| <i>renD</i> | orf, hypothetical protein | 3,55 | 0,0003658 |
| <i>ygjJ</i> | orf, hypothetical protein | 3,55 | 0,0004479 |
| --- | intergenic region | 3,55 | 8,90E-04 |
| --- | intergenic region | 3,55 | 8,63E-02 |
| --- | intergenic region | 3,54 | 2,26E-02 |
| --- | intergenic region | 3,52 | 9,83E-02 |
| --- | intergenic region | 3,52 | 0,0001122 |
| Z5924 | orf; Unknown function | 3,51 | 2,66E-03 |
| --- | intergenic region | 3,51 | 2,71E-03 |
| --- | intergenic region | 3,48 | 0,01431 |
| --- | intergenic region | 3,48 | 6,99e-06 |
| <i>yehB</i> | putative outer membrane protein | 3,48 | 0,0008587 |
| <i>rzpD</i> | bacteriophage lambda endopeptidase homolog | 3,47 | 0,003165 |
| <i>ygbF</i> | orf, hypothetical protein | 3,46 | 1,19E-04 |
| <i>rzpR</i> | lipoprotein Rz1 precursor | 3,45 | 0,0002034 |
| <i>hslR // yrfH</i> | hypothetical protein | 3,45 | 0,003761 |
| --- | intergenic region | 3,45 | 2,01E-02 |
| <i>yihO</i> | putative permease | 3,44 | 1,88E-02 |
| <i>yohG</i> | orf, hypothetical protein | 3,43 | 2,86E-03 |
| --- | intergenic region | 3,43 | 2,21E-03 |
| <i>mcrC</i> | component of McrBC 5-methylcytosine restriction system, expands range of sequences restricted | 3,43 | 1,20E-03 |
| --- | intergenic region | 3,42 | 3,97e-06 |
| <i>yddL</i> | putative outer membrane porin protein | 3,42 | 1,86E-02 |
| --- | intergenic region | 3,42 | 0,0002639 |
| --- | intergenic region | 3,42 | 2,89E-03 |
| <i>sfmF</i> | putative fimbrial-like protein | 3,42 | 8,47e-05 |
| <i>yqeH</i> | orf, hypothetical protein | 3,41 | 1,96E-02 |

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|---------------------|--|------|-----------|
| --- | intergenic region | 3,40 | 5,38E-04 |
| <i>gmm // wcaH</i> | GDP-mannose mannosyl hydrolase | 3,38 | 2,97E-03 |
| <i>clpB</i> | heat shock protein | 3,38 | 1,70E-02 |
| <i>yegZ</i> | orf, hypothetical protein | 3,37 | 5,10E-04 |
| <i>hslV</i> | heat shock protein hslVU, proteasome-related peptidase subunit | 3,36 | 0,005641 |
| --- | intergenic region | 3,35 | 5,94E-03 |
| <i>yfdQ</i> | orf, hypothetical protein | 3,35 | 5,39E-04 |
| ECs2704 | hypothetical protein | 3,34 | 2,05E-03 |
| <i>ykfJ</i> | orf, hypothetical protein | 3,33 | 1,31E-02 |
| <i>frc // yfdW</i> | putative enzyme | 3,32 | 7,90E-03 |
| c0500 | Hypothetical protein | 3,32 | 2,25E-03 |
| <i>aroM</i> | protein of aro operon, regulated by aroR | 3,32 | 3,73E-02 |
| --- | intergenic region | 3,31 | 4,60E-03 |
| --- | intergenic region | 3,31 | 1,36E-03 |
| <i>viaA</i> | Hypothetical protein viaA | 3,31 | 1,10E-02 |
| <i>ydfI</i> | Hypothetical oxidoreductase ydfI | 3,30 | 1,11E-03 |
| <i>ybdN</i> | orf, hypothetical protein | 3,29 | 3,76E-03 |
| <i>fimE</i> | recombinase involved in phase variation; regulator for fimA | 3,29 | 5,11E-03 |
| <i>pgaC // ycdQ</i> | orf, hypothetical protein | 3,29 | 3,23E-04 |
| <i>yfhL</i> | orf, hypothetical protein | 3,28 | 4,60E-03 |
| <i>agaB</i> | PTS system, cytoplasmic, N-acetylgalactosamine-specific IIB component 1 (EIIB-AGA) | 3,27 | 1,23E-03 |
| <i>ddg // lpxP</i> | putative heat shock protein | 3,26 | 0,0001223 |
| <i>sgcR</i> | putative DEOR-type transcriptional regulator | 3,26 | 3,29E-02 |
| --- | intergenic region | 3,26 | 2,82E-02 |
| --- | intergenic region | 3,25 | 0,001715 |
| <i>yebO</i> | orf, hypothetical protein | 3,25 | 2,44e-05 |
| --- | intergenic region | 3,25 | 9,50E-02 |
| <i>ygcG</i> | orf, hypothetical protein | 3,25 | 1,45E-03 |
| --- | orf, hypothetical protein | 3,23 | 7,91E-04 |
| <i>yfjH</i> | putative histone | 3,23 | 2,12e-07 |
| <i>yecT</i> | orf, hypothetical protein | 3,23 | 0,000193 |
| <i>flxA</i> | orf, hypothetical protein | 3,23 | 6,29e-06 |
| <i>arnC</i> | putative sugar transferase | 3,22 | 4,59E-04 |
| c3022 | orf; Unknown function | 3,22 | 5,75E-02 |
| <i>viaR</i> | putative 3-hexulose-6-phosphate isomerase | 3,22 | 5,38E-04 |
| <i>pphB</i> | protein phosphatase 2 | 3,22 | 1,89E-02 |
| <i>ycjF</i> | orf, hypothetical protein | 3,22 | 0,01395 |
| --- | intergenic region | 3,20 | 2,67E-02 |
| --- | intergenic region | 3,20 | 9,63e-06 |
| --- | intergenic region | 3,19 | 3,56E-02 |
| <i>gadY</i> | MG1655_IS183_b4452 /SEG=NC_000913:+3662494,3662598 /LEN=104 | 3,19 | 3,81E-02 |
| --- | intergenic region | 3,18 | 1,08E-03 |
| --- | intergenic region | 3,18 | 1,73E-02 |
| --- | intergenic region | 3,17 | 0,01139 |
| --- | intergenic region | 3,17 | 0,0008631 |

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|---------------------|--|------|-----------|
| <i>ybaA</i> | orf, hypothetical protein | 3,16 | 0,0001485 |
| <i>eaeH</i> | attaching and effacing protein, pathogenesis factor | 3,16 | 6,13E-02 |
| --- | intergenic region | 3,15 | 8,3e-06 |
| <i>dicB</i> | inhibition of cell division | 3,15 | 4,20E-02 |
| --- | intergenic region | 3,14 | 1,84E-03 |
| --- | intergenic region | 3,14 | 3,75E-03 |
| <i>ydiN</i> | putative amino acidamine transport protein | 3,14 | 0,0003836 |
| <i>yghF</i> | putative general secretion pathway for protein export (GSP) | 3,14 | 0,004096 |
| --- | intergenic region | 3,14 | 0,0008332 |
| <i>ykgA</i> | putative ARAC-type regulatory protein | 3,13 | 8,62E-04 |
| <i>ycjX</i> | putative EC 2.1 enzymes | 3,12 | 0,02617 |
| <i>ybbY</i> | putative transport | 3,11 | 5,23E-04 |
| --- | intergenic region | 3,11 | 0,003716 |
| <i>yfaH</i> | orf, hypothetical protein | 3,11 | 0,0001593 |
| <i>yiiG</i> | orf, hypothetical protein | 3,09 | 2,41E-03 |
| c3379 | Hypothetical protein | 3,08 | 0,000106 |
| c4110 | Hypothetical protein | 3,08 | 0,002835 |
| <i>hokA</i> | small toxic membrane polypeptide | 3,08 | 1,21E-02 |
| --- | intergenic region | 3,07 | 0,000181 |
| c0468 | putative transferase | 3,07 | 1,18E-02 |
| <i>gcl</i> | glyoxylate carboligase | 3,06 | 2,57E-02 |
| --- | intergenic region | 3,03 | 7,80E-02 |
| --- | intergenic region | 3,03 | 0,0004179 |
| <i>ybbW</i> | orf; Unknown function | 3,03 | 2,93E-03 |
| <i>bglI</i> | 2-component transcriptional regulator | 3,03 | 0,003271 |
| <i>yfdT</i> | orf, hypothetical protein | 3,03 | 2,44E-02 |
| ECs5533 | hypothetical protein | 3,02 | 0,0001572 |
| --- | intergenic region | 3,01 | 1,88E-02 |
| --- | intergenic region | 3,01 | 4,67E-02 |
| <i>arpB</i> | Putative conserved protein | 3,01 | 2,17E-04 |
| <i>symE</i> | orf, hypothetical protein | 3,01 | 1,16E-02 |
| --- | intergenic region | 3,00 | 1,05e-05 |
| <i>tfaQ // tfaR</i> | tail fiber assembly protein homolog from lambdoid prophage Rac | 2,99 | 1,92E-03 |
| <i>yfbK</i> | orf, hypothetical protein | 2,99 | 9,13E-04 |
| <i>yncG</i> | putative transferase | 2,99 | 1,61E-02 |
| <i>yjjQ</i> | putative regulator | 2,99 | 3,09E-03 |
| --- | intergenic region | 2,99 | 2,19E-02 |
| --- | intergenic region | 2,98 | 2,25E-03 |
| <i>eutQ</i> | orf, hypothetical protein | 2,98 | 2,38E-02 |
| <i>intD</i> | prophage DLP12 integrase | 2,98 | 1,82E-03 |
| <i>slp</i> | outer membrane protein induced after carbon starvation | 2,97 | 0,001916 |
| <i>ybfP</i> | putative pectinase | 2,97 | 0,0002143 |
| --- | intergenic region | 2,97 | 1,05E-02 |
| --- | intergenic region | 2,97 | 9,84E-04 |
| <i>yjiV</i> | orf, hypothetical protein | 2,96 | 7,89E-04 |

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|---------------------|---|------|-----------|
| <i>yciF</i> | putative structural proteins | 2,94 | 2,24E-03 |
| <i>yahL</i> | orf, hypothetical protein | 2,94 | 0,0001854 |
| <i>yjbl</i> | orf, hypothetical protein | 2,93 | 0,003567 |
| <i>sfmA</i> | putative fimbrial-like protein | 2,93 | 2,41E-03 |
| --- | intergenic region | 2,93 | 0,0001678 |
| <i>pitB</i> | low-affinity phosphate transport | 2,92 | 1,71E-03 |
| <i>eutD</i> | ethanolamine utilization; homolog of Salmonella acetylbutyryl P transferase | 2,92 | 9,63E-03 |
| --- | orf, hypothetical protein | 2,91 | 3,66e-05 |
| --- | intergenic region | 2,90 | 0,0002253 |
| Z3843 | orf; Unknown function | 2,90 | 0,0006109 |
| <i>yddV</i> | Putative conserved protein | 2,89 | 1,23E-02 |
| --- | intergenic region | 2,88 | 0,0001324 |
| <i>pgaB // ycdR</i> | orf, hypothetical protein | 2,88 | 7,56E-04 |
| <i>idnO</i> | 5-keto-D-gluconate 5-reductase | 2,87 | 8,33E-02 |
| --- | intergenic region | 2,86 | 9,44E-03 |
| <i>gcl</i> | glyoxylate carboligase | 2,85 | 6,21e-06 |
| <i>yabP</i> | orf, hypothetical protein | 2,85 | 4,33E-03 |
| --- | intergenic region | 2,85 | 0,002428 |
| <i>mdtJ // ydgF</i> | possible chaperone | 2,85 | 0,003043 |
| --- | intergenic region | 2,85 | 0,0006903 |
| <i>ybhJ</i> | Hypothetical protein ybhJ | 2,85 | 5,28E-03 |
| --- | intergenic region | 2,84 | 1,38E-03 |
| <i>yjhE</i> | orf, hypothetical protein | 2,84 | 0,0004574 |
| <i>yqcE</i> | putative transport protein | 2,83 | 0,0007259 |
| c2574 | Hypothetical protein | 2,83 | 0,0004788 |
| <i>yafE</i> | putative biotin synthesis protein | 2,83 | 4,36E-02 |
| <i>ynjI</i> | orf; Unknown function | 2,83 | 2,74E-02 |
| --- | orf, hypothetical protein | 2,83 | 7,22E-03 |
| <i>yjgX</i> | orf, hypothetical protein | 2,82 | 0,0001469 |
| c2092 | Hypothetical protein | 2,82 | 0,0002685 |
| <i>ybeD</i> | orf, hypothetical protein | 2,82 | 0,02535 |
| <i>sfmH</i> | involved in fimbrial assembly | 2,82 | 0,0004204 |
| <i>idnD</i> | L-idonate dehydrogenase | 2,81 | 0,0002632 |
| <i>sfmC</i> | putative chaperone | 2,81 | 4,67E-02 |
| <i>ynaA</i> | putative alpha helix protein | 2,80 | 8,07E-03 |
| <i>ydfV</i> | orf, hypothetical protein | 2,80 | 4,24E-02 |
| <i>gspE // yheG</i> | YheG | 2,80 | 0,0001773 |
| Z3066 | orf; Unknown function | 2,80 | 0,004664 |
| --- | putative outer membrane protein | 2,79 | 1,98E-03 |
| --- | intergenic region | 2,78 | 1,12E-02 |
| --- | intergenic region | 2,78 | 2,43E-03 |
| --- | intergenic region | 2,77 | 8,07E-03 |
| <i>agaC</i> | PTS system N-acetylgalactosamine-specific IIC component 1 | 2,77 | 6,97E-03 |
| <i>glxR</i> | putative oxidoreductase | 2,76 | 4,15e-06 |
| <i>rzpR</i> | putative Rac prophage endopeptidase | 2,75 | 9,97E-03 |

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|---------------------|--|------|-----------|
| <i>yhjA</i> | putative cytochrome C peroxidase (EC 1.11.1) | 2,75 | 0,02595 |
| <i>hscC // ybeW</i> | DnaK-like protein | 2,75 | 9,96e-06 |
| --- | intergenic region | 2,75 | 1,21E-02 |
| --- | Hypothetical protein | 2,75 | 0,0001916 |
| <i>c2903</i> | Hypothetical protein | 2,73 | 0,0003254 |
| <i>yjlL</i> | putative transport protein, cryptic, orf, joins former <i>yjiZ</i> and <i>yjlL</i> | 2,73 | 0,001326 |
| --- | intergenic region | 2,73 | 1,82E-02 |
| <i>yfbE</i> | putative enzyme | 2,72 | 5,56e-06 |
| <i>ybcW</i> | orf, hypothetical protein | 2,72 | 0,003525 |
| <i>xapB</i> | xanthosine permease | 2,72 | 4,86E-02 |
| <i>lldD</i> | L-lactate dehydrogenase | 2,72 | 0,008499 |
| <i>ompG</i> | Outer membrane protein G precursor | 2,71 | 8,86E-03 |
| <i>ydjH</i> | putative kinase | 2,71 | 6,29e-06 |
| --- | intergenic region | 2,71 | 9,13e-06 |
| <i>ECs2095</i> | orf, hypothetical protein | 2,70 | 1,66E-03 |
| --- | intergenic region | 2,70 | 7,29E-02 |
| --- | intergenic region | 2,69 | 0,000158 |
| <i>yqiK</i> | putative membrane protein | 2,68 | 8,49E-02 |
| <i>yggF</i> | Putative conserved protein | 2,67 | 6,26E-03 |
| <i>yahl</i> | putative kinase (EC 2.7.2.2). | 2,67 | 1,66E-03 |
| --- | intergenic region | 2,67 | 2,19E-02 |
| <i>yaiA</i> | orf, hypothetical protein | 2,67 | 3,54E-03 |
| --- | intergenic region | 2,66 | 0,007057 |
| --- | intergenic region | 2,66 | 1,73E-02 |
| <i>aceK</i> | isocitrate dehydrogenase kinasephosphatase | 2,65 | 0,01494 |
| <i>csgC</i> | putative curli production protein | 2,65 | 2,05E-02 |
| <i>nsrR // yjeB</i> | orf, hypothetical protein | 2,64 | 9,45E-03 |
| --- | intergenic region | 2,64 | 5,83E-02 |
| --- | intergenic region | 2,64 | 0,0004294 |
| <i>rpiR</i> | transcriptional repressor of <i>rpiB</i> expression | 2,64 | 1,43E-02 |
| <i>insF</i> | Transposase | 2,64 | 1,28E-03 |
| <i>ECs5460</i> | hypothetical protein | 2,63 | 0,0001035 |
| <i>c1702</i> | Hypothetical protein | 2,63 | 0,0005127 |
| <i>ydjG</i> | hypothetical protein | 2,62 | 3,37E-03 |
| <i>arnA</i> | putative transformylase | 2,62 | 8,52E-02 |
| <i>gadC // xasA</i> | acid sensitivity protein, putative transporter | 2,62 | 0,0003264 |
| <i>hslU</i> | heat shock protein hslVU, ATPase subunit, homologous to chaperones | 2,62 | 0,005712 |
| --- | intergenic region | 2,61 | 0,0009013 |
| --- | intergenic region | 2,61 | 6,70E-03 |
| <i>insD // yaiX</i> | orf, hypothetical protein | 2,61 | 7,79e-06 |
| <i>dos</i> | putative sensor kinase | 2,61 | 8,68E-03 |
| <i>evgA</i> | putative positive transcription regulator (sensor EvgS) | 2,60 | 8,35E-03 |
| --- | intergenic region | 2,60 | 4,47E-02 |
| <i>pqqL</i> | putative zinc protease | 2,60 | 3,91E-02 |
| --- | intergenic region | 2,60 | 1,48E-03 |

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|---------------------|---|------|-----------|
| <i>leuO</i> | probable transcriptional activator for leuABCD operon | 2,59 | 1,40E-02 |
| <i>yghS</i> | orf, hypothetical protein | 2,58 | 6,29e-06 |
| --- | intergenic region | 2,58 | 1,86E-03 |
| <i>sfmD</i> | putative outer membrane protein, export function | 2,57 | 1,09E-02 |
| --- | intergenic region | 2,57 | 0,0001916 |
| <i>bglH</i> | putative receptor protein | 2,57 | 2,10E-02 |
| <i>ydjI</i> | putative aldolase | 2,57 | 1,23E-03 |
| --- | intergenic region | 2,56 | 0,0002182 |
| <i>livF</i> | ATP-binding component of leucine transport | 2,55 | 0,01927 |
| --- | intergenic region | 2,55 | 0,0002793 |
| --- | intergenic region | 2,55 | 9,14E-02 |
| --- | intergenic region | 2,55 | 1,52E-02 |
| --- | intergenic region | 2,55 | 0,0004068 |
| --- | intergenic region | 2,54 | 0,0004068 |
| <i>bssS</i> | orf, hypothetical protein | 2,54 | 0,0007124 |
| <i>pgaA</i> | putative outer membrane protein | 2,54 | 9,97E-03 |
| --- | intergenic region | 2,53 | 0,0001518 |
| <i>hsI</i> | hypothetical protein | 2,53 | 0,02095 |
| <i>yjaA</i> | orf, hypothetical protein | 2,52 | 0,0008101 |
| --- | Hypothetical protein | 2,52 | 0,01222 |
| --- | intergenic region | 2,52 | 0,0002447 |
| c3233 | Hypothetical protein | 2,51 | 0,006487 |
| --- | intergenic region | 2,51 | 0,0003683 |
| --- | intergenic region | 2,51 | 8,96E-02 |
| <i>mdtI // ydgE</i> | possible chaperone | 2,50 | 0,002313 |
| --- | intergenic region | 2,50 | 0,0004318 |
| <i>essQ</i> | Lysis protein S homolog from lambdoid prophage Qin | 2,50 | 0,0002376 |
| --- | intergenic region | 2,50 | 0,0004471 |
| --- | intergenic region | 2,49 | 1,65E-02 |
| <i>htpG</i> | chaperone Hsp90, heat shock protein C 62.5 | 2,48 | 0,0005809 |
| <i>focA_2</i> | intergenic region | 2,48 | 4,69E-02 |
| <i>ydhW</i> | orf, hypothetical protein | 2,48 | 0,001382 |
| <i>yfcU</i> | putative outer membrane protein | 2,48 | 0,0001334 |
| c4805 | Hypothetical protein | 2,48 | 0,001864 |
| <i>ycgG</i> | putative proteases | 2,47 | 6,87E-02 |
| <i>gspD</i> | YheF | 2,47 | 0,0001532 |
| <i>yhcG</i> | orf, hypothetical protein | 2,46 | 4,77E-02 |
| --- | intergenic region | 2,46 | 9,05E-03 |
| <i>eutT</i> | orf, hypothetical protein | 2,46 | 2,76E-02 |
| <i>ymfA</i> | orf, hypothetical protein | 2,46 | 0,0002422 |
| <i>rzpQ</i> | orf, hypothetical protein | 2,45 | 0,0001881 |
| --- | intergenic region | 2,45 | 0,003793 |
| --- | intergenic region | 2,44 | 8,80E-02 |
| <i>ydhT</i> | Hypothetical protein | 2,44 | 2,30E-02 |
| --- | intergenic region | 2,44 | 6,02E-02 |

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|---------------------|---|------|-----------|
| c5088 | Hypothetical protein | 2,44 | 0,005479 |
| <i>ypjA</i> | putative ATP-binding component of a transport system | 2,43 | 9,83E-02 |
| --- | intergenic region | 2,43 | 3,99e-05 |
| <i>Int</i> | apolipoprotein N-acyltransferase, copper homeostasis protein, inner membrane | 2,43 | 0,01616 |
| <i>pgaD // ycdP</i> | orf, hypothetical protein | 2,42 | 1,53E-03 |
| <i>hlyE</i> | hemolysin E | 2,42 | 0,007884 |
| <i>sanA</i> | vancomycin sensitivity | 2,41 | 2,47E-02 |
| --- | intergenic region | 2,41 | 5,63E-02 |
| <i>livG</i> | ATP-binding component of high-affinity branched-chain amino acid transport system | 2,41 | 0,03372 |
| --- | intergenic region | 2,41 | 0,0001855 |
| <i>yjcS</i> | orf, hypothetical protein | 2,41 | 0,0002218 |
| --- | intergenic region | 2,41 | 0,0005196 |
| <i>rdlC</i> | antisense RNA, trans-acting regulator of <i>ldrC</i> translation | 2,40 | 3,56E-02 |
| --- | intergenic region | 2,40 | 0,004718 |
| <i>ycfZ</i> | homolog of virulence factor | 2,40 | 0,0007277 |
| <i>yheL</i> | orf, hypothetical protein | 2,39 | 0,002033 |
| <i>wcaI</i> | putative colanic biosynthesis glycosyl transferase | 2,39 | 6,58E-02 |
| --- | intergenic region | 2,39 | 6,02E-03 |
| --- | orf, hypothetical protein | 2,38 | 0,0004842 |
| c4645 | Hypothetical protein | 2,38 | 0,0001027 |
| <i>yfbL</i> | putative aminopeptidase | 2,37 | 0,0002304 |
| <i>gspl // yheH</i> | putative export protein H | 2,37 | 0,006227 |
| <i>yiaS</i> | putative epimerasealdolase | 2,37 | 5,35E-03 |
| c3917 | Hypothetical protein | 2,37 | 0,000242 |
| --- | intergenic region | 2,37 | 1,18E-02 |
| --- | intergenic region | 2,37 | 0,003221 |
| <i>dnaK</i> | chaperone Hsp70; DNA biosynthesis; autoregulated heat shock proteins | 2,36 | 0,003518 |
| --- | intergenic region | 2,36 | 0,0007019 |
| <i>tfaS</i> | hypothetical protein | 2,36 | 8,23E-03 |
| <i>agaD</i> | PTS system, N-acetylgalactosamine-specific IID component | 2,34 | 0,0001435 |
| <i>cpsB</i> | mannose-1-phosphate guanyltransferase | 2,34 | 4,99E-03 |
| c5135 | Hypothetical protein | 2,34 | 4,43E-03 |
| <i>yaiS</i> | orf, hypothetical protein | 2,34 | 0,0005076 |
| <i>yjcC</i> | Hypothetical protein <i>yjcC</i> | 2,34 | 1,70E-02 |
| <i>yhjQ</i> | orf, hypothetical protein | 2,33 | 1,83E-02 |
| <i>ycgF</i> | orf, hypothetical protein | 2,33 | 0,002497 |
| <i>tdcF // yhaR</i> | hypothetical protein | 2,33 | 0,006821 |
| <i>yiaW</i> | orf, hypothetical protein | 2,33 | 7,04E-02 |
| <i>ybeX</i> | putative transport protein | 2,33 | 0,008417 |
| <i>ynbD</i> | putative enzymes | 2,32 | 4,07E-02 |
| <i>gspl // yheI</i> | putative export protein I | 2,32 | 0,0005118 |
| <i>ykgD</i> | putative ARAC-type regulatory protein | 2,31 | 7,26E-03 |
| <i>matC // yagY</i> | orf, hypothetical protein | 2,31 | 0,001541 |
| --- | intergenic region | 2,31 | 0,0003658 |

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|---------------------|---|------|-----------|
| <i>matB // yagZ</i> | orf, hypothetical protein | 2,30 | 1,74E-02 |
| <i>c3234</i> | orf, hypothetical protein | 2,30 | 0,00481 |
| --- | intergenic region | 2,30 | 0,0004156 |
| <i>dppA</i> | dipeptide transport protein | 2,30 | 6,09E-02 |
| <i>yaiT</i> | orf, hypothetical protein | 2,29 | 3,53E-02 |
| <i>ygcW</i> | putative oxidoreductase | 2,29 | 0,0001547 |
| --- | intergenic region | 2,29 | 0,000536 |
| --- | intergenic region | 2,28 | 4,43E-03 |
| --- | intergenic region | 2,28 | 0,004219 |
| <i>yncG</i> | Hypothetical protein | 2,28 | 1,9e-05 |
| <i>rlmE // rrmJ</i> | cell division protein | 2,27 | 0,002048 |
| <i>ompN</i> | putative outer membrane protein | 2,27 | 5,13E-03 |
| <i>yghE</i> | putative general secretion pathway for protein export (GSP) | 2,26 | 0,004369 |
| <i>ygaQ</i> | orf, hypothetical protein | 2,26 | 1,72E-02 |
| <i>intB</i> | prophage P4 integrase | 2,26 | 0,0002358 |
| <i>yagX</i> | putative enzyme | 2,26 | 0,000284 |
| <i>yhcE</i> | orf, hypothetical protein | 2,25 | 4,85E-02 |
| <i>yffW</i> | orf, hypothetical protein | 2,25 | 5,96E-02 |
| --- | intergenic region | 2,25 | 0,001857 |
| <i>yfgG</i> | orf, hypothetical protein | 2,25 | 0,000218 |
| <i>dsdX</i> | D-serine permease | 2,25 | 0,0005873 |
| <i>yegJ</i> | orf, hypothetical protein | 2,25 | 0,000106 |
| <i>ilvG</i> | acetolactate synthase II, valine insensitive, large subunit, silent in K-12 | 2,24 | 0,0001018 |
| <i>yahB</i> | orf; Unknown function | 2,24 | 0,0004143 |
| --- | intergenic region | 2,24 | 0,0002704 |
| --- | intergenic region | 2,23 | 0,0004553 |
| <i>yhiM</i> | orf, hypothetical protein | 2,23 | 2,62E-03 |
| --- | intergenic region | 2,22 | 7,83E-03 |
| <i>yhcF</i> | putative transcriptional regulator | 2,22 | 7,83E-02 |
| <i>yfbP</i> | orf, hypothetical protein | 2,21 | 0,0002422 |
| <i>wzxC</i> | probable export protein | 2,21 | 0,001971 |
| --- | intergenic region | 2,21 | 0,0007132 |
| --- | intergenic region | 2,21 | 0,001044 |
| <i>lon</i> | DNA-binding, ATP-dependent protease La; heat shock K-protein | 2,21 | 0,007312 |
| --- | intergenic region | 2,21 | 0,0007362 |
| --- | intergenic region | 2,21 | 0,0003416 |
| --- | intergenic region | 2,20 | 0,0005135 |
| <i>yffU</i> | orf, hypothetical protein | 2,20 | 1,74E-02 |
| <i>yedS</i> | putative outer membrane protein | 2,20 | 0,0003012 |
| <i>agal</i> | putative galactosamine-6-phosphate isomerase | 2,19 | 0,0003032 |
| <i>yiaG</i> | orf, hypothetical protein | 2,19 | 0,0008884 |
| --- | intergenic region | 2,19 | 0,009166 |
| <i>yraJ</i> | putative outer membrane protein | 2,19 | 7,09e-06 |
| --- | intergenic region | 2,19 | 0,001597 |
| <i>ybeY</i> | orf, hypothetical protein | 2,19 | 0,002248 |

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|---------------------|---|------|-----------|
| <i>yhbE</i> | orf, hypothetical protein | 2,19 | 0,0004101 |
| <i>intQ</i> | putative transposase | 2,19 | 0,0001681 |
| <i>caiC</i> | probable crotonobetainecarnitine-CoA ligase | 2,18 | 1,54E-02 |
| ECs1706 | hypothetical protein | 2,18 | 0,0008466 |
| c3023 | Hypothetical protein | 2,18 | 0,02398 |
| --- | orf, hypothetical protein | 2,17 | 2,18E-02 |
| <i>ygaY</i> | putative transport protein | 2,17 | 0,001785 |
| --- | intergenic region | 2,17 | 6,48E-02 |
| <i>pptA // ydcE</i> | orf, hypothetical protein | 2,17 | 6,51E-02 |
| --- | intergenic region | 2,17 | 0,0002118 |
| <i>yddK</i> | putative glycoprotein | 2,17 | 0,000193 |
| --- | intergenic region | 2,17 | 0,0001904 |
| --- | intergenic region | 2,17 | 0,004192 |
| <i>yehK</i> | orf; Unknown function | 2,17 | 2,55E-02 |
| <i>sugE</i> | suppresses groEL, may be chaperone | 2,16 | 0,0001677 |
| <i>bisZ // torZ</i> | biotin sulfoxide reductase 2 | 2,16 | 2,44E-03 |
| --- | intergenic region | 2,16 | 0,0001354 |
| <i>yaiP</i> | polysaccharide metabolism | 2,15 | 0,001494 |
| <i>aroL</i> | shikimate kinase II | 2,15 | 8,72E-03 |
| <i>livM</i> | high-affinity branched-chain amino acid transport | 2,15 | 0,0297 |
| --- | intergenic region | 2,15 | 0,000195 |
| <i>yedW</i> | putative 2-component transcriptional regulator | 2,15 | 3,96E-03 |
| --- | intergenic region | 2,15 | 0,003837 |
| <i>dsdA</i> | D-serine dehydratase (deaminase) | 2,14 | 1,23E-02 |
| --- | intergenic region | 2,14 | 0,001031 |
| <i>arnD // yfbH</i> | orf, hypothetical protein | 2,14 | 0,000149 |
| <i>yjiV</i> | inhibits McrE 5-methylcytosine restriction system | 2,14 | 3,27E-02 |
| <i>idnR</i> | L-idonate transcriptional regulator | 2,13 | 4,05E-02 |
| <i>ybhJ</i> | putative enzyme | 2,13 | 5,67E-02 |
| --- | intergenic region | 2,13 | 0,005418 |
| <i>yieL</i> | putative xylanase | 2,13 | 0,0001646 |
| --- | intergenic region | 2,12 | 0,005889 |
| <i>ybbV</i> | orf, hypothetical protein | 2,12 | 0,0005523 |
| <i>ygjK</i> | putative isomerase | 2,12 | 0,0003965 |
| --- | intergenic region | 2,12 | 0,002901 |
| <i>insL</i> | IS186 hypothetical protein | 2,12 | 0,004605 |
| <i>rdlB</i> | antisense RNA, trans-acting regulator of ldrB translation | 2,12 | 5,33E-02 |
| --- | intergenic region | 2,12 | 1,18E-02 |
| <i>ftsW</i> | cell division; membrane protein involved in shape determination | 2,12 | 3,96E-02 |
| <i>chiA</i> | hypothetical protein | 2,11 | 4,91E-02 |
| <i>gtrA</i> | hypothetical protein | 2,11 | 0,001593 |
| <i>yoaC</i> | orf, hypothetical protein | 2,11 | 3,02E-02 |
| <i>yheM</i> | orf, hypothetical protein | 2,10 | 0,0004318 |
| <i>yjdl</i> | orf, hypothetical protein | 2,10 | 0,005894 |
| <i>ycbQ</i> | putative fimbrial-like protein | 2,10 | 2,03E-02 |

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|---------------------|--|------|-----------|
| c0018 | Putative glutamate dehydrogenase | 2,10 | 0,04418 |
| <i>tdcG</i> | putative L-serine dehydratase | 2,09 | 0,02417 |
| <i>gfcA // ymcD</i> | orf, hypothetical protein | 2,09 | 0,0002862 |
| --- | intergenic region | 2,09 | 0,00013 |
| <i>uidC</i> | membrane-associated protein | 2,09 | 0,0008201 |
| --- | hypothetical protein | 2,08 | 0,01653 |
| <i>ygcU 4</i> | orf, hypothetical protein | 2,08 | 9,71E-02 |
| <i>csgB</i> | minor curlin subunit precursor, similar ro CsgA | 2,08 | 0,0002285 |
| --- | intergenic region | 2,07 | 7,19E-02 |
| c2913 | Hypothetical protein | 2,07 | 0,001909 |
| --- | intergenic region | 2,07 | 0,0004722 |
| <i>nhaR</i> | transcriptional activator of <i>nhaA</i> | 2,07 | 8,26E-03 |
| <i>yjeT</i> | orf, hypothetical protein | 2,05 | 0,002835 |
| <i>yfiL</i> | orf, hypothetical protein | 2,05 | 0,0006861 |
| <i>bcsZ // yhjM</i> | putative endoglucanase | 2,05 | 6,83E-02 |
| <i>yjdI</i> | orf, hypothetical protein | 2,04 | 0,003369 |
| c0497 | Hypothetical protein | 2,04 | 0,0009365 |
| <i>yicO</i> | orf, hypothetical protein | 2,04 | 0,0002673 |
| <i>hisP</i> | ATP-binding component of histidine transport | 2,04 | 0,0454 |
| ECs0347 | orf, hypothetical protein | 2,04 | 0,02319 |
| <i>gspK</i> | putative export protein J | 2,04 | 0,0003613 |
| --- | intergenic region | 2,04 | 0,00293 |
| <i>tdcE</i> | probable formate acetyltransferase 3 | 2,03 | 0,03329 |
| <i>ydhX</i> | putative oxidoreductase, Fe-S subunit | 2,03 | 0,005165 |
| --- | intergenic region | 2,03 | 0,0003168 |
| <i>envR</i> | putative transcriptional regulator | 2,02 | 0,001813 |
| <i>recF</i> | ssDNA and dsDNA binding, ATP binding | 2,02 | 0,04306 |
| <i>mdtO // yjcQ</i> | putative enzyme | 2,02 | 0,0009664 |
| <i>rbsR</i> | regulator for <i>rbs</i> operon | 2,02 | 0,0359 |
| <i>yhbX</i> | putative alkaline phosphatase I | 2,02 | 0,0005934 |
| <i>gltF</i> | regulator of <i>gltBDF</i> operon, induction of <i>Ntr</i> enzymes | 2,02 | 0,0001072 |
| <i>yfaL</i> | putative ATP-binding component of a transport system | 2,01 | 1,74E-02 |
| --- | intergenic region | 2,00 | 0,0008756 |
| <i>yneL</i> | orf, hypothetical protein | 2,00 | 0,0001076 |
| --- | orf, hypothetical protein | 2,00 | 0,0001058 |
| <i>yrdD</i> | hypothetical protein | 1,99 | 8,86E-02 |
| --- | intergenic region | 1,99 | 9,28E-02 |
| <i>pppA</i> | putative peptidase | 1,99 | 0,007618 |
| <i>ycbU</i> | hypothetical protein | 1,98 | 4,85E-02 |
| c2201 | Hypothetical protein | 1,98 | 0,0002819 |
| --- | intergenic region | 1,98 | 9,04E-03 |
| --- | intergenic region | 1,98 | 0,001113 |
| <i>rimN // yrdC</i> | orf, hypothetical protein | 1,98 | 0,001095 |
| <i>rsxB</i> | hypothetical protein | 1,98 | 0,001722 |
| <i>wcaL</i> | putative colanic acid biosynthesis glycosyl transferase | 1,97 | 0,0001526 |

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|---------------------|---|------|-----------|
| <i>yggC</i> | putative kinase | 1,97 | 3,28E-02 |
| <i>dos</i> | conserved protein | 1,97 | 5,44E-02 |
| --- | intergenic region | 1,97 | 0,002433 |
| <i>ilvM</i> | acetolactate synthase II, valine insensitive, small subunit | 1,96 | 0,001117 |
| --- | intergenic region | 1,96 | 0,001151 |
| <i>gspG // hofG</i> | putative general protein secretion protein | 1,96 | 0,0004517 |
| <i>yjgG_1</i> | orf, hypothetical protein | 1,96 | 3,91E-02 |
| <i>mcrB</i> | component of McrBC 5-methylcytosine restriction system | 1,96 | 9,97E-03 |
| <i>glxK // ybbZ</i> | hypothetical protein | 1,96 | 0,0001474 |
| <i>fecR</i> | regulator for fec operon, periplasmic | 1,96 | 0,04025 |
| --- | intergenic region | 1,96 | 4,92E-02 |
| <i>yrdB</i> | orf, hypothetical protein | 1,95 | 0,001089 |
| --- | intergenic region | 1,95 | 9,62e-05 |
| <i>inaA</i> | pH-inducible protein involved in stress response | 1,95 | 0,0001074 |
| --- | intergenic region | 1,94 | 0,0003092 |
| <i>dpiA</i> | sequence similarity to Shigella regulator | 1,94 | 0,001707 |
| <i>idnT</i> | L-idonate transporter | 1,94 | 0,002758 |
| --- | intergenic region | 1,94 | 2,53E-02 |
| --- | orf, hypothetical protein | 1,94 | 0,0003352 |
| <i>ybeQ</i> | orf, hypothetical protein | 1,94 | 3,06E-02 |
| <i>yehK</i> | Hypothetical protein | 1,94 | 0,0003953 |
| <i>yhjQ</i> | Uncharacterized conserved protein | 1,93 | 8,57E-02 |
| <i>cobC // phpB</i> | homolog of Salmonella cobC, a phosphohistidine protein | 1,93 | 0,01536 |
| <i>Z4614</i> | orf; Unknown function | 1,93 | 0,03025 |
| <i>yfdK</i> | orf, hypothetical protein | 1,93 | 0,0001593 |
| --- | intergenic region | 1,93 | 0,001509 |
| <i>c3935</i> | Hypothetical protein | 1,93 | 0,0258 |
| <i>yqjB</i> | orf, hypothetical protein | 1,92 | 5,95E-02 |
| <i>prlC</i> | oligopeptidase A | 1,92 | 0,02824 |
| --- | intergenic region | 1,92 | 0,001313 |
| <i>yjiT</i> | orf, hypothetical protein | 1,92 | 9,83E-02 |
| --- | intergenic region | 1,92 | 0,00071 |
| <i>xanQ // ygfO</i> | putative transport protein | 1,92 | 0,002916 |
| --- | intergenic region | 1,92 | 0,000139 |
| --- | intergenic region | 1,92 | 0,000448 |
| --- | intergenic region | 1,91 | 0,0002006 |
| --- | intergenic region | 1,91 | 0,0003957 |
| <i>ycdU</i> | putative transport system permease protein | 1,90 | 0,01045 |
| <i>yiaN</i> | putative membrane protein | 1,90 | 0,0009069 |
| <i>yjbN</i> | Hypothetical protein yjbN | 1,90 | 0,001771 |
| --- | orf, hypothetical protein | 1,90 | 0,0005519 |
| <i>yehH</i> | molybdate metabolism regulator, first fragment | 1,90 | 0,003433 |
| <i>yzgL</i> | orf, hypothetical protein | 1,90 | 0,02131 |
| <i>yjfC</i> | Hypothetical protein yjfC | 1,89 | 0,0003804 |
| <i>mltA</i> | Membrane-bound lytic murein transglycosylase A precursor | 1,89 | 0,0004565 |

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|---------------------|--|------|-----------|
| <i>ygfK</i> | putative oxidoreductase, Fe-S subunit | 1,89 | 0,01962 |
| --- | intergenic region | 1,89 | 0,0003514 |
| --- | intergenic region | 1,89 | 0,001792 |
| --- | intergenic region | 1,89 | 0,000127 |
| --- | intergenic region | 1,88 | 0,01365 |
| <i>proP</i> | low-affinity transport system; proline permease II | 1,88 | 0,0004333 |
| --- | intergenic region | 1,88 | 0,0009047 |
| <i>wcaK</i> | putative galactokinase (EC 2.7.1.6). | 1,88 | 7,08E-02 |
| --- | intergenic region | 1,88 | 0,001134 |
| <i>yjeH</i> | putative transport | 1,88 | 0,0003794 |
| --- | intergenic region | 1,88 | 0,0006109 |
| <i>ycbT</i> | FimH-like protein | 1,88 | 6,16e-05 |
| <i>gtrB</i> | putative glycan biosynthesis enzyme | 1,87 | 0,001866 |
| c0438 | Hypothetical protein | 1,87 | 0,0003897 |
| <i>cedA</i> | hypothetical protein | 1,87 | 2,28E-02 |
| <i>ylbF</i> | putative carboxylase | 1,87 | 0,0008014 |
| c0824 | intergenic region | 1,87 | 0,02129 |
| <i>yddJ</i> | orf, hypothetical protein | 1,87 | 0,0009365 |
| <i>macB // ybjZ</i> | Hypothetical protein | 1,87 | 0,03489 |
| <i>tnaB</i> | low affinity tryptophan permease | 1,87 | 0,001144 |
| --- | intergenic region | 1,87 | 0,0002837 |
| <i>ribE // ribH</i> | riboflavin synthase, beta chain | 1,87 | 0,001833 |
| <i>yfiV</i> | orf, hypothetical protein | 1,86 | 0,0004534 |
| <i>yfiR</i> | orf, hypothetical protein | 1,86 | 0,005016 |
| --- | intergenic region | 1,86 | 0,02034 |
| <i>rffC // wecD</i> | orf, hypothetical protein | 1,86 | 0,001845 |
| --- | intergenic region | 1,86 | 0,005403 |
| --- | intergenic region | 1,86 | 0,001004 |
| <i>aldH // puuC</i> | aldehyde dehydrogenase, prefers NADP over NAD | 1,86 | 0,004133 |
| <i>aroE</i> | dehydroshikimate reductase | 1,85 | 0,00289 |
| <i>ydfO</i> | orf, hypothetical protein | 1,85 | 0,04899 |
| <i>ais</i> | protein induced by aluminum | 1,85 | 0,003742 |
| <i>yjcB</i> | orf, hypothetical protein | 1,85 | 0,01384 |
| --- | intergenic region | 1,85 | 9,98E-02 |
| --- | intergenic region | 1,85 | 0,003742 |
| --- | intergenic region | 1,85 | 0,0001201 |
| <i>grpE</i> | phage lambda replication; host DNA synthesis; heat shock protein; protein repair | 1,84 | 0,006156 |
| <i>bcsC // yhjL</i> | putative oxidoreductase subunit | 1,84 | 0,0003824 |
| <i>ybgO</i> | orf, hypothetical protein | 1,84 | 0,0001382 |
| <i>ycfI</i> | orf, hypothetical protein | 1,84 | 0,003034 |
| <i>dnaA</i> | DNA biosynthesis; initiation of chromosome replication; can be transcription regulator | 1,84 | 0,002966 |
| --- | intergenic region | 1,84 | 0,001757 |
| --- | intergenic region | 1,84 | 0,0009582 |
| --- | intergenic region | 1,83 | 0,0005294 |

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|---------------------|--|------|-----------|
| <i>yjeS</i> | orf, hypothetical protein | 1,83 | 0,0005347 |
| <i>gatR</i> | split galactitol utilization operon repressor, fragment 2 | 1,83 | 7,96E-03 |
| <i>ygcE</i> | putative kinase | 1,83 | 0,002709 |
| --- | intergenic region | 1,83 | 6,03E-02 |
| --- | IS911 hypothetical protein | 1,83 | 0,003304 |
| --- | intergenic region | 1,83 | 0,03951 |
| <i>ygcU</i> | putative oxidoreductase subunit | 1,82 | 0,003241 |
| <i>tesC // ybaW</i> | orf, hypothetical protein | 1,82 | 0,00163 |
| --- | intergenic region | 1,82 | 0,005193 |
| <i>wza</i> | Putative conserved protein | 1,82 | 0,0002059 |
| <i>fhuA</i> | outer membrane protein receptor for ferrichrome, colicin M, and phages T1, T5, and phi80 | 1,82 | 0,04489 |
| <i>ydjI</i> | putative oxidoreductase | 1,82 | 0,0002979 |
| <i>dnaE</i> | DNA polymerase III, alpha subunit | 1,82 | 0,004306 |
| --- | intergenic region | 1,82 | 0,000937 |
| --- | intergenic region | 1,82 | 0,009001 |
| <i>yedS</i> | hypothetical protein | 1,82 | 0,001562 |
| <i>yieK</i> | putative isomerase | 1,81 | 0,0003627 |
| --- | intergenic region | 1,81 | 0,001373 |
| <i>insF</i> | IS3 putative transposase | 1,81 | 0,0003473 |
| <i>wcaM</i> | orf, hypothetical protein | 1,81 | 0,000195 |
| --- | intergenic region | 1,81 | 0,0022 |
| <i>iclR</i> | repressor of aceBA operon | 1,81 | 0,0006471 |
| <i>yiiX</i> | orf, hypothetical protein | 1,81 | 0,0001043 |
| <i>prfH</i> | probable peptide chain release factor | 1,81 | 0,0002364 |
| <i>rnhB</i> | RNAse HII, degrades RNA of DNA-RNA hybrids | 1,81 | 0,01509 |
| --- | intergenic region | 1,80 | 0,004006 |
| <i>ybeZ</i> | putative ATP-binding protein in pho regulon | 1,80 | 0,01619 |
| <i>deaD</i> | inducible ATP-independent RNA helicase | 1,80 | 0,0003899 |
| --- | intergenic region | 1,80 | 0,01869 |
| <i>yaiO</i> | orf, hypothetical protein | 1,80 | 0,0008587 |
| --- | intergenic region | 1,80 | 0,007077 |
| <i>rbsK</i> | ribokinase | 1,79 | 0,03226 |
| <i>intE</i> | prophage e14 integrase | 1,79 | 0,0002032 |
| <i>cspH</i> | cold shock-like protein | 1,79 | 0,03907 |
| --- | intergenic region | 1,79 | 0,001072 |
| <i>mltB</i> | Membrane-bound lytic murein transglycosylase B precursor | 1,79 | 0,0002905 |
| --- | intergenic region | 1,79 | 0,00837 |
| --- | intergenic region | 1,79 | 0,02704 |
| <i>hflX</i> | GTP - binding subunit of protease specific for phage lambda cII repressor | 1,79 | 0,001043 |
| <i>ygiZ</i> | orf, hypothetical protein | 1,78 | 0,0009504 |
| --- | intergenic region | 1,78 | 0,01525 |
| <i>bgIB</i> | phospho-beta-glucosidase B; cryptic | 1,78 | 0,000302 |
| <i>yfiN</i> | orf, hypothetical protein | 1,78 | 0,003557 |
| --- | intergenic region | 1,78 | 0,001001 |

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|---------------------|--|------|-----------|
| <i>ypjA</i> | orf, hypothetical protein | 1,77 | 9,49E-02 |
| c4226 | intergenic region | 1,77 | 0,01219 |
| <i>yeaR</i> | orf, hypothetical protein | 1,77 | 0,001985 |
| <i>yheN</i> | orf, hypothetical protein | 1,77 | 0,0005672 |
| <i>yicO</i> | orf; Unknown function | 1,77 | 0,000211 |
| <i>gtrS</i> | putative ligase | 1,76 | 0,003723 |
| <i>yqhG</i> | orf; Unknown function | 1,76 | 0,00259 |
| <i>yghR</i> | orf, hypothetical protein | 1,76 | 0,0002221 |
| --- | intergenic region | 1,76 | 7,16E-02 |
| <i>mepA</i> | murein DD-endopeptidase, penicillin-insensitive | 1,76 | 0,00459 |
| --- | intergenic region | 1,76 | 0,002219 |
| <i>cchA // eutM</i> | detox protein | 1,76 | 0,0001018 |
| --- | intergenic region | 1,76 | 0,0005758 |
| --- | intergenic region | 1,76 | 0,002983 |
| <i>yehM</i> | orf, hypothetical protein | 1,76 | 0,001749 |
| <i>yagN</i> | orf, hypothetical protein | 1,75 | 0,0006574 |
| <i>glpX</i> | unknown function in glycerol metabolism | 1,75 | 0,003539 |
| <i>yafQ</i> | orf, hypothetical protein | 1,75 | 8,24E-02 |
| <i>ybgQ</i> | putative outer membrane protein | 1,75 | 0,01514 |
| <i>yihR</i> | putative aldose-1-epimerase (EC 5.1.3.3) | 1,75 | 0,0008958 |
| <i>mreC</i> | Hypothetical protein | 1,75 | 0,02336 |
| c1324 | Hypothetical protein | 1,75 | 0,000379 |
| <i>ylbE</i> | orf, hypothetical protein | 1,75 | 0,0003663 |
| --- | intergenic region | 1,75 | 0,0007086 |
| --- | intergenic region | 1,75 | 0,001472 |
| <i>ydiM</i> | putative transport system permease protein | 1,74 | 0,000961 |
| <i>fdrA</i> | involved in protein transport; multicopy suppressor of dominant negative <i>ftsH</i> mutants | 1,74 | 0,001152 |
| <i>entD</i> | enterochelin synthetase, component D | 1,74 | 0,02481 |
| <i>mreD</i> | rod shape-determining protein | 1,74 | 0,01674 |
| <i>ftsL</i> | cell division protein; ingrowth of wall at septum | 1,74 | 8,47e-05 |
| --- | intergenic region | 1,74 | 0,0003133 |
| --- | intergenic region | 1,74 | 0,009118 |
| <i>cspA</i> | cold shock protein 7.4, transcriptional activator of <i>hns</i> | 1,74 | 0,0002262 |
| --- | intergenic region | 1,73 | 0,02096 |
| <i>ydhU</i> | orf, hypothetical protein | 1,73 | 0,005146 |
| <i>uidC</i> | orf; Unknown function | 1,73 | 0,005239 |
| <i>secM // yacA</i> | orf, hypothetical protein | 1,73 | 0,0004537 |
| --- | intergenic region | 1,73 | 0,04383 |
| <i>rtn</i> | orf, hypothetical protein | 1,73 | 0,0003073 |
| --- | intergenic region | 1,72 | 0,008614 |
| <i>yfcQ</i> | orf, hypothetical protein | 1,72 | 0,00614 |
| <i>infA</i> | protein chain initiation factor IF-1 | 1,72 | 0,01005 |
| --- | intergenic region | 1,72 | 0,01731 |
| <i>malT</i> | positive regulator of <i>mal</i> regulon | 1,72 | 0,0006336 |
| <i>ybcC</i> | orf, hypothetical protein | 1,72 | 2,67E-02 |

| | | | |
|---------------------|--|------|-----------|
| <i>ftsN</i> | essential cell division protein | 1,72 | 0,003165 |
| <i>ycgE // ycgE</i> | putative transcriptional regulator | 1,72 | 4,85E-02 |
| --- | intergenic region | 1,72 | 0,002813 |
| <i>ygfE // zapA</i> | orf, hypothetical protein | 1,72 | 0,0001547 |
| c2371 | Hypothetical protein | 1,72 | 0,002283 |
| <i>ycgG</i> | Conserved hypothetical protein | 1,71 | 0,0007255 |
| --- | intergenic region | 1,71 | 0,01399 |
| <i>hemA</i> | glutamyl-tRNA reductase | 1,71 | 0,0002414 |
| <i>gapC</i> | glyceraldehyde-3-phosphate dehydrogenase (second fragment) | 1,71 | 0,005403 |
| <i>yejM</i> | putative sulfatase | 1,71 | 0,003573 |
| <i>cysE</i> | serine acetyltransferase | 1,71 | 0,002899 |
| --- | putative pump protein | 1,71 | 0,000894 |
| <i>yggD</i> | putative transcriptional regulator | 1,71 | 8,29E-02 |
| --- | intergenic region | 1,70 | 0,0005269 |
| <i>ftsQ</i> | cell division protein; ingrowth of wall at septum | 1,70 | 0,0001221 |
| <i>ybeU</i> | putative tRNA ligase | 1,70 | 0,002928 |
| <i>ybbN</i> | putative thioredoxin-like protein | 1,70 | 0,03358 |
| <i>yjiX</i> | orf, hypothetical protein | 1,70 | 0,008553 |
| <i>ytfP</i> | orf, hypothetical protein | 1,70 | 0,005183 |
| <i>rimP // yhbC</i> | orf, hypothetical protein | 1,70 | 0,0007693 |
| <i>wcaJ</i> | putative colanic acid biosynthesis UDP-glucose lipid carrier transferase | 1,70 | 0,0007044 |
| <i>arnT</i> | 4-amino-4-deoxy-L-arabinose transferase (lipid A modification) | 1,69 | 0,001087 |
| --- | intergenic region | 1,69 | 0,01799 |
| <i>djlC</i> | orf, hypothetical protein | 1,69 | 0,02038 |
| <i>dapE</i> | N-succinyl-diaminopimelate deacylase | 1,69 | 0,0152 |
| <i>ypfN</i> | orf; Unknown function | 1,69 | 0,006811 |
| <i>fdol</i> | formate dehydrogenase, cytochrome B556 (FDO) subunit | 1,69 | 0,000135 |
| <i>zntR</i> | putative transcriptional regulator | 1,69 | 0,03831 |
| <i>ycjZ</i> | putative transcriptional regulator LYSR-type | 1,69 | 0,001397 |
| --- | intergenic region | 1,69 | 0,001757 |
| --- | intergenic region | 1,68 | 0,0001774 |
| <i>groEL</i> | GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock protein | 1,68 | 0,0125 |
| <i>wecH // yiaH</i> | orf, hypothetical protein | 1,68 | 9,53E-02 |
| --- | intergenic region | 1,68 | 0,00975 |
| <i>rssA // ychK</i> | orf, hypothetical protein | 1,68 | 0,008964 |
| <i>ydcV</i> | Hypothetical ABC transporter permease protein ydcV | 1,68 | 0,001693 |
| <i>yqiC</i> | orf, hypothetical protein | 1,68 | 0,005261 |
| <i>yjaH</i> | orf, hypothetical protein | 1,68 | 0,006666 |
| --- | intergenic region | 1,68 | 0,002529 |
| --- | intergenic region | 1,68 | 0,006183 |
| --- | intergenic region | 1,68 | 0,002465 |
| <i>yraH</i> | putative fimbrial-like protein | 1,68 | 0,002433 |
| <i>yejO</i> | Hypothetical protein | 1,68 | 0,004158 |
| <i>rsxC</i> | putative membrane protein | 1,68 | 0,03951 |
| c0485 | Hypothetical protein | 1,68 | 0,0007452 |

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|----------------------|---|------|-----------|
| --- | intergenic region | 1,67 | 0,01181 |
| <i>npr // ptsO</i> | phosphocarrier protein HPr-like NPr, nitrogen related, exchanges phosphate with Enzyme I, Hpr | 1,67 | 0,0004594 |
| <i>yibQ</i> | orf, hypothetical protein | 1,67 | 0,007588 |
| <i>oppC</i> | homolog of Salmonella oligopeptide transport permease protein | 1,67 | 0,0003658 |
| <i>rbsB</i> | D-ribose periplasmic binding protein | 1,67 | 0,01299 |
| <i>mutL</i> | enzyme in methyl-directed mismatch repair | 1,67 | 0,0002603 |
| <i>hnr // rssB</i> | Hnr protein | 1,67 | 0,002336 |
| --- | intergenic region | 1,67 | 0,007075 |
| <i>yaaY</i> | orf, hypothetical protein | 1,67 | 0,03817 |
| <i>ycgY</i> | orf, hypothetical protein | 1,67 | 0,004679 |
| <i>yraK</i> | partial putative fimbrial protein | 1,66 | 0,001146 |
| <i>yafN</i> | orf, hypothetical protein | 1,66 | 0,0008409 |
| <i>c3200 // yfdP</i> | orf, hypothetical protein | 1,66 | 0,001676 |
| <i>yegR</i> | orf, hypothetical protein | 1,66 | 0,0003695 |
| --- | intergenic region | 1,66 | 0,001079 |
| <i>npl // yhbM</i> | putative control proteins | 1,66 | 0,0001018 |
| <i>yacC</i> | hypothetical protein | 1,66 | 0,002078 |
| --- | intergenic region | 1,65 | 0,02626 |
| <i>ycgF</i> | orf, hypothetical protein | 1,65 | 0,002076 |
| <i>yphF</i> | putative LACI-type transcriptional regulator | 1,65 | 0,0007135 |
| --- | intergenic region | 1,65 | 0,0005429 |
| <i>ecnB</i> | entericidin B | 1,65 | 0,00874 |
| <i>wecF // wzyE</i> | TDP-Fuc4NAc:lipidII transferase; synthesis of enterobacterial common antigen (ECA) | 1,65 | 0,003384 |
| Z2403 | orf, hypothetical protein | 1,65 | 0,000428 |
| --- | intergenic region | 1,65 | 0,002112 |
| --- | intergenic region | 1,64 | 0,01956 |
| --- | intergenic region | 1,64 | 0,0007053 |
| <i>agal</i> | putative galactosamine-6-phosphate isomerase | 1,64 | 0,009279 |
| --- | intergenic region | 1,64 | 0,0004055 |
| <i>yebA</i> | orf, hypothetical protein | 1,64 | 0,01592 |
| --- | intergenic region | 1,64 | 0,01954 |
| --- | intergenic region | 1,64 | 0,002127 |
| <i>yiaT</i> | putative outer membrane protein | 1,64 | 0,002484 |
| <i>ppdD</i> | prelipin peptidase dependent protein | 1,64 | 0,000179 |
| <i>yjgM</i> | orf, hypothetical protein | 1,64 | 0,0005143 |
| c5270 | Hypothetical protein | 1,64 | 0,003452 |
| <i>murG</i> | UDP-N-acetylglucosamine:N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase | 1,64 | 0,0001706 |
| <i>yciM</i> | putative heat shock protein | 1,64 | 0,005531 |
| <i>lpxB</i> | tetraacyldisaccharide-1-P; lipid A biosynthesis, penultimate step | 1,64 | 0,01218 |
| --- | intergenic region | 1,64 | 0,001207 |
| --- | intergenic region | 1,64 | 0,0007976 |
| <i>ycgN</i> | orf, hypothetical protein | 1,63 | 0,002855 |
| ECs5181 | hypothetical protein | 1,63 | 0,001005 |
| Z5430 | orf; Unknown function | 1,63 | 0,00783 |

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|---------------------|--|------|-----------|
| <i>ycjW</i> | putative LACI-type transcriptional regulator | 1,63 | 0,002748 |
| c0062 | Hypothetical protein | 1,63 | 0,03806 |
| <i>gppA</i> | guanosine pentaphosphatase; exopolyphosphatase | 1,63 | 0,005183 |
| c4584 | Hypothetical protein | 1,63 | 0,001273 |
| <i>yneF</i> | orf, hypothetical protein | 1,62 | 0,009526 |
| --- | intergenic region | 1,62 | 0,0009233 |
| <i>lacA</i> | thiogalactoside acetyltransferase | 1,62 | 0,001313 |
| --- | intergenic region | 1,62 | 0,00353 |
| <i>sieB</i> | phage superinfection exclusion protein | 1,62 | 0,0006869 |
| --- | intergenic region | 1,62 | 0,001777 |
| <i>ybgP</i> | putative chaperone | 1,62 | 0,01407 |
| --- | intergenic region | 1,61 | 0,0004039 |
| --- | intergenic region | 1,61 | 0,0009936 |
| <i>yffO</i> | orf, hypothetical protein | 1,61 | 0,0002364 |
| <i>ygdQ</i> | putative transport protein | 1,61 | 0,004397 |
| --- | intergenic region | 1,61 | 0,0001213 |
| --- | intergenic region | 1,61 | 0,002194 |
| ECs1673 | hypothetical protein | 1,61 | 0,004555 |
| <i>yraK</i> | putative fimbrial protein | 1,61 | 0,003976 |
| --- | intergenic region | 1,61 | 0,02129 |
| --- | intergenic region | 1,61 | 0,005892 |
| --- | intergenic region | 1,61 | 0,008793 |
| <i>yiiF</i> | orf, hypothetical protein | 1,61 | 0,0005742 |
| <i>rfaL</i> | O-antigen ligase; lipopolysaccharide core biosynthesis | 1,61 | 0,005736 |
| <i>ycbS</i> | partial fimbrial usher protein | 1,61 | 0,0006164 |
| <i>phoE</i> | outer membrane pore protein E (E,Ic,NmpAB) | 1,61 | 8,22E-02 |
| <i>fdoH</i> | formate dehydrogenase-O, iron-sulfur subunit | 1,60 | 0,001236 |
| <i>intZ</i> | putative prophage integrase | 1,60 | 0,004985 |
| <i>intK</i> | orf, hypothetical protein | 1,60 | 0,0137 |
| <i>yjeK</i> | orf, hypothetical protein | 1,60 | 0,001562 |
| --- | intergenic region | 1,60 | 0,0005532 |
| <i>yhdP</i> | orf, hypothetical protein | 1,60 | 0,0008256 |
| <i>lptC // yrbK</i> | orf, hypothetical protein | 1,60 | 0,001211 |
| --- | intergenic region | 1,60 | 0,00794 |
| <i>dam</i> | DNA adenine methylase | 1,60 | 0,00819 |
| <i>yqhG</i> | orf; Unknown function | 1,60 | 0,0009821 |
| --- | intergenic region | 1,60 | 0,001211 |
| <i>rffH</i> | glucose-1-phosphate thymidyltransferase | 1,60 | 0,01449 |
| <i>rhIE</i> | putative ATP-dependent RNA helicase | 1,60 | 0,01486 |
| <i>ompN</i> | partial putative outer membrane protein | 1,60 | 0,006897 |
| <i>rfaZ</i> | lipopolysaccharide core biosynthesis | 1,60 | 0,01852 |
| <i>yegl</i> | putative chaperonin | 1,59 | 0,0163 |
| <i>yihM</i> | orf, hypothetical protein | 1,59 | 0,001666 |
| <i>yehM</i> | orf; Unknown function | 1,59 | 0,002892 |
| c4808 | Hypothetical protein | 1,59 | 0,003438 |

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|----------------------|--|------|-----------|
| c1624 | Hypothetical protein | 1,59 | 0,006046 |
| <i>wecD</i> | Lipopolysaccharide biosynthesis protein rffC | 1,59 | 0,02199 |
| --- | intergenic region | 1,59 | 0,02068 |
| <i>wzxE</i> | putative cytochrome | 1,59 | 0,002879 |
| <i>gspO // hofD</i> | leader peptidase | 1,59 | 0,0007675 |
| --- | intergenic region | 1,59 | 0,01685 |
| <i>adrA</i> | orf, hypothetical protein | 1,59 | 0,001396 |
| <i>pspG</i> | orf, hypothetical protein | 1,59 | 0,02578 |
| <i>yael</i> | orf, hypothetical protein | 1,58 | 0,001381 |
| <i>oppB</i> | oligopeptide transport permease protein | 1,58 | 0,0007498 |
| <i>pdxA</i> | pyridoxine biosynthesis | 1,58 | 0,004556 |
| <i>groES // groS</i> | GroES, 10 Kd chaperone binds to Hsp60 in pres. Mg-ATP, suppressing its ATPase activity | 1,58 | 0,04773 |
| <i>nusB</i> | transcription termination; L factor | 1,58 | 0,03595 |
| --- | intergenic region | 1,58 | 0,01031 |
| --- | intergenic region | 1,58 | 0,002776 |
| --- | intergenic region | 1,58 | 0,03412 |
| <i>folK</i> | 7,8-dihydro-6-hydroxymethylpterin- pyrophosphokinase | 1,58 | 0,02121 |
| <i>rseP // yaeL</i> | hypothetical protein | 1,58 | 0,001604 |
| <i>yjbl</i> | orf, hypothetical protein | 1,58 | 0,008385 |
| <i>mraY</i> | phospho-N-acetylmuramoyl-pentapeptide transferase? | 1,57 | 0,004253 |
| ECs0305 | putative transcriptional regulator LYSR-type | 1,57 | 0,0009576 |
| ECs0442 | unknown | 1,57 | 0,001932 |
| --- | intergenic region | 1,57 | 0,02177 |
| <i>acrE</i> | transmembrane protein affects septum formation and cell membrane permeability | 1,57 | 0,03366 |
| <i>coaE</i> | putative DNA repair protein | 1,57 | 0,0005398 |
| <i>mreC</i> | rod shape-determining protein | 1,57 | 0,03483 |
| <i>kdsC // yrbI</i> | orf, hypothetical protein | 1,57 | 0,000445 |
| <i>ycjV</i> | putative ATP-binding component of a transport system | 1,57 | 0,009034 |
| <i>uvrD</i> | DNA-dependent ATPase I and helicase II | 1,57 | 0,002033 |
| <i>pdxA</i> | 4-hydroxythreonine-4-phosphate dehydrogenase | 1,57 | 0,00314 |
| --- | intergenic region | 1,57 | 0,007341 |
| <i>ygfl</i> | partial putative transcriptional regulator LYSR-type | 1,56 | 0,006788 |
| <i>bgfI</i> | PTS system beta-glucosides, enzyme II, cryptic | 1,56 | 0,01854 |
| <i>yphE</i> | putative ATP-binding component of a transport system | 1,56 | 0,004141 |
| --- | intergenic region | 1,56 | 0,00476 |
| <i>ispU // yaeS</i> | hypothetical protein | 1,56 | 0,005301 |
| <i>puuB</i> | probable oxidoreductase | 1,56 | 0,02178 |
| <i>rem</i> | orf, hypothetical protein | 1,56 | 0,002194 |
| <i>yneK</i> | orf, hypothetical protein | 1,56 | 0,02104 |
| <i>dnaB</i> | replicative DNA helicase; part of primosome | 1,56 | 0,01155 |
| <i>ylbE</i> | intergenic region | 1,55 | 0,02278 |
| --- | intergenic region | 1,55 | 0,03365 |
| <i>yfcO</i> | orf, hypothetical protein | 1,55 | 0,001744 |
| --- | intergenic region | 1,55 | 0,01028 |

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|-----------------------------|--|------|-----------|
| <i>yfdL</i> | putative RNA polymerase beta | 1,55 | 0,006223 |
| --- | intergenic region | 1,55 | 0,001665 |
| --- | intergenic region | 1,55 | 0,002944 |
| <i>xerC</i> | site-specific recombinase, acts on <i>cer</i> sequence of <i>ColE1</i> , effects chromosome segregation at cell division | 1,55 | 0,00146 |
| <i>acrF</i> | N-terminal fragment of integral transmembrane protein involved with acridine resistance | 1,55 | 0,006574 |
| --- | intergenic region | 1,55 | 0,0323 |
| <i>apaG</i> | orf, hypothetical protein | 1,55 | 0,002428 |
| <i>dnaN</i> | DNA polymerase III, beta-subunit | 1,55 | 0,01438 |
| <i>yoeF7</i> | orf; Unknown function | 1,55 | 0,008193 |
| <i>fdhE</i> | affects formate dehydrogenase-N | 1,55 | 0,0004574 |
| <i>ftsH // hflB</i> | degrades sigma32, integral membrane peptidase, cell division protein | 1,55 | 0,01046 |
| --- | intergenic region | 1,55 | 0,0004398 |
| --- | intergenic region | 1,54 | 0,005586 |
| <i>hsdS</i> | specificity determinant for <i>hsdM</i> and <i>hsdR</i> | 1,54 | 0,003057 |
| <i>fepE</i> | ferric enterobactin (enterochelin) transport | 1,54 | 0,003548 |
| <i>holA // holA</i> | DNA polymerase III, delta subunit | 1,54 | 0,04253 |
| <i>ydeH</i> | orf, hypothetical protein | 1,54 | 0,002384 |
| c4720 | Hypothetical protein | 1,54 | 0,0304 |
| --- | intergenic region | 1,54 | 0,02777 |
| ECs5364 | hypothetical protein | 1,54 | 0,001323 |
| <i>ydbH</i> | orf, hypothetical protein | 1,54 | 0,00303 |
| --- | intergenic region | 1,53 | 0,0004427 |
| <i>murD</i> | UDP-N-acetylmuramoylalanine-D-glutamate ligase | 1,53 | 0,001761 |
| --- | intergenic region | 1,53 | 0,02864 |
| <i>ygeR</i> | putative lipoprotein | 1,53 | 0,001534 |
| <i>mgrB // yobG</i> | orf, hypothetical protein | 1,53 | 0,01537 |
| <i>yiaV</i> | putative membrane protein | 1,53 | 0,0005932 |
| <i>rffD // wecC</i> | UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase; synthesis of enterobacterial common antigen (ECA) | 1,53 | 0,01805 |
| <i>nohB // nohD // nohQ</i> | bacteriophage DNA packaging protein | 1,53 | 0,0007259 |
| <i>ykgL</i> | orf, hypothetical protein | 1,53 | 0,009033 |
| <i>yafK</i> | orf, hypothetical protein | 1,53 | 0,04326 |
| --- | intergenic region | 1,53 | 0,00212 |
| c2215 | Hypothetical protein | 1,52 | 0,005146 |
| <i>dusB // yhdG</i> | putative dehydrogenase | 1,52 | 0,00368 |
| <i>yheO</i> | orf, hypothetical protein | 1,52 | 0,001655 |
| <i>insB</i> | IS1 protein <i>InsB</i> | 1,52 | 0,001149 |
| <i>hemA</i> | intergenic region | 1,52 | 0,006288 |
| <i>yadE</i> | Hypothetical protein <i>yadE</i> precursor | 1,52 | 0,001382 |
| <i>aroF</i> | 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (DAHP synthetase, tyrosine repressible) | 1,52 | 0,001158 |
| <i>bcsB // yhjN</i> | orf, hypothetical protein | 1,52 | 0,001249 |
| <i>ftsI</i> | septum formation; penicillin-binding protein 3; peptidoglycan synthetase | 1,52 | 0,0005481 |
| c1303 | Hypothetical protein | 1,52 | 0,001058 |

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|---------------------|---|------|-----------|
| <i>ttcA // ydaO</i> | orf, hypothetical protein | 1,52 | 0,01733 |
| <i>poxA // yjeA</i> | putative lysyl-tRNA synthetase | 1,52 | 0,01278 |
| <i>yhaM</i> | orf, hypothetical protein | 1,52 | 0,02678 |
| <i>yhjR</i> | orf, hypothetical protein | 1,51 | 0,007851 |
| --- | intergenic region | 1,51 | 0,03603 |
| <i>ybjL</i> | putative transport protein | 1,51 | 0,00273 |
| <i>setA</i> | putative transport protein | 1,51 | 0,00101 |
| <i>yagF</i> | putative dehydratase | 1,51 | 0,00644 |
| <i>osmB</i> | osmotically inducible lipoprotein | 1,51 | 0,01928 |
| <i>alr</i> | alanine racemase 1 | 1,51 | 0,0009235 |
| <i>rpoH</i> | RNA polymerase, sigma(32) factor; regulation of proteins induced at high temperatures | 1,51 | 0,001368 |
| <i>rsxA</i> | hypothetical protein | 1,51 | 0,006105 |
| c2063 | Hypothetical protein | 1,51 | 0,02355 |
| c1535 | Putative conserved protein | 1,51 | 0,02919 |
| --- | intergenic region | 1,51 | 0,002377 |
| --- | intergenic region | 1,51 | 0,01546 |
| --- | intergenic region | 1,51 | 0,00154 |
| <i>dicC</i> | regulator of <i>dicB</i> | 1,50 | 0,04287 |
| <i>mioC</i> | initiation of chromosome replication | 1,50 | 0,02849 |
| --- | intergenic region | 1,50 | 0,006654 |
| <i>oppD</i> | homolog of Salmonella ATP-binding protein of oligopeptide ABC transport system | 1,50 | 0,002501 |
| <i>tpiA</i> | triosephosphate isomerase | 1,50 | 0,0117 |
| <i>pmbA</i> | maturation of antibiotic MccB17, see <i>tld</i> genes | 1,50 | 0,01158 |
| <i>thrC</i> | threonine synthase | 1,50 | 0,01666 |
| <i>hycF</i> | probable iron-sulfur protein of hydrogenase 3 (part of FHL complex) | 1,50 | 0,001325 |
| c0640 | intergenic region | 1,50 | 0,00449 |
| <i>nanR // yhcK</i> | putative FADA-type transcriptional regulator | 1,50 | 0,004719 |
| <i>galP</i> | galactose-proton symport of transport system | 1,50 | 0,02247 |
| <i>yfcE</i> | orf, hypothetical protein | 1,50 | 0,0007112 |
| <i>ybiC</i> | putative dehydrogenase | 1,50 | 0,004853 |
| --- | intergenic region | 1,50 | 0,01248 |
| <i>yccS</i> | orf, hypothetical protein | 1,50 | 0,03208 |
| <i>yieF</i> | orf, hypothetical protein | 1,50 | 0,009605 |
| <i>hisI</i> | phosphoribosyl-amp cyclohydrolase; phosphoribosyl-ATP pyrophosphatase | 1,50 | 0,006479 |
| <i>argI</i> | ornithine carbamoyltransferase 1 | 1,50 | 0,002879 |
| Z5883 | orf; Unknown function | 1,51 | 0,03763 |
| <i>glpD</i> | Aerobic glycerol-3-phosphate dehydrogenase | 1,51 | 0,007426 |
| c1337 | Hypothetical protein | 1,51 | 0,01367 |
| --- | intergenic region | 1,51 | 0,02351 |
| <i>rimJ</i> | acetylation of N-terminal alanine of 30S ribosomal subunit protein S5 | 1,51 | 0,01036 |
| <i>coaD</i> | hypothetical protein | 1,51 | 0,0118 |
| c1673 | Hypothetical protein | 1,51 | 0,01494 |
| <i>yffS</i> | orf, hypothetical protein | 1,51 | 0,002562 |
| c0397 | InsB protein | 1,51 | 0,0008262 |

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|---------------------|--|------|-----------|
| <i>xthA</i> | exonuclease III | 1,51 | 0,0007362 |
| <i>phrB</i> | deoxyribodipyrimidine photolyase (photoreactivation) | 1,51 | 0,01941 |
| <i>hyaD</i> | processing of HyaA and HyaB proteins | 1,51 | 0,01356 |
| ECs0827 | unknown protein encoded by prophage CP-933K | 1,51 | 0,001468 |
| <i>rspA</i> | starvation sensing protein | 1,51 | 0,0197 |
| <i>emrB</i> | multidrug resistance; probably membrane translocase | 1,51 | 0,04418 |
| <i>ymfL</i> | Hypothetical protein ymfL | 1,51 | 0,00169 |
| <i>menE</i> | O-succinylbenzoic acid--CoA ligase | 1,52 | 0,02398 |
| ECs4964 | hypothetical protein | 1,52 | 0,004005 |
| <i>metG</i> | methionine tRNA synthetase | 1,52 | 0,00958 |
| <i>bglX</i> | beta-D-glucoside glucohydrolase, periplasmic | 1,52 | 0,001118 |
| <i>proC</i> | pyrroline-5-carboxylate reductase | 1,52 | 0,0004515 |
| ECs1584 | hypothetical protein | 1,52 | 0,004532 |
| ECs1173 | hypothetical protein | 1,52 | 0,001731 |
| <i>ilvL</i> | ilvGEDA operon leader peptide | 1,52 | 0,02243 |
| <i>emtA // mltE</i> | murein transglycosylase E | 1,52 | 0,03231 |
| --- | intergenic region | 1,52 | 0,03938 |
| c1980 | Hypothetical protein | 1,52 | 0,02043 |
| <i>mpaA // ycjI</i> | putative carboxypeptidase | 1,52 | 0,0137 |
| <i>rdgC</i> | orf, hypothetical protein | 1,52 | 0,01395 |
| <i>ydjK</i> | Hypothetical protein | 1,52 | 0,003269 |
| Z3866 | orf; Unknown function | 1,53 | 0,01335 |
| <i>mviM // yceM</i> | putative virulence factor | 1,53 | 0,03505 |
| <i>ypfG</i> | Hypothetical protein | 1,53 | 0,04565 |
| <i>yfaU</i> | orf, hypothetical protein | 1,53 | 0,001547 |
| <i>artP</i> | ATP-binding component of 3rd arginine transport system | 1,53 | 0,0002997 |
| <i>pdxH</i> | pyridoxinephosphate oxidase | 1,53 | 0,0005865 |
| <i>ruvA</i> | Holliday junction helicase subunit B; branch migration; repair | 1,53 | 0,005795 |
| --- | intergenic region | 1,53 | 0,006444 |
| c1062 | Hypothetical protein | 1,53 | 0,008597 |
| <i>galU</i> | glucose-1-phosphate uridylyltransferase | 1,53 | 0,0005572 |
| ECs0839 | putative tail component of prophage CP-933K | 1,53 | 0,0008673 |
| <i>cpdB</i> | Putative conserved protein | 1,53 | 0,001019 |
| <i>ychn</i> | orf, hypothetical protein | 1,53 | 0,003277 |
| ECs2041 | orf, hypothetical protein | 1,53 | 0,0006392 |
| <i>trpB</i> | Tryptophan synthase beta chain | 1,53 | 0,006778 |
| <i>adhC // frmA</i> | alcohol dehydrogenase class III; formaldehyde dehydrogenase, glutathione-dependent | 1,53 | 0,000686 |
| <i>ansP</i> | L-asparagine permease | 1,53 | 0,03203 |
| --- | intergenic region | 1,53 | 0,005518 |
| c1452 | Hypothetical protein | 1,53 | 0,009397 |
| <i>glmM</i> | Protein mrsA | 1,53 | 0,004429 |
| <i>malQ</i> | 4-alpha-glucanotransferase | 1,53 | 0,01424 |
| <i>ynjH</i> | orf, hypothetical protein | 1,53 | 0,01666 |
| --- | intergenic region | 1,54 | 0,003977 |
| <i>syd</i> | interacts with secY | 1,54 | 0,001916 |

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|---------------------|--|------|-----------|
| <i>bioB</i> | Biotin synthase | 1,54 | 0,0005567 |
| <i>ribA</i> | GTP cyclohydrolase II | 1,54 | 0,006118 |
| --- | intergenic region | 1,54 | 0,004728 |
| <i>malP</i> | Maltodextrin phosphorylase | 1,54 | 0,02501 |
| <i>ygiN</i> | orf, hypothetical protein | 1,54 | 0,01062 |
| --- | Hypothetical protein | 1,54 | 0,001141 |
| <i>hycC</i> | membrane-spanning protein of hydrogenase 3 (part of FHL complex) | 1,54 | 0,002386 |
| <i>emrR // mprA</i> | regulator of plasmid mcrB operon (microcin B17 synthesis) | 1,54 | 0,008809 |
| --- | intergenic region | 1,54 | 0,01339 |
| <i>baeR</i> | transcriptional response regulatory protein (sensor BaeS) | 1,54 | 0,001509 |
| <i>sbcB</i> | exonuclease I, 3 --> 5 specific; deoxyribosephosphodiesterase | 1,54 | 0,007884 |
| --- | intergenic region | 1,54 | 0,00958 |
| <i>mdoG // opgG</i> | periplasmic glucans biosynthesis protein | 1,54 | 0,006851 |
| <i>ldrB</i> | small toxic polypeptide | 1,55 | 0,02429 |
| --- | intergenic region | 1,55 | 0,001874 |
| c4811 | Hypothetical protein | 1,55 | 0,02035 |
| <i>cutC</i> | intergenic region | 1,55 | 0,0005333 |
| c1224 | Transposase insF for insertion sequence IS3ABCDEfA | 1,55 | 0,002884 |
| c1498 | Hypothetical protein | 1,55 | 0,002925 |
| <i>flgN</i> | protein of flagellar biosynthesis | 1,55 | 0,0006336 |
| <i>ltaE // ybjU</i> | putative arylsulfatase | 1,55 | 0,0005958 |
| <i>cysU</i> | Sulfate transport system permease protein cysT | 1,55 | 0,003702 |
| <i>rlmL</i> | Hypothetical protein ycbY | 1,55 | 0,02038 |
| --- | intergenic region | 1,55 | 0,0005035 |
| --- | Bacteriophage P1 gene repA | 1,55 | 0,002892 |
| <i>yegT</i> | putative nucleoside permease protein | 1,55 | 0,00868 |
| ECs4997 | translational regulator | 1,55 | 0,001031 |
| <i>ybiH</i> | putative transcriptional regulator | 1,55 | 0,01891 |
| <i>ycaR</i> | orf, hypothetical protein | 1,55 | 0,008568 |
| <i>ivy // ykfE</i> | orf, hypothetical protein | 1,55 | 0,0024 |
| <i>ggt</i> | gamma-glutamyltranspeptidase | 1,55 | 0,00101 |
| <i>hisH</i> | glutamine amidotransferase subunit of heterodimer with HisF = imidazole glycerol phosphate synthase holoenzyme | 1,55 | 0,00402 |
| ECs2633 | putative phage replication protein | 1,55 | 0,0259 |
| <i>allR // ybbU</i> | putative regulator | 1,55 | 0,0002422 |
| c3545 | Hypothetical protein | 1,55 | 0,002405 |
| <i>ynfA</i> | orf, hypothetical protein | 1,56 | 0,0005958 |
| <i>mltE</i> | Hypothetical protein | 1,56 | 0,01933 |
| <i>hokD // mokP</i> | polypeptide destructive to membrane potential | 1,56 | 0,002465 |
| <i>glpK</i> | Glycerol kinase | 1,56 | 0,02036 |
| --- | intergenic region | 1,56 | 0,02395 |
| ECs1593 | putative head-tail adaptor | 1,56 | 0,003935 |
| ECs2201 | unknown protein encoded within prophage CP-9330 | 1,56 | 0,01504 |
| <i>mipA // yeaF</i> | hypothetical protein | 1,56 | 0,00293 |
| <i>yiaD</i> | putative outer membrane protein | 1,56 | 0,04784 |

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|---------------------|---|------|-----------|
| --- | hypothetical protein | 1,56 | 0,0495 |
| <i>yicH</i> | orf, hypothetical protein | 1,56 | 0,01275 |
| <i>nhoA</i> | putative N-hydroxyarylamine O-acetyltransferase | 1,56 | 0,002443 |
| <i>ybgH</i> | Hypothetical transporter ybgH | 1,56 | 0,0002178 |
| <i>yecM</i> | orf, hypothetical protein | 1,56 | 0,0005658 |
| <i>nfnB</i> | oxygen-insensitive NAD(P)H nitroreductase | 1,56 | 0,0001825 |
| <i>fadL</i> | long-chain fatty acid transport protein (outer membrane flp protein) | 1,56 | 0,002002 |
| <i>tynA</i> | copper amine oxidase (tyramine oxidase) | 1,56 | 0,01024 |
| <i>spy</i> | periplasmic protein related to spheroblast formation | 1,56 | 0,00257 |
| <i>ydhB</i> | putative transcriptional regulator LYSR-type | 1,56 | 0,0006903 |
| <i>lysP</i> | lysine-specific permease | 1,56 | 0,02316 |
| <i>ytfF</i> | putative transmembrane subunit | 1,57 | 0,003452 |
| <i>ddlA</i> | D-alanine-D-alanine ligase A | 1,57 | 0,0003205 |
| <i>ygaC</i> | orf, hypothetical protein | 1,57 | 0,02804 |
| <i>yeeS</i> | putative DNA repair protein, RADC family | 1,57 | 0,00343 |
| <i>tyrP</i> | tyrosine-specific transport system | 1,57 | 0,04154 |
| <i>eutC</i> | ethanolamine ammonia-lyase, light chain | 1,57 | 0,002728 |
| <i>ybgR // zitB</i> | Putative conserved protein | 1,57 | 0,01937 |
| <i>cheY</i> | chemotaxis regulator transmits chemoreceptor signals to flagellar motor components | 1,57 | 0,0002639 |
| <i>dacC</i> | D-alanyl-D-alanine carboxypeptidase; penicillin-binding protein 6 | 1,57 | 0,007006 |
| <i>phnA</i> | PhnA protein | 1,57 | 0,001004 |
| --- | intergenic region | 1,57 | 0,01486 |
| <i>mobA</i> | molybdopterin ---> molybdopterin-guanine dinucleotide, protein Ar | 1,57 | 0,001006 |
| <i>pfkB</i> | 6-phosphofructokinase II; suppressor of pfkA | 1,57 | 0,01266 |
| <i>hyfE</i> | hydrogenase 4 membrane subunit | 1,57 | 0,0006213 |
| <i>ybjC</i> | orf, hypothetical protein | 1,57 | 0,000229 |
| <i>yeeR</i> | orf, hypothetical protein | 1,57 | 0,0009849 |
| <i>yaaW</i> | putative oxidoreductase | 1,57 | 0,0004849 |
| <i>pspE</i> | phage shock protein | 1,57 | 0,02789 |
| <i>yciK</i> | putative oxidoreductase | 1,57 | 0,0003977 |
| <i>ycdP</i> | putative protease | 1,57 | 0,01587 |
| --- | intergenic region | 1,57 | 0,01992 |
| <i>marA</i> | multiple antibiotic resistance; transcriptional activator of defense systems | 1,57 | 0,005353 |
| <i>ygaM</i> | orf, hypothetical protein | 1,57 | 0,0276 |
| <i>hisA</i> | N-(5-phospho-L-ribosyl-formimino)-5-amino-1-(5-phosphoribosyl)-4-imidazolecarboxamide isomerase | 1,57 | 0,001866 |
| <i>ydgl</i> | putative arginineornithine antiporter | 1,57 | 0,01488 |
| <i>ssuD // ycbN</i> | Alkanesulfonate monooxygenase | 1,58 | 0,01233 |
| <i>yjel</i> | orf, hypothetical protein | 1,58 | 0,01196 |
| <i>speC</i> | ornithine decarboxylase isozyme | 1,58 | 0,005124 |
| ECs4971 | hypothetical protein | 1,58 | 0,0003073 |
| <i>tar</i> | methyl-accepting chemotaxis protein II, aspartate sensor receptor | 1,58 | 0,0009238 |
| <i>mak // yajF</i> | Hypothetical protein yajF | 1,58 | 0,01351 |
| <i>kilW</i> | Lambda Regulatory protein CIII | 1,58 | 0,00071 |
| --- | intergenic region | 1,58 | 0,01092 |

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|---------------------|---|------|-----------|
| <i>mrp</i> | putative ATPase | 1,58 | 0,008809 |
| <i>aceE</i> | pyruvate dehydrogenase (decarboxylase component) | 1,58 | 0,001904 |
| <i>araC</i> | transcriptional regulator for ara operon | 1,58 | 0,01352 |
| <i>mdaA // nfsA</i> | modulator of drug activity A | 1,58 | 0,0003352 |
| <i>ubiF</i> | 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase | 1,58 | 0,003728 |
| <i>argP // iciA</i> | replication initiation inhibitor, binds to 13-mers at oriC | 1,58 | 0,01385 |
| <i>hdhA</i> | 7-alpha-hydroxysteroid dehydrogenase | 1,59 | 0,002231 |
| <i>cheB</i> | response regulator for chemotaxis (cheA sensor); protein methylesterase | 1,59 | 0,00115 |
| <i>thiJ // yajL</i> | 4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate synthesis | 1,59 | 0,003709 |
| <i>guaB</i> | Inosine-5-monophosphate dehydrogenase | 1,59 | 0,001229 |
| <i>nudK // yffH</i> | orf, hypothetical protein | 1,59 | 0,01711 |
| <i>c1602</i> | Hypothetical protein | 1,59 | 0,00194 |
| <i>mukB</i> | Cell division protein mukB | 1,59 | 0,001388 |
| <i>yidP</i> | putative transcriptional regulator | 1,59 | 0,004785 |
| --- | orf, hypothetical protein | 1,59 | 0,007246 |
| <i>frsA</i> | orf, hypothetical protein | 1,60 | 0,04734 |
| --- | intergenic region | 1,60 | 0,007006 |
| <i>bglA</i> | 6-phospho-beta-glucosidase A; cryptic | 1,60 | 0,0009944 |
| <i>mscS // yggB</i> | putative transport protein | 1,60 | 0,001134 |
| <i>phnA // yjdM</i> | orf, hypothetical protein | 1,60 | 0,004879 |
| <i>ftnA</i> | cytoplasmic ferritin (an iron storage protein) | 1,60 | 0,00338 |
| <i>rph</i> | RNase PH | 1,60 | 0,006778 |
| <i>c2257</i> | Hypothetical protein | 1,60 | 0,005361 |
| <i>fliQ</i> | flagellar biosynthesis | 1,60 | 0,00975 |
| <i>ygiE</i> | Zinc transporter zupT | 1,60 | 0,007185 |
| <i>c14613</i> | putative tail component of prophage CP-9330 | 1,60 | 0,00634 |
| <i>purR</i> | transcriptional repressor for pur regulon, glyA, glnB, prsA, speA | 1,60 | 0,006126 |
| <i>kdsA</i> | 2-dehydro-3-deoxyphosphooctulonate aldolase | 1,60 | 0,0003098 |
| <i>mliC // ydhA</i> | orf, hypothetical protein | 1,60 | 0,000929 |
| <i>c2484</i> | Hypothetical protein | 1,60 | 0,01438 |
| <i>yncE</i> | putative receptor | 1,60 | 0,03299 |
| <i>menC</i> | o-succinylbenzoyl-CoA synthase; conversion of chorismate to 2-o-succinylbenzoyl-CoA | 1,60 | 0,01036 |
| <i>yiiM</i> | orf, hypothetical protein | 1,61 | 0,0489 |
| <i>cynT</i> | carbonic anhydrase | 1,61 | 0,0001173 |
| <i>ECs1096</i> | putative endolysin of prophage CP-9330 | 1,61 | 0,00119 |
| <i>modA</i> | Molybdate-binding periplasmic protein precursor | 1,61 | 0,01921 |
| <i>yicL</i> | putative permease transporter | 1,61 | 0,0005771 |
| <i>ECs1093</i> | putative lipoprotein Rz1 protein precursor | 1,61 | 0,01407 |
| <i>cheR</i> | response regulator for chemotaxis; protein glutamate methyltransferase | 1,61 | 0,002193 |
| <i>ybhB</i> | orf, hypothetical protein | 1,61 | 0,001577 |
| <i>pheL</i> | leader peptide of chorismate mutase-P-prephenate dehydratase | 1,61 | 0,02479 |
| <i>yjiU</i> | Hypothetical protein yjiU | 1,61 | 0,001373 |
| <i>abgB</i> | hypothetical protein | 1,61 | 0,0006777 |
| <i>narP</i> | nitratennitrite response regulator (sensor NarQ) | 1,61 | 0,0007362 |

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|----------------------|--|------|-----------|
| --- | intergenic region | 1,61 | 0,000406 |
| <i>ycbW</i> | orf, hypothetical protein | 1,61 | 0,001658 |
| --- | intergenic region | 1,62 | 0,001341 |
| <i>pntA</i> | pyridine nucleotide transhydrogenase, alpha subunit | 1,62 | 0,0001051 |
| <i>htrB // lpxL</i> | heat shock protein | 1,62 | 0,004664 |
| <i>trxB</i> | thioredoxin reductase | 1,62 | 0,03653 |
| <i>kbl</i> | 2-amino-3-ketobutyrate CoA ligase (glycine acetyltransferase) | 1,62 | 0,002146 |
| <i>c3554</i> | Hypothetical protein | 1,62 | 0,009987 |
| <i>c2439</i> | Hypothetical protein | 1,62 | 0,00194 |
| <i>rpmE2 // ykgM</i> | putative ribosomal protein | 1,62 | 0,003809 |
| <i>ppiC</i> | peptidyl-prolyl cis-trans isomerase C (rotamase C) | 1,62 | 0,007672 |
| <i>phnI</i> | phosphonate metabolism | 1,62 | 0,01179 |
| <i>fliD</i> | flagellar biosynthesis; filament capping protein; enables filament assembly | 1,63 | 0,004345 |
| <i>yebE</i> | orf, hypothetical protein | 1,63 | 0,02741 |
| <i>kdpB</i> | Potassium-transporting ATPase B chain | 1,63 | 0,003364 |
| <i>bglX</i> | Periplasmic beta-glucosidase precursor | 1,63 | 0,0002958 |
| --- | intergenic region | 1,63 | 0,002433 |
| <i>argA</i> | N-acetylglutamate synthase; amino acid acetyltransferase | 1,63 | 0,001005 |
| <i>Z1189</i> | orf; Unknown function | 1,63 | 0,007815 |
| <i>yadI</i> | putative PTS enzyme II B component | 1,63 | 0,03752 |
| <i>degQ</i> | serine endoprotease | 1,63 | 0,001382 |
| <i>ygaD</i> | orf, hypothetical protein | 1,63 | 0,000308 |
| <i>metC</i> | cystathionine beta-lyase (beta-cystathionase) | 1,63 | 0,0005569 |
| <i>kdtA</i> | 3-deoxy-D-manno-octulosonic-acid transferase (KDO transferase) | 1,63 | 0,003177 |
| <i>prsA</i> | phosphoribosylpyrophosphate synthetase | 1,63 | 0,01079 |
| <i>bioC</i> | biotin biosynthesis; reaction prior to pimeloyl CoA | 1,64 | 0,006178 |
| <i>cynR</i> | cyn operon positive regulator | 1,64 | 0,002405 |
| <i>ygjM</i> | orf, hypothetical protein | 1,64 | 0,0002489 |
| <i>arsC</i> | Arsenate reductase | 1,64 | 0,002485 |
| <i>ileS</i> | Isoleucyl-tRNA synthetase | 1,64 | 0,0009176 |
| <i>acnB</i> | aconitate hydratase B | 1,64 | 0,04421 |
| <i>lysR</i> | positive regulator for lys | 1,64 | 0,003762 |
| <i>hhN</i> | putative enzyme | 1,64 | 0,02762 |
| <i>cyaR</i> | MG1655_ryeE_b4438 /SEG=NC_000913:+2165134,2165219 /LEN=85 | 1,64 | 0,002901 |
| <i>c5447</i> | Hypothetical protein | 1,64 | 0,001382 |
| <i>EybaK</i> | orf, hypothetical protein | 1,64 | 0,000212 |
| <i>fbp</i> | fructose-bisphosphatase | 1,64 | 0,0008818 |
| <i>hisD</i> | Histidinol dehydrogenase | 1,64 | 0,0008841 |
| <i>yfaZ</i> | orf, hypothetical protein | 1,64 | 0,01908 |
| <i>ECs2963</i> | unknown protein encoded within prophage CP-9330 | 1,64 | 0,00314 |
| <i>pdxK</i> | pyridoxalpyridoxinepyridoxamine kinase | 1,64 | 0,001142 |
| <i>ydfG</i> | putative oxidoreductase | 1,64 | 0,006156 |
| <i>che</i> | chemotactic response; CheY protein phosphatase; antagonist of CheY as switch regulator | 1,64 | 0,0016 |
| <i>hycB</i> | Formate hydrogenlyase subunit 2 | 1,64 | 0,003572 |

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|---------------------|---|------|-----------|
| <i>yidA</i> | orf, hypothetical protein | 1,64 | 0,008101 |
| <i>exoX</i> | hypothetical protein | 1,64 | 0,0003772 |
| --- | intergenic region | 1,65 | 0,01531 |
| <i>EynfH</i> | putative DMSO reductase anchor subunit | 1,65 | 0,003005 |
| <i>hisL</i> | his operon leader peptide | 1,65 | 0,0446 |
| <i>udp</i> | uridine phosphorylase | 1,65 | 0,01092 |
| <i>yfcS</i> | Hypothetical fimbrial chaperone yfcS precursor | 1,65 | 0,0006642 |
| ECs1509 | unknown protein encoded by prophage CP-933N | 1,65 | 0,003392 |
| c0283 | Hypothetical protein | 1,65 | 0,001534 |
| <i>panB</i> | 3-methyl-2-oxobutanoate hydroxymethyltransferase | 1,65 | 0,001927 |
| <i>ycfP</i> | orf, hypothetical protein | 1,65 | 0,03505 |
| <i>fimD</i> | outer membrane protein; export and assembly of type 1 fimbriae, interrupted | 1,65 | 0,003762 |
| <i>eutR</i> | putative ARAC-type regulatory protein | 1,65 | 0,003837 |
| <i>murQ</i> | putative regulator | 1,65 | 0,01875 |
| <i>yidE</i> | putative transport protein | 1,66 | 0,01888 |
| <i>dkgB</i> | 2,5-diketo-D-gluconate reductase B | 1,66 | 0,0001018 |
| ECs1088 | unknown protein encoded by prophage CP-933O | 1,66 | 0,001349 |
| c5008 | Hypothetical protein | 1,66 | 0,01927 |
| c2230 | Hypothetical protein | 1,66 | 0,002401 |
| c0754 | Hypothetical protein | 1,66 | 0,02468 |
| <i>ydgH</i> | orf, hypothetical protein | 1,66 | 0,0002696 |
| <i>yfcB</i> | putative adenine-specific methylase | 1,66 | 0,0008409 |
| <i>eutL</i> | orf, hypothetical protein | 1,66 | 0,001084 |
| <i>yafM</i> | orf, hypothetical protein | 1,67 | 0,02623 |
| c4942 | Hypothetical protein | 1,67 | 0,03391 |
| <i>ynjD</i> | putative ATP-binding component of a transport system | 1,67 | 0,0002952 |
| <i>ygiM</i> | orf, hypothetical protein | 1,67 | 0,005638 |
| <i>ybjK</i> | putative DEOR-type transcriptional regulator | 1,67 | 0,001284 |
| <i>ynaJ</i> | orf, hypothetical protein | 1,67 | 0,02591 |
| <i>rlmI // yccW</i> | putative oxidoreductase | 1,67 | 0,01562 |
| ECs4272 | orf; hypothetical protein | 1,67 | 0,0008555 |
| <i>ybhQ</i> | orf, hypothetical protein | 1,67 | 0,0005518 |
| <i>ybiU</i> | orf, hypothetical protein | 1,67 | 0,01374 |
| <i>yejK</i> | protein present in spermidine nucleoids | 1,67 | 0,0008763 |
| <i>hiuH</i> | orf, hypothetical protein | 1,67 | 0,0005016 |
| <i>lipA</i> | lipoate synthesis, sulfur insertion? | 1,68 | 0,00121 |
| <i>dcrB</i> | hypothetical protein | 1,68 | 0,0001844 |
| <i>ECyqjI</i> | orf, hypothetical protein | 1,68 | 0,001708 |
| <i>sppA</i> | protease IV, a signal peptide peptidase | 1,68 | 0,0004019 |
| <i>orn // yjeR</i> | hypothetical protein | 1,68 | 0,0003007 |
| <i>mtIA</i> | PTS system, mannitol-specific IIABC component | 1,68 | 0,0005465 |
| <i>fimH</i> | minor fimbrial subunit, D-mannose specific adhesin | 1,68 | 0,0008897 |
| <i>yfbU</i> | orf, hypothetical protein | 1,68 | 0,009592 |
| --- | hypothetical protein | 1,68 | 0,0006188 |
| <i>gabT</i> | 4-aminobutyrate aminotransferase | 1,68 | 0,001031 |

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|---------------------|---|------|-----------|
| <i>narY</i> | Respiratory nitrate reductase 2 beta chain | 1,68 | 0,002621 |
| <i>ybhA</i> | putative phosphatase | 1,68 | 0,003 |
| <i>dld</i> | D-lactate dehydrogenase, FAD protein, NADH independent | 1,68 | 0,005796 |
| <i>ygiS</i> | putative transport periplasmic protein | 1,68 | 0,01424 |
| <i>yqhC</i> | putative ARAC-type regulatory protein | 1,68 | 0,0005269 |
| <i>ydcQ</i> | Hypothetical protein | 1,68 | 0,000355 |
| c3190 | Hypothetical protein | 1,69 | 0,001173 |
| <i>pnuC</i> | required for NMN transport | 1,69 | 0,01114 |
| <i>ackA</i> | acetate kinase | 1,69 | 0,01156 |
| <i>yihN</i> | putative resistance protein (transport) | 1,69 | 0,0008587 |
| <i>ubiF</i> | hypothetical protein | 1,69 | 0,02678 |
| <i>abgA // ydaJ</i> | putative aminohydrolase | 1,69 | 0,00104 |
| <i>ycfD</i> | orf, hypothetical protein | 1,69 | 0,002072 |
| <i>purA</i> | adenylosuccinate synthetase | 1,69 | 0,0003646 |
| <i>hisC</i> | histidinol-phosphate aminotransferase | 1,69 | 0,001248 |
| c4898 | Hypothetical protein | 1,69 | 0,009164 |
| <i>thiH</i> | Thiazole biosynthesis protein thiH | 1,70 | 0,01396 |
| <i>ybfA</i> | orf, hypothetical protein | 1,70 | 0,04257 |
| <i>moeA</i> | Molybdopterin biosynthesis protein moeA | 1,70 | 0,004454 |
| <i>relB</i> | negative regulator of translation | 1,70 | 0,0004114 |
| <i>gpt</i> | guanine-hypoxanthine phosphoribosyltransferase | 1,70 | 0,006178 |
| <i>rhtB // yigK</i> | hypothetical protein | 1,70 | 0,008028 |
| <i>yihU</i> | putative dehydrogenase | 1,71 | 0,0003366 |
| <i>dgoK</i> | 2-oxo-3-deoxygalactonate kinase | 1,71 | 0,004152 |
| c4437 | Hypothetical protein | 1,71 | 0,009279 |
| <i>rpoS</i> | RNA polymerase, sigma S (sigma38) factor; synthesis of many growth phase related proteins | 1,71 | 8,34E-02 |
| <i>yhjC</i> | putative transcriptional regulator LYSR-type | 1,71 | 0,01787 |
| <i>guaA</i> | GMP synthase (glutamine-hydrolyzing) | 1,71 | 0,0007268 |
| <i>yccX</i> | orf, hypothetical protein | 1,71 | 0,02558 |
| <i>ymdB</i> | putative polyprotein | 1,72 | 0,04919 |
| <i>ompA</i> | Outer membrane protein A precursor | 1,72 | 0,003373 |
| <i>gntP</i> | gluconate transport system permease 3 | 1,72 | 0,007246 |
| c1453 | Putative head-tail joining protein of prophage | 1,72 | 0,002382 |
| <i>hemB</i> | 5-aminolevulinatase dehydratase = porphobilinogen synthase | 1,72 | 0,0002435 |
| <i>proS</i> | Prolyl-tRNA synthetase | 1,73 | 0,001405 |
| <i>yidB //</i> | Hypothetical protein yidB | 1,73 | 0,001877 |
| <i>tus</i> | DNA-binding protein; inhibition of replication at Ter sites | 1,73 | 0,0005076 |
| c1588 | Lambda K, tail component | 1,73 | 0,0005105 |
| <i>potF</i> | Putrescine-binding periplasmic protein precursor | 1,73 | 0,0001855 |
| <i>gmhA // lpcA</i> | phosphoheptose isomerase | 1,73 | 0,0002164 |
| <i>cysS</i> | cysteine tRNA synthetase | 1,73 | 0,006005 |
| <i>fadH // ygjL</i> | putative NADPH dehydrogenase | 1,73 | 0,02501 |
| <i>marB</i> | multiple antibiotic resistance protein | 1,74 | 0,00348 |
| c4552 | Transposase insC for insertion element IS2ADFIK | 1,74 | 0,001592 |
| <i>araD</i> | L-ribulose-5-phosphate 4-epimerase | 1,74 | 0,00063 |

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|---------------------|--|------|-----------|
| <i>anmK</i> | orf, hypothetical protein | 1,74 | 0,000217 |
| <i>kdsB</i> | CTP: CMP-3-deoxy-D-manno-octulosonate transferase | 1,74 | 0,001053 |
| <i>lacZ</i> | Beta-galactosidase | 1,74 | 0,0007112 |
| <i>sohB</i> | putative protease | 1,74 | 0,006872 |
| <i>aroH</i> | 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (DAHP synthetase, tryptophan repressible) | 1,74 | 0,02014 |
| <i>yjhP</i> | putative methyltransferase | 1,74 | 0,01016 |
| c1106 | Putative acylphosphatase | 1,74 | 0,03235 |
| <i>dcp</i> | dipeptidyl carboxypeptidase II | 1,74 | 4,46E-02 |
| <i>ygjP</i> | orf, hypothetical protein | 1,74 | 0,0003953 |
| <i>yeaK</i> | orf, hypothetical protein | 1,74 | 1,52E-02 |
| <i>yjhQ</i> | orf, hypothetical protein | 1,75 | 0,00273 |
| <i>potF</i> | periplasmic putrescine-binding protein; permease protein | 1,75 | 0,004405 |
| <i>yhhM</i> | putative receptor | 1,75 | 7,31E-02 |
| c0284 | Conserved hypothetical protein | 1,75 | 0,000229 |
| <i>gatZ</i> | Putative tagatose 6-phosphate kinase gatZ | 1,75 | 0,006479 |
| ECs1112 | putative minor tail protein | 1,75 | 0,01079 |
| c4571 | Hypothetical protein yfjX | 1,75 | 0,0003244 |
| c3651 | Hypothetical protein | 1,75 | 0,0002575 |
| <i>fliR</i> | Hypothetical protein | 1,76 | 0,0009986 |
| <i>yncJ</i> | orf, hypothetical protein | 1,76 | 0,0049 |
| <i>cbpM // yccD</i> | orf, hypothetical protein | 1,76 | 0,01364 |
| <i>ybdG</i> | putative transport | 1,76 | 4,52E-02 |
| <i>ycdQ</i> | orf, hypothetical protein | 1,76 | 0,0004698 |
| <i>cysG</i> | uroporphyrinogen III methylase; sirohaeme biosynthesis | 1,76 | 0,005753 |
| <i>ccmH</i> | possible subunit of heme lyase | 1,76 | 0,003879 |
| <i>eco</i> | ecotin, a serine protease inhibitor | 1,76 | 9,28E-02 |
| <i>leuL</i> | leu operon leader peptide | 1,76 | 0,004192 |
| <i>manA</i> | mannose-6-phosphate isomerase | 1,76 | 0,001728 |
| <i>ycdF</i> | orf, hypothetical protein | 1,76 | 0,001375 |
| <i>malE</i> | Maltose-binding periplasmic protein precursor | 1,76 | 0,002829 |
| <i>metK</i> | methionine adenosyltransferase 1 (AdoMet synthetase); methyl and propylamine donor, corepressor of met genes | 1,76 | 0,0101 |
| <i>purP // yieG</i> | putative membrane transport protein | 1,77 | 0,01395 |
| <i>frmB // yaiM</i> | putative S-formylglutathione hydrolase | 1,77 | 4,50E-02 |
| <i>yaaA</i> | orf, hypothetical protein | 1,77 | 5,65E-02 |
| <i>ychM</i> | putative sulfate transporter | 1,77 | 0,003331 |
| <i>yeiP</i> | putative elongation factor | 1,77 | 0,0005567 |
| <i>eutK</i> | orf, hypothetical protein | 1,77 | 4,30E-02 |
| <i>purN</i> | phosphoribosylglycinamide formyltransferase 1 | 1,77 | 0,0003708 |
| <i>bioA</i> | 7,8-diaminopelargonic acid synthetase | 1,77 | 0,0008684 |
| Z2978 | putative replication protein for prophage CP-933T | 1,78 | 0,0006833 |
| ECs1549 | putative major tail subunit | 1,78 | 0,01572 |
| <i>cynS</i> | cyanate aminohydrolase, cyanase | 1,78 | 0,0001213 |
| --- | intergenic region | 1,78 | 0,02051 |
| <i>yidB</i> | orf, hypothetical protein | 1,78 | 0,001358 |

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|---------------------|--|------|-----------|
| <i>elbB // yhbL</i> | sigma cross-reacting protein 27A (SCRP-27A) | 1,78 | 0,001308 |
| <i>purC</i> | phosphoribosylaminoimidazole-succinocarboxamide synthetase = SAICAR synthetase | 1,78 | 0,005685 |
| <i>glnG</i> | response regulator for gln (sensor glnL) (nitrogen regulator I, NRI) | 1,78 | 0,001457 |
| <i>pspF</i> | psp operon transcriptional activator | 1,78 | 0,004237 |
| <i>deoA</i> | hypothetical protein | 1,78 | 0,03574 |
| <i>torA</i> | trimethylamine N-oxide reductase subunit | 1,78 | 0,0004376 |
| <i>argG</i> | argininosuccinate synthetase | 1,78 | 7,95E-02 |
| <i>chaA</i> | sodium-calciumproton antiporter | 1,79 | 0,01447 |
| <i>yidR</i> | orf, hypothetical protein | 1,79 | 0,01036 |
| <i>osmC</i> | osmotically inducible protein | 1,79 | 0,01472 |
| <i>ycbG</i> | putative dehydrogenase | 1,79 | 0,01156 |
| <i>yeaD</i> | orf, hypothetical protein | 1,79 | 0,002622 |
| <i>pyrD</i> | Dihydroorotate dehydrogenase | 1,79 | 0,0001018 |
| <i>hdfR // yifA</i> | regulator of pssA | 1,79 | 0,0007705 |
| --- | Hypothetical protein | 1,79 | 0,01987 |
| <i>msrA</i> | peptide methionine sulfoxide reductase | 1,79 | 0,0007009 |
| <i>yraQ</i> | orf, hypothetical protein | 1,80 | 0,0007334 |
| <i>ypfH</i> | orf, hypothetical protein | 1,80 | 0,00158 |
| <i>ycaM</i> | putative transport | 1,80 | 0,002231 |
| <i>yeeF</i> | putative amino acidamine transport protein | 1,81 | 0,02663 |
| c4300 | Hypothetical protein | 1,81 | 0,01082 |
| <i>hipB</i> | persistence to inhibition of murein or DNA biosynthesis; regulatory protein | 1,81 | 6,14E-02 |
| <i>frwC</i> | PTS system, fructose-like enzyme II component | 1,81 | 0,0005481 |
| <i>glnA</i> | Glutamine synthetase | 1,81 | 3,53E-02 |
| <i>ynjA</i> | orf, hypothetical protein | 1,81 | 0,01565 |
| <i>metG</i> | Methionyl-tRNA synthetase | 1,81 | 0,00103 |
| <i>hdfR // yifA</i> | orf, hypothetical protein | 1,81 | 0,03141 |
| c4424 | Putative adhesin | 1,82 | 0,0006372 |
| <i>yfaX</i> | putative regulator | 1,82 | 0,008863 |
| <i>glnP</i> | glutamine high-affinity transport system; membrane component | 1,82 | 0,04328 |
| <i>rsmF // yebU</i> | putative nucleolar proteins | 1,82 | 0,005114 |
| <i>uspD // yitT</i> | putative regulator | 1,82 | 0,00473 |
| <i>rhaR</i> | positive regulator for rhaRS operon | 1,82 | 0,0006869 |
| <i>qseB // ygiX</i> | putative 2-component transcriptional regulator | 1,82 | 0,0003734 |
| <i>bioF</i> | 8-amino-7-oxononanoate synthase | 1,82 | 0,001896 |
| <i>carB</i> | Carbamoyl-phosphate synthase large chain | 1,83 | 0,004405 |
| c4195 | Hypothetical protein | 1,83 | 0,00635 |
| <i>mtfA // yeel</i> | orf, hypothetical protein | 1,83 | 0,01569 |
| <i>speB</i> | agmatinase | 1,83 | 0,001481 |
| <i>ymgG</i> | orf, hypothetical protein | 1,83 | 1,14E-02 |
| c4772 | Hypothetical protein | 1,83 | 0,001672 |
| --- | intergenic region | 1,83 | 0,01668 |
| <i>ycaO</i> | orf, hypothetical protein | 1,83 | 0,00525 |
| <i>purP</i> | putative membrane transport protein | 1,84 | 0,009789 |

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|---------------------|--|------|-----------|
| <i>kdpB</i> | ATPase of high-affinity potassium transport system, B chain | 1,84 | 0,001593 |
| <i>yqhD</i> | putative oxidoreductase | 1,84 | 0,00868 |
| <i>aes // ybaC</i> | putative lipase | 1,84 | 0,005683 |
| <i>hisD</i> | L-histidinal:NAD+ oxidoreductase; L-histidinol:NAD+ oxidoreductase | 1,84 | 0,003359 |
| <i>malM</i> | periplasmic protein of mal regulon | 1,84 | 0,0002091 |
| <i>mdaB</i> | modulator of drug activity B | 1,84 | 2,75E-02 |
| <i>argC</i> | N-acetyl-gamma-glutamylphosphate reductase | 1,84 | 0,000406 |
| --- | putative major tail subunit encoded within prophage CP-933V | 1,85 | 0,001685 |
| <i>pspA</i> | phage shock protein, inner membrane protein | 1,85 | 0,0001035 |
| --- | putative holin protein | 1,85 | 0,002282 |
| <i>thiM</i> | hydroxyethylthiazole kinase | 1,86 | 0,0007983 |
| <i>ldcA</i> | hypothetical protein | 1,86 | 0,0006057 |
| <i>ulaG // yjfR</i> | orf, hypothetical protein | 1,86 | 9,74E-02 |
| <i>ogrK</i> | prophage P2 ogr protein | 1,86 | 0,00282 |
| <i>xthA</i> | exonuclease III | 1,86 | 0,001697 |
| <i>potD</i> | spermidineputrescine periplasmic transport protein | 1,87 | 8,86E-02 |
| <i>ynjB</i> | orf, hypothetical protein | 1,87 | 0,01447 |
| <i>mdtA</i> | putative membrane protein | 1,87 | 0,003012 |
| <i>ydcO</i> | putative membrane transport protein | 1,87 | 0,000249 |
| <i>rpiA</i> | ribosephosphate isomerase, constitutive | 1,87 | 6,27E-02 |
| <i>yegB</i> | Hypothetical transport protein yegB | 1,87 | 2,99E-02 |
| <i>sseA</i> | putative thiosulfate sulfurtransferase | 1,87 | 0,02293 |
| <i>cfa</i> | cyclopropane fatty acyl phospholipid synthase | 1,87 | 0,003963 |
| ECs3935 | putative kinase | 1,87 | 4,51E-02 |
| <i>eda</i> | 2-keto-3-deoxygluconate 6-phosphate aldolase and 2-keto-4-hydroxyglutarate aldolase | 1,88 | 0,0003106 |
| <i>hisD</i> | L-histidinal:NAD+ oxidoreductase; L-histidinol:NAD+ oxidoreductase | 1,88 | 6,02E-02 |
| <i>narH</i> | Respiratory nitrate reductase 1 beta chain | 1,88 | 0,0239 |
| <i>yibI</i> | Hypothetical protein yibI | 1,88 | 0,0227 |
| <i>ycdW</i> | putative dehydrogenase | 1,89 | 0,0001875 |
| <i>ccbB</i> | orf, hypothetical protein | 1,89 | 0,0004919 |
| <i>ydcH</i> | orf, hypothetical protein | 1,89 | 0,01758 |
| <i>ydbK</i> | putative oxidoreductase, Fe-S subunit | 1,89 | 0,04764 |
| <i>ushA</i> | UDP-sugar hydrolase (5-nucleotidase) | 1,89 | 0,002905 |
| <i>hisB</i> | imidazoleglycerolphosphate dehydratase and histidinol-phosphate phosphatase | 1,90 | 0,0002392 |
| <i>ygcB</i> | orf; hypothetical protein | 1,90 | 0,0002399 |
| <i>nadA</i> | quinolinate synthetase, A protein | 1,90 | 0,0008295 |
| <i>rimO // yliG</i> | orf, hypothetical protein | 1,90 | 0,02223 |
| <i>sotB // ydeA</i> | sugar efflux transporter; L-arabinose and isopropyl-b-D-thiogalactopyranoside exporter protein | 1,90 | 0,0001406 |
| <i>ybiN</i> | orf, hypothetical protein | 1,90 | 0,0008017 |
| <i>mug // ygfF</i> | orf, hypothetical protein | 1,90 | 0,002825 |
| <i>yaeH</i> | putative structural protein | 1,90 | 0,01666 |
| <i>narL</i> | pleiotrophic regulation of anaerobic respiration: response regulator for nar, frd, dms and tor genes | 1,91 | 0,02268 |
| <i>malZ</i> | Maltodextrin glucosidase | 1,91 | 0,0003353 |

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|---------------------|---|------|-----------|
| <i>yibO</i> | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase | 1,91 | 0,009592 |
| <i>ybjP</i> | putative lipoprotein | 1,91 | 0,004501 |
| <i>yhaK</i> | orf, hypothetical protein | 1,91 | 0,003303 |
| <i>yfbT</i> | putative phosphatase | 1,92 | 0,007265 |
| <i>metR</i> | regulator for metE and methH | 1,92 | 0,0005958 |
| <i>yggS</i> | orf, hypothetical protein | 1,92 | 0,002239 |
| c2149 | Hypothetical protein | 1,92 | 0,005052 |
| --- | intergenic region | 1,92 | 0,0002257 |
| <i>pgsA</i> | phosphatidylglycerophosphate synthetase = CDP-1,2-diacyl-sn-glycerol-3-phosphate phosphatidyl transferase | 1,92 | 7,08E-02 |
| <i>qmcA // ybbK</i> | putative protease | 1,92 | 0,0202 |
| <i>yccF</i> | orf, hypothetical protein | 1,92 | 0,0002447 |
| <i>argF</i> | ornithine carbamoyltransferase 2, chain F | 1,92 | 7,28E-03 |
| <i>yeaO</i> | orf, hypothetical protein | 1,93 | 0,0116 |
| <i>yqjH</i> | orf, hypothetical protein | 1,93 | 0,0001317 |
| <i>malX</i> | PTS system, maltose and glucose-specific IIBC component | 1,93 | 0,0005016 |
| --- | intergenic region | 1,93 | 0,04287 |
| Z0115 | orf, hypothetical protein | 1,93 | 0,003072 |
| --- | intergenic region | 1,93 | 0,0175 |
| <i>ade // yicP</i> | putative adenine deaminase | 1,93 | 0,0002988 |
| <i>yceH</i> | orf, hypothetical protein | 1,93 | 0,003465 |
| <i>yijO</i> | putative ARAC-type regulatory protein | 1,94 | 0,0006279 |
| c2623 | hypothetical protein | 1,94 | 0,006119 |
| <i>menC</i> | O-succinylbenzoate-CoA synthase | 1,94 | 0,0003938 |
| --- | intergenic region | 1,94 | 0,02455 |
| <i>acpD // azoR</i> | acyl carrier protein phosphodiesterase | 1,95 | 7,98E-03 |
| c5055 | Hypothetical protein | 1,95 | 0,004429 |
| <i>cspD</i> | stress induced DNA replication inhibitor. | 1,95 | 0,0003055 |
| <i>nupC</i> | permease of transport system for 3 nucleosides | 1,95 | 0,00114 |
| <i>hemL</i> | glutamate-1-semialdehyde aminotransferase (aminomutase) | 1,95 | 0,002052 |
| c5343 | Hypothetical protein | 1,95 | 0,001807 |
| <i>glnH</i> | periplasmic glutamine-binding protein; permease | 1,95 | 0,0003097 |
| <i>ccmG // dsbE</i> | disulfide oxidoreductase | 1,96 | 0,001524 |
| <i>gnd</i> | gluconate-6-phosphate dehydrogenase, decarboxylating | 1,96 | 0,0006967 |
| <i>yajQ</i> | orf, hypothetical protein | 1,96 | 4,36E-02 |
| <i>thiD</i> | phosphomethylpyrimidine kinase | 1,96 | 0,0002686 |
| <i>yeaC</i> | orf, hypothetical protein | 1,98 | 0,006768 |
| <i>mutS</i> | methyl-directed mismatch repair | 1,98 | 0,0005975 |
| <i>hycl</i> | Hydrogenase 3 maturation protease | 1,99 | 0,0003641 |
| <i>malZ</i> | maltodextrin glucosidase | 1,99 | 0,0004574 |
| <i>hokB</i> | small toxic membrane polypeptide | 1,99 | 0,007164 |
| <i>mokB</i> | regulatory peptide whose translation enables hokB expression | 1,99 | 0,02443 |
| <i>gldD</i> | glycolate oxidase subunit D | 2,00 | 0,002465 |
| <i>hybD</i> | Hydrogenase 2 maturation protease | 2,00 | 0,0003829 |
| <i>ynfG</i> | putative oxidoreductase Fe-S subunit | 2,01 | 0,009549 |
| <i>flgM</i> | anti-FlhA (anti-sigma) factor; also known as RflB protein | 2,02 | 8,24E-02 |

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|---------------------|--|------|-----------|
| <i>ydbC</i> | putative dehydrogenase | 2,02 | 0,03723 |
| <i>ccmH</i> | Cytochrome c-type biogenesis protein ccmH precursor | 2,02 | 3,78E-02 |
| <i>asnA</i> | asparagine synthetase A | 2,02 | 0,007391 |
| <i>yccU</i> | orf; Unknown function | 2,02 | 0,00217 |
| <i>purK</i> | phosphoribosylaminoimidazole carboxylase = AIR carboxylase, CO(2)-fixing subunit | 2,02 | 0,002646 |
| <i>yiiS</i> | orf, hypothetical protein | 2,03 | 0,0002995 |
| <i>yffR</i> | orf, hypothetical protein | 2,03 | 0,000171 |
| <i>ycaC</i> | orf, hypothetical protein | 2,03 | 0,009032 |
| <i>nikR // yhhG</i> | hypothetical protein | 2,03 | 0,01431 |
| <i>msrB // yeaA</i> | orf, hypothetical protein | 2,03 | 0,003328 |
| <i>pta</i> | phosphotransacetylase | 2,03 | 0,002823 |
| <i>xylF</i> | xylose binding protein transport system | 2,03 | 0,0002206 |
| <i>maf // yceF</i> | orf, hypothetical protein | 2,03 | 5,44E-02 |
| <i>c3976</i> | Hypothetical protein yhcI | 2,03 | 0,002001 |
| <i>yffQ</i> | orf, hypothetical protein | 2,04 | 0,001853 |
| <i>nupG</i> | transport of nucleosides, permease protein | 2,04 | 0,007407 |
| <i>yqcA</i> | orf, hypothetical protein | 2,04 | 0,003763 |
| <i>c2806</i> | Hypothetical protein | 2,05 | 0,0008884 |
| <i>cysS</i> | Cysteinyl-tRNA synthetase | 2,05 | 0,002166 |
| <i>c0869</i> | Hypothetical protein | 2,06 | 0,006936 |
| <i>ytfE</i> | orf, hypothetical protein | 2,06 | 0,0002164 |
| <i>c2528</i> | Hypothetical protein | 2,06 | 0,0004973 |
| <i>menB</i> | dihydroxynaphtoic acid synthetase | 2,06 | 0,0009404 |
| <i>moeB</i> | molybdopterin biosynthesis | 2,07 | 0,0003658 |
| <i>pepN</i> | Aminopeptidase N | 2,08 | 0,0005865 |
| <i>sppA</i> | Protease IV | 2,09 | 5,13E-02 |
| <i>uspC // yecG</i> | putative regulator | 2,09 | 0,02797 |
| <i>mrr</i> | restriction of methylated adenine | 2,09 | 0,0001845 |
| <i>ppsA</i> | phosphoenolpyruvate synthase | 2,10 | 0,02574 |
| <i>puuD</i> | probable amidotransferase subunit | 2,10 | 0,002901 |
| <i>tdh</i> | threonine dehydrogenase | 2,11 | 8,22E-02 |
| <i>moeB</i> | molybdopterin biosynthesis | 2,12 | 0,01225 |
| --- | intergenic region | 2,12 | 0,0002135 |
| <i>flhA</i> | flagellar biosynthesis; possible export of flagellar proteins | 2,12 | 9,18E-03 |
| <i>dgoR</i> | putative FADA-type transcriptional regulator | 2,12 | 9,71E-02 |
| <i>ybiA</i> | orf, hypothetical protein | 2,13 | 0,02141 |
| <i>ymfl</i> | hypothetical protein | 2,13 | 5,66E-02 |
| <i>cheA</i> | sensory transducer kinase between chemo- signal receptors and CheB and CheY | 2,13 | 0,0001267 |
| <i>aceF</i> | pyruvate dehydrogenase (dihydrolipoyltransacetylase component) | 2,13 | 0,0007294 |
| <i>ycaD</i> | putative transport | 2,13 | 0,006696 |
| <i>c3305</i> | Hypothetical protein | 2,13 | 0,008633 |
| <i>yeaN</i> | putative amino acidamine transport protein | 2,13 | 2,33E-02 |
| <i>purB</i> | adenylosuccinate lyase | 2,14 | 0,000106 |
| <i>bglA</i> | 6-phospho-beta-glucosidase bglA | 2,16 | 6,56E-02 |

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|---------------------|--|------|-----------|
| <i>artI</i> | arginine 3rd transport system periplasmic binding protein | 2,16 | 0,00039 |
| <i>guaB</i> | IMP dehydrogenase | 2,16 | 0,0009367 |
| <i>ghrB // yiaE</i> | putative dehydrogenase | 2,16 | 4,50E-03 |
| <i>yiaK</i> | putative dehydrogenase | 2,17 | 0,00071 |
| <i>ybhL</i> | orf, hypothetical protein | 2,17 | 0,002979 |
| <i>yegQ</i> | orf, hypothetical protein | 2,17 | 0,007006 |
| <i>ycbC</i> | orf, hypothetical protein | 2,18 | 9,62e-05 |
| <i>yghU</i> | orf, hypothetical protein | 2,18 | 0,003469 |
| <i>erpA // yadR</i> | orf, hypothetical protein | 2,18 | 0,01368 |
| <i>kdgK</i> | ketodeoxygluconokinase | 2,20 | 2,02E-02 |
| <i>ynfF</i> | putative oxidoreductase major subunit | 2,21 | 0,04326 |
| <i>grxB</i> | glutaredoxin 2 | 2,21 | 0,0035 |
| <i>ycil</i> | orf, hypothetical protein | 2,21 | 0,0003544 |
| <i>ccmF</i> | cytochrome c-type biogenesis protein | 2,21 | 0,006081 |
| <i>ybdF</i> | orf, hypothetical protein | 2,21 | 0,002096 |
| <i>gltS</i> | glutamate transport | 2,22 | 1,41E-02 |
| <i>araA6</i> | L-arabinose isomerase | 2,22 | 0,001113 |
| <i>soxS</i> | regulation of superoxide response regulon | 2,22 | 0,008198 |
| <i>yddG</i> | orf, hypothetical protein | 2,22 | 1,63E-02 |
| <i>insH</i> | IS5 transposase | 2,23 | 0,0006358 |
| <i>hmpA</i> | dihydropteridine reductase, ferrisiderophore reductase activity | 2,24 | 1,73E-02 |
| <i>stpA</i> | DNA-binding protein; H-NS-like protein; chaperone activity; RNA splicing? | 2,24 | 0,0577 |
| <i>yegD</i> | putative heat shock protein | 2,24 | 9,13E-02 |
| <i>arsB</i> | arsenical pump membrane protein | 2,24 | 0,0008587 |
| <i>gcvP</i> | Glycine dehydrogenase (decarboxylating) | 2,25 | 0,001665 |
| <i>ychH</i> | orf, hypothetical protein | 2,25 | 0,01904 |
| <i>fimF</i> | fimbrial morphology | 2,26 | 0,0001318 |
| <i>yniA</i> | orf, hypothetical protein | 2,27 | 0,04309 |
| <i>yfeH</i> | putative cytochrome oxidase | 2,27 | 8,46E-02 |
| <i>iraP // yaiB</i> | orf, hypothetical protein | 2,27 | 0,02307 |
| <i>glyA</i> | serine hydroxymethyltransferase | 2,28 | 4,78E-02 |
| --- | intergenic region | 2,28 | 0,001877 |
| <i>glgS</i> | glycogen biosynthesis, rpoS dependent | 2,28 | 0,00842 |
| <i>fliS</i> | flagellar biosynthesis; repressor of class 3a and 3b operons (RfIA activity) | 2,30 | 1,44E-03 |
| <i>nrdA</i> | ribonucleoside diphosphate reductase 1, alpha subunit, B1 | 2,30 | 0,0005269 |
| <i>ybiB</i> | putative enzyme | 2,31 | 0,001446 |
| <i>arsR</i> | transcriptional repressor of chromosomal ars operon | 2,31 | 0,001109 |
| <i>fimC</i> | periplasmic chaperone, required for type 1 fimbriae | 2,34 | 0,002612 |
| <i>araB</i> | L-ribulokinase | 2,35 | 0,0001462 |
| <i>gst</i> | glutathionine S-transferase | 2,35 | 0,0005688 |
| <i>yahN</i> | putative cytochrome subunit of dehydrogenase | 2,36 | 0,03423 |
| <i>ydjX</i> | orf, hypothetical protein | 2,36 | 0,03882 |
| <i>c3354</i> | Hypothetical protein | 2,38 | 1,27E-02 |
| <i>argD</i> | acetylornithine delta-aminotransferase | 2,39 | 4,54E-03 |

| | | | |
|---------------------|--|------|-----------|
| <i>yfcB</i> | Hypothetical adenine-specific methylase yfcB | 2,39 | 6,95E-04 |
| <i>torR</i> | response transcriptional regulator for torA (sensor TorS) | 2,39 | 8,75E-03 |
| <i>degP //htrA</i> | periplasmic serine protease Do; heat shock protein HtrA | 2,39 | 0,00013 |
| <i>dgoR</i> | regulator protein for dgo operon | 2,41 | 9,56e-06 |
| <i>yifE</i> | orf, hypothetical protein | 2,41 | 1,21E-02 |
| <i>purF</i> | amidophosphoribosyltransferase = PRPP amidotransferase | 2,41 | 3,91E-02 |
| <i>caiF</i> | transcriptional regulator of cai operon | 2,41 | 0,03358 |
| <i>codA</i> | cytosine deaminase | 2,43 | 2,67E-02 |
| <i>fimG</i> | fimbrial morphology | 2,44 | 2,68E-02 |
| <i>flhB</i> | putative part of export apparatus for flagellar proteins | 2,45 | 2,51E-03 |
| --- | intergenic region | 2,47 | 0,00203 |
| <i>ccmA</i> | ATP binding protein of heme exporter A | 2,49 | 0,03596 |
| c2356 | Hypothetical protein | 2,52 | 2,11E-03 |
| <i>ptsA</i> | PEP-protein phosphotransferase system enzyme I | 2,54 | 0,0244 |
| <i>cheW</i> | positive regulator of CheA protein activity | 2,54 | 1,72e-05 |
| <i>artJ</i> | arginine 3rd transport system periplasmic binding protein | 2,55 | 2,82E-03 |
| <i>metE</i> | tetrahydropteroyltriglutamate methyltransferase | 2,56 | 3,35E-02 |
| <i>yfaE</i> | orf, hypothetical protein | 2,59 | 3,35E-02 |
| <i>fliP</i> | flagellar biosynthesis | 2,61 | 1,40E-02 |
| <i>sad // yneI</i> | putative aldehyde dehydrogenase | 2,63 | 5,57E-02 |
| <i>csiE</i> | stationary phase inducible protein | 2,64 | 9,39E-02 |
| <i>yliJ</i> | putative transferase | 2,64 | 4,86E-02 |
| <i>uspG // ybdQ</i> | orf, hypothetical protein | 2,66 | 0,007215 |
| <i>purM</i> | phosphoribosylaminoimidazole synthetase = AIR synthetase | 2,67 | 0,0002245 |
| <i>malF</i> | part of maltose permease, periplasmic | 2,68 | 0,0008101 |
| --- | intergenic region | 2,68 | 0,000171 |
| <i>pyrL</i> | pyrBI operon leader peptide | 2,70 | 8,09E-03 |
| <i>pyrD</i> | dihydro-orotate dehydrogenase | 2,77 | 0,0002135 |
| <i>nrdB</i> | Ribonucleoside-diphosphate reductase 1 beta chain | 2,78 | 2,15e-06 |
| <i>pyrC</i> | dihydro-orotase | 2,79 | 7,89E-02 |
| <i>xanP // yicE</i> | putative transport protein | 2,80 | 0,0004562 |
| <i>moeA</i> | molybdopterin biosynthesis | 2,80 | 0,005557 |
| <i>ydiA</i> | orf, hypothetical protein | 2,84 | 4,08e-05 |
| <i>purH</i> | phosphoribosylaminoimidazolecarboxamideformyltransferase | 2,85 | 8,05E-02 |
| <i>purL</i> | phosphoribosylformyl-glycineamide synthetase = FGAM synthetase | 2,87 | 1,10E-02 |
| <i>melA</i> | alpha-galactosidase | 2,91 | 0,007381 |
| <i>ccmC</i> | heme exporter protein C | 2,93 | 0,007618 |
| c2839 | Hypothetical protein | 2,94 | 5,96E-02 |
| <i>ycgK</i> | orf, hypothetical protein | 2,96 | 0,0003221 |
| <i>guaB</i> | IMP dehydrogenase | 2,97 | 0,0002253 |
| <i>guaC</i> | GMP reductase | 2,98 | 1,12E-03 |
| --- | intergenic region | 2,99 | 4,25E-02 |
| <i>malG /</i> | part of maltose permease, inner membrane | 3,00 | 4,85E-02 |
| <i>nupC</i> | Nucleoside permease nupC | 3,01 | 1,99E-03 |
| <i>purL</i> | phosphoribosylformyl-glycineamide synthetase = FGAM synthetase | 3,03 | 0,0001492 |

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|---------------------|--|------|-----------|
| <i>yeaU</i> | putative tartrate dehydrogenase | 3,03 | 1,41E-02 |
| <i>uhpT</i> | hexose phosphate transport protein | 3,04 | 0,01212 |
| <i>malk</i> | Maltosemaltodextrin transport ATP-binding protein malk | 3,04 | 0,0001639 |
| --- | intergenic region | 3,05 | 0,0001018 |
| <i>yjcD</i> | Hypothetical protein yjcD | 3,06 | 0,0002615 |
| <i>ycaK</i> | orf, hypothetical protein | 3,07 | 2,24E-04 |
| <i>malk</i> | ATP-binding component of transport system for maltose | 3,07 | 0,000393 |
| <i>fimI</i> | Fimbrin-like protein fimI precursor | 3,08 | 0,001905 |
| <i>ccmD</i> | heme exporter protein C | 3,11 | 0,002726 |
| <i>phoH</i> | PhoH protein | 3,20 | 0,001813 |
| <i>ftnB // yecl</i> | ferritin-like protein | 3,24 | 0,0005502 |
| <i>ptsA</i> | PEP-protein phosphotransferase system enzyme I | 3,26 | 0,001884 |
| <i>c2740</i> | Hypothetical protein | 3,27 | 0,03023 |
| <i>nrdB</i> | ribonucleoside-diphosphate reductase 1, beta subunit, B2 | 3,31 | 1,09E-03 |
| <i>flgL</i> | flagellar biosynthesis; hook-filament junction protein | 3,33 | 1,31E-04 |
| <i>upp</i> | uracil phosphoribosyltransferase | 3,34 | 6,54E-03 |
| --- | intergenic region | 3,40 | 0,0008587 |
| <i>c2742</i> | Hypothetical protein | 3,49 | 0,01741 |
| <i>ccmE</i> | cytochrome c biogenesis, possible subunit of a heme lyase | 3,55 | 0,003766 |
| <i>pta</i> | Phosphate acetyltransferase | 3,58 | 8,56E-03 |
| <i>flgK</i> | flagellar biosynthesis, hook-filament junction protein 1 | 3,69 | 5,22E-04 |
| <i>uraA</i> | uracil transport | 3,76 | 0,0001371 |
| <i>cdaR // yaeG</i> | hypothetical protein | 3,78 | 1,97E-03 |
| <i>c1905</i> | Hypothetical protein | 3,82 | 0,03406 |
| <i>yedE</i> | putative transport system permease protein | 3,87 | 0,0003007 |
| <i>cueO</i> | hypothetical protein | 3,87 | 0,0004033 |
| <i>flgJ</i> | flagellar biosynthesis | 3,97 | 1,87e-06 |
| <i>purD</i> | phosphoribosylglycinamide synthetase = GAR synthetase | 4,06 | 6,99E-02 |
| <i>flgI</i> | homolog of Salmonella P-ring of flagella basal body | 4,10 | 4,24E-04 |
| <i>ydjZ</i> | orf, hypothetical protein | 4,11 | 0,02101 |
| <i>yedF</i> | orf, hypothetical protein | 4,21 | 1,43E-02 |
| <i>fdnH</i> | formate dehydrogenase-N, nitrate-inducible, iron-sulfur beta subunit | 4,25 | 0,04814 |
| <i>codB /</i> | cytosine permeasetransport | 4,33 | 5,09E-04 |
| <i>copA</i> | putative ATPase | 4,33 | 0,001387 |
| <i>fliO</i> | flagellar biosynthesis | 4,37 | 7,39e-09 |
| <i>fliJ</i> | flagellar fliJ protein | 4,49 | 5,27E-05 |
| <i>napB</i> | cytochrome c-type protein | 4,52 | 0,026 |
| <i>malS</i> | alpha-amylase | 4,57 | 0,0008142 |
| <i>fliH</i> | Flagellar assembly protein fliH | 4,72 | 1,65E-04 |
| <i>fdnI</i> | formate dehydrogenase-N, nitrate-inducible, cytochrome B556(Fdn) gamma subunit | 4,78 | 0,01874 |
| <i>fliI</i> | flagellum-specific ATP synthase | 4,83 | 4,97E-05 |
| <i>ydjY</i> | orf, hypothetical protein | 4,83 | 0,02398 |
| <i>carB /</i> | carbamoyl-phosphate synthase large subunit | 4,84 | 5,05E-03 |
| <i>gudD // ygcX</i> | Glucarate dehydratase | 4,89 | 7,09E-04 |
| <i>c0039</i> | Hypothetical protein | 5,11 | 8,33E-04 |

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|---------------------|--|-------|----------|
| <i>purT</i> | phosphoribosylglycinamide formyltransferase 2 | 5,18 | 9,34E-03 |
| <i>fliK</i> | flagellar hook-length control protein | 5,23 | 1,86E-05 |
| <i>fimA</i> | major type 1 subunit fimbrin (pilin) | 5,39 | 5,02E-03 |
| <i>fliF</i> | flagellar biosynthesis; basal-body MS(membrane and supramembrane)-ring and collar protein | 5,70 | 9,20E-04 |
| <i>ynjE</i> | putative thiosulfate sulfur transferase | 6,02 | 0,002108 |
| <i>fliM</i> | flagellar biosynthesis, component of motor switch and energizing, enabling rotation and determining its direction | 6,11 | 2,09E-05 |
| <i>fliZ</i> | orf, hypothetical protein | 6,29 | 3,55E-04 |
| <i>flgH</i> | flagellar biosynthesis, basal-body outer-membrane L (lipopolysaccharide layer) ring protein | 6,31 | 3,90E-05 |
| <i>garD // yhaG</i> | (D)-galactarate dehydrogenase | 6,40 | 0,002281 |
| <i>carA</i> | carbamoyl-phosphate synthetase, glutamine (small) subunit | 6,80 | 6,52E-04 |
| <i>fliG</i> | flagellar biosynthesis, component of motor switching and energizing, enabling rotation and determining its direction | 1,00 | 5,37e-09 |
| <i>fliN</i> | flagellar biosynthesis, component of motor switch and energizing, enabling rotation and determining its direction | 7,21 | 6,97E-05 |
| <i>narJ</i> | nitrate reductase 1, delta subunit, assembly function | 7,84 | 0,04466 |
| <i>pyrI</i> | aspartate carbamoyltransferase, regulatory subunit | 8,90 | 1,54E-02 |
| <i>gudX // ygcY</i> | putative (D)-glucarate dehydratase 2 | 9,16 | 5,27E-05 |
| <i>fliL</i> | flagellar biosynthesis | 9,20 | 1,16e-08 |
| <i>flgF</i> | flagellar biosynthesis, cell-proximal portion of basal-body rod | 9,24 | 1,06E-04 |
| <i>narI</i> | nitrate reductase 1, cytochrome b(NR), gamma subunit | 9,42 | 0,02706 |
| <i>fliA</i> | flagellar biosynthesis; alternative sigma factor 28; regulation of flagellar operons | 9,99 | 1,23E-05 |
| <i>flgA</i> | flagellar biosynthesis; assembly of basal-body periplasmic P ring | 10,38 | 3,03E-05 |
| <i>flgG</i> | flagellar biosynthesis, cell-distal portion of basal-body rod | 10,38 | 1,49E-06 |
| <i>garK // yhaD</i> | glycerate kinase I | 12,48 | 2,44E-05 |
| <i>pyrB</i> | aspartate carbamoyltransferase, catalytic subunit | 12,64 | 1,89E-02 |
| <i>garR</i> | tartronate semialdehyde reductase (TSAR) | 13,12 | 7,24E-04 |
| <i>flgF</i> | Flagellar basal-body rod protein flgF | 14,12 | 6,51E-06 |
| <i>flgE</i> | flagellar biosynthesis, hook protein | 16,66 | 1,17E-06 |
| <i>flgD</i> | flagellar biosynthesis, initiation of hook assembly | 19,47 | 2,55E-06 |
| <i>flgC</i> | flagellar biosynthesis, cell-proximal portion of basal-body rod | 22,49 | 1,80E-06 |
| <i>flgB</i> | flagellar biosynthesis, cell-proximal portion of basal-body rod | 25,19 | 3,36E-06 |
| <i>garL // yhaF</i> | alpha-dehydro-beta-deoxy-D-glucarate aldolase | 27,30 | 1,97E-03 |
| <i>gudP</i> | putative D-glucarate permease (MFS family) | 27,49 | 1,11E-04 |
| --- | intergenic region | 41,41 | 2,19E-06 |
| <i>garP // yhaU</i> | putative transport protein | 43,50 | 1,90E-03 |

4. Anàlisi transcriptòmica mutant MG1655E_vs_wt

Taula 4. Gens expressats diferencialment en un mutant *holE* (MG1655E) respecte a la soca salvatge (MG1655) amb un FC>1,5. En diferents intensitats de vermell s'indiquen els gens que es troben induïts respecte a la soca salvatge i en verd els que es troben reprimits.

| Gene.Symbol | Target.Description | FC_E_vs_WT | adj.P.Val |
|---------------------|--|------------|-----------|
| <i>nanC // yjhA</i> | orf, hypothetical protein | 3,78 | 0,03261 |
| <i>yghJ</i> | putative endoglucanase | 3,29 | 0,01827 |
| <i>ycaC</i> | orf, hypothetical protein | 3,24 | 0,00034 |
| <i>hchA // yedU</i> | orf, hypothetical protein | 3,13 | 0,00034 |
| <i>yobA</i> | orf, hypothetical protein | 3,04 | 2,18E-04 |
| <i>otsB</i> | trehalose-6-phosphate phosphatase, biosynthetic | 3,02 | 0,000953 |
| <i>pyrB</i> | aspartate carbamoyltransferase, catalytic subunit | 2,94 | 0,03235 |
| <i>ybgA</i> | orf, hypothetical protein | 2,93 | 0,002044 |
| --- | intergenic region | 2,90 | 0,001446 |
| <i>yghJ</i> | orf, hypothetical protein | 2,89 | 0,01623 |
| <i>yebZ</i> | putative resistance protein | 2,89 | 2,18E-04 |
| <i>ygaM</i> | orf, hypothetical protein | 2,88 | 0,01451 |
| <i>yebY</i> | orf, hypothetical protein | 2,86 | 2,99E-04 |
| <i>yegS</i> | orf, hypothetical protein | 2,81 | 0,000553 |
| <i>yhcO</i> | orf, hypothetical protein | 2,77 | 0,004017 |
| <i>otsA</i> | trehalose-6-phosphate synthase | 2,73 | 0,00206 |
| <i>osmF</i> | putative transport system permease protein | 2,71 | 0,000553 |
| <i>pyrI</i> | aspartate carbamoyltransferase, regulatory subunit | 2,66 | 0,01621 |
| <i>ycgB</i> | putative sporulation protein | 2,64 | 0,007448 |
| <i>katE</i> | catalase; hydroperoxidase HP(III) | 2,62 | 0,000936 |
| <i>yodD</i> | orf, hypothetical protein | 2,59 | 0,002367 |
| <i>yahO</i> | Hypothetical protein yahO precursor | 2,58 | 0,002979 |
| <i>yfcG</i> | putative S-transferase | 2,58 | 0,002642 |
| --- | intergenic region | 2,57 | 0,002892 |
| <i>nanM // yjhT</i> | orf, hypothetical protein | 2,54 | 0,0118 |
| <i>ybdK</i> | orf, hypothetical protein | 2,53 | 0,000972 |
| <i>narU</i> | nitrite extrusion protein 2 | 2,49 | 0,01625 |
| c2623 | hypothetical protein | 2,49 | 0,000219 |
| <i>bhc</i> | outer membrane lipoprotein (lipocalin) | 2,47 | 0,01333 |
| <i>uhpT</i> | hexose phosphate transport protein | 2,47 | 0,01489 |
| <i>ybhP</i> | orf, hypothetical protein | 2,47 | 0,004509 |
| <i>ybgS</i> | putative homeobox protein | 2,47 | 0,002324 |
| <i>yeaG</i> | orf, hypothetical protein | 2,46 | 0,008017 |
| <i>yiaG</i> | orf, hypothetical protein | 2,45 | 0,01381 |
| <i>yehX</i> | putative ATP-binding component of a transport system | 2,44 | 0,000587 |
| <i>tnaB</i> | low affinity tryptophan permease | 2,43 | 0,000553 |
| <i>ydhS</i> | orf, hypothetical protein | 2,43 | 0,008745 |
| <i>osmE</i> | activator of ntrL gene | 2,42 | 0,00223 |
| <i>gadW // yhiW</i> | putative ARAC-type regulatory protein | 2,41 | 0,000587 |
| <i>psuG // yeiN</i> | orf, hypothetical protein | 2,39 | 0,003066 |
| <i>yohF</i> | Putative conserved protein | 2,39 | 0,0013 |
| <i>yeaH</i> | Hypothetical protein yeaH | 2,38 | 0,004098 |
| <i>ybjP</i> | putative lipoprotein | 2,38 | 0,00034 |

| | | | |
|---------------------|--|------|----------|
| <i>rbbA // yhiH</i> | ribosome-associated ATPase, ATP-binding domain (N-terminal) | 2,31 | 0,001592 |
| <i>ycaP</i> | orf, hypothetical protein | 2,30 | 0,000516 |
| <i>borD // borW</i> | putative Bor protein of prophage CP-933X | 2,30 | 0,02375 |
| <i>msyB</i> | acidic protein suppresses mutants lacking function of protein export | 2,25 | 0,00034 |
| <i>yehY</i> | putative transport system permease protein | 2,22 | 0,00034 |
| <i>yhjD</i> | orf, hypothetical protein | 2,22 | 0,007026 |
| <i>amyA</i> | cytoplasmic alpha-amylase | 2,21 | 0,003805 |
| <i>yhbO</i> | orf, hypothetical protein | 2,19 | 0,000846 |
| <i>ydeN</i> | putative sulfatase | 2,18 | 0,01893 |
| <i>yhhJ</i> | putative transporter | 2,17 | 0,002293 |
| --- | intergenic region | 2,16 | 0,002132 |
| <i>gadX // yhiX</i> | putative ARAC-type regulatory protein | 2,16 | 0,000637 |
| <i>yeaQ</i> | orf, hypothetical protein | 2,15 | 0,00421 |
| <i>elaB</i> | orf, hypothetical protein | 2,13 | 0,00121 |
| <i>hiuH</i> | orf, hypothetical protein | 2,12 | 0,004751 |
| <i>poxB</i> | pyruvate oxidase | 2,12 | 0,02265 |
| <i>ybiO</i> | putative transport protein | 2,11 | 0,004977 |
| <i>ryeB</i> | Hypothetical protein | 2,09 | 0,00034 |
| <i>yohK</i> | putative serotonin transporter | 2,09 | 0,02456 |
| <i>ycdS</i> | putative transport protein | 2,08 | 0,000472 |
| <i>dps</i> | global regulator, starvation conditions | 2,08 | 0,002066 |
| <i>ycdT</i> | putative ATP-binding component of a transport system | 2,07 | 0,000882 |
| <i>artI</i> | arginine 3rd transport system periplasmic binding protein | 2,07 | 6,42E-02 |
| <i>ygaU</i> | orf, hypothetical protein | 2,07 | 0,001732 |
| <i>tam</i> | hypothetical protein | 2,05 | 0,002245 |
| <i>yfdC</i> | putative transport protein | 2,02 | 0,002979 |
| <i>ydaM</i> | orf, hypothetical protein | 2,01 | 0,01388 |
| <i>yjdl</i> | orf, hypothetical protein | 2,01 | 0,02456 |
| <i>yjdl</i> | orf, hypothetical protein | 2,01 | 0,01008 |
| c2130 | Hypothetical protein | 2,01 | 0,000854 |
| <i>osmC</i> | osmotically inducible protein | 2,00 | 0,002428 |
| <i>ycgK</i> | orf, hypothetical protein | 1,99 | 0,004685 |
| <i>yghA</i> | putative oxidoreductase | 1,99 | 0,006907 |
| <i>malS</i> | alpha-amylase | 1,99 | 0,02165 |
| <i>talA</i> | transaldolase A | 1,98 | 0,004293 |
| <i>yegP</i> | orf, hypothetical protein | 1,98 | 0,001065 |
| <i>melA</i> | alpha-galactosidase | 1,96 | 0,01163 |
| <i>psiF</i> | induced by phosphate starvation | 1,95 | 0,002072 |
| --- | intergenic region | 1,95 | 0,003229 |
| <i>yahK</i> | putative oxidoreductase | 1,93 | 0,000936 |
| <i>hlyE</i> | hemolysin E | 1,93 | 0,001993 |
| <i>phnB // yjdN</i> | orf, hypothetical protein | 1,93 | 0,01014 |
| <i>xyIF</i> | xylose binding protein transport system | 1,93 | 0,02481 |
| <i>bfr</i> | bacterioferrin, an iron storage homoprotein | 1,91 | 0,000342 |
| <i>ycdJ</i> | orf; Unknown function | 1,90 | 0,004294 |

| | | | |
|---------------------|--|------|----------|
| <i>slp</i> | outer membrane protein induced after carbon starvation | 1,90 | 0,01833 |
| <i>araA</i> | L-arabinose isomerase | 1,90 | 0,000644 |
| <i>artQ</i> | arginine 3rd transport system permease protein | 1,88 | 0,003066 |
| <i>hokB</i> | small toxic membrane polypeptide | 1,88 | 0,04793 |
| <i>gadE // yhiE</i> | orf, hypothetical protein | 1,87 | 0,0133 |
| <i>yedP</i> | orf, hypothetical protein | 1,87 | 0,004077 |
| <i>osmB</i> | osmotically inducible lipoprotein | 1,84 | 0,000548 |
| <i>phr</i> | deoxyribodipyrimidine photolyase (photoreactivation) | 1,83 | 0,002351 |
| <i>fic</i> | induced in stationary phase, recognized by rpoS, affects cell division | 1,83 | 0,005181 |
| <i>ybhB</i> | orf, hypothetical protein | 1,82 | 0,000786 |
| --- | intergenic region | 1,82 | 0,001713 |
| <i>erfK</i> | orf, hypothetical protein | 1,82 | 0,001837 |
| <i>hdhA</i> | 7-alpha-hydroxysteroid dehydrogenase | 1,78 | 0,000731 |
| <i>yphA</i> | orf, hypothetical protein | 1,78 | 0,04781 |
| <i>aldB</i> | aldehyde dehydrogenase B (lactaldehyde dehydrogenase) | 1,78 | 0,01455 |
| <i>ykgC</i> | putative oxidoreductase | 1,77 | 0,002293 |
| <i>araF</i> | L-arabinose-binding periplasmic protein | 1,77 | 0,00206 |
| <i>appY</i> | regulatory protein affecting appA and other genes | 1,76 | 0,02018 |
| <i>IsrF // yneB</i> | putative aldolase | 1,76 | 0,000516 |
| <i>ynhG</i> | orf, hypothetical protein | 1,75 | 0,00173 |
| <i>spy</i> | periplasmic protein related to spheroblast formation | 1,75 | 0,00034 |
| <i>IsrG</i> | orf, hypothetical protein | 1,74 | 0,000936 |
| <i>ydhY</i> | putative oxidoreductase, Fe-S subunit | 1,74 | 0,03321 |
| <i>ycdU</i> | putative transport system permease protein | 1,74 | 0,03235 |
| <i>chaB</i> | cation transport regulator | 1,74 | 0,0082 |
| <i>ynfD</i> | orf, hypothetical protein | 1,73 | 0,000936 |
| <i>gadB</i> | glutamate decarboxylase isozyme | 1,73 | 0,04243 |
| <i>yehW</i> | putative transport system permease protein | 1,73 | 0,01683 |
| --- | intergenic region | 1,72 | 0,003 |
| <i>ybhO</i> | Hypothetical protein ybhO | 1,72 | 0,003941 |
| <i>tktB</i> | transketolase 2 isozyme | 1,71 | 0,02315 |
| <i>yggE</i> | putative actin | 1,71 | 0,003303 |
| <i>ycdK</i> | orf, hypothetical protein | 1,70 | 0,004977 |
| <i>hmpA</i> | dihydropteridine reductase, ferrisiderophore reductase activity | 1,70 | 0,007026 |
| <i>yqaE</i> | orf, hypothetical protein | 1,70 | 0,006886 |
| --- | intergenic region | 1,70 | 0,03778 |
| <i>erfK</i> | Protein erfKsrfK precursor | 1,70 | 0,001156 |
| <i>ygiW</i> | orf, hypothetical protein | 1,69 | 0,008235 |
| <i>ompT</i> | outer membrane protein 3b (a), protease VII | 1,69 | 0,003807 |
| <i>ivy // ykfE</i> | orf, hypothetical protein | 1,69 | 0,000936 |
| <i>araB</i> | L-ribulokinase | 1,69 | 0,007848 |
| <i>degP // htrA</i> | periplasmic serine protease Do; heat shock protein HtrA | 1,68 | 0,001495 |
| <i>dacC</i> | D-alanyl-D-alanine carboxypeptidase; penicillin-binding protein 6 | 1,68 | 0,000723 |
| <i>araG</i> | ATP-binding component of high-affinity L-arabinose transport system | 1,68 | 0,01146 |
| <i>dkgA</i> | hypothetical protein | 1,68 | 0,002462 |

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|---------------------|---|------|----------|
| <i>ydcJ</i> | orf; Unknown function | 1,68 | 0,008329 |
| --- | intergenic region | 1,67 | 0,02269 |
| <i>ybaS</i> | putative glutaminase | 1,66 | 0,007448 |
| <i>yeal</i> | orf, hypothetical protein | 1,66 | 0,003066 |
| <i>kbaY</i> | tagatose-bisphosphate aldolase 2 | 1,66 | 0,03303 |
| <i>yqjG</i> | putative transferase | 1,66 | 0,009277 |
| <i>ygdI</i> | orf, hypothetical protein | 1,66 | 0,02837 |
| <i>ybaY</i> | glycoproteinpolysaccharide metabolism | 1,65 | 0,03261 |
| <i>ygaC</i> | orf, hypothetical protein | 1,64 | 0,02108 |
| <i>hdeB</i> | orf, hypothetical protein | 1,63 | 0,006157 |
| <i>osmY</i> | hyperosmotically inducible periplasmic protein | 1,63 | 0,0118 |
| <i>cfa</i> | cyclopropane fatty acyl phospholipid synthase | 1,62 | 0,002158 |
| <i>uspD // yiiT</i> | putative regulator | 1,62 | 0,004977 |
| --- | intergenic region | 1,62 | 0,002925 |
| <i>cbpA</i> | curved DNA-binding protein; functions closely related to DnaJ | 1,62 | 0,002979 |
| <i>yiaO</i> | putative solute-binding transport protein | 1,62 | 0,007055 |
| <i>prf // ydcW</i> | putative aldehyde dehydrogenase | 1,62 | 0,02769 |
| <i>bolA</i> | possible regulator of murein genes | 1,61 | 0,01852 |
| --- | intergenic region | 1,61 | 0,01434 |
| --- | intergenic region | 1,61 | 0,009456 |
| c1618 | Hypothetical protein | 1,61 | 0,01718 |
| <i>hyaA</i> | hydrogenase-1 small subunit | 1,61 | 0,006466 |
| <i>hdeA</i> | orf, hypothetical protein | 1,61 | 0,005 |
| <i>yceK</i> | orf, hypothetical protein | 1,60 | 0,00495 |
| <i>yehE</i> | orf, hypothetical protein | 1,60 | 0,03334 |
| <i>ydcV</i> | Hypothetical ABC transporter permease protein ydcV | 1,59 | 0,03989 |
| <i>yeiA</i> | putative oxidoreductase | 1,59 | 0,01381 |
| <i>ytjA</i> | orf; Unknown function | 1,59 | 0,02048 |
| <i>artP</i> | ATP-binding component of 3rd arginine transport system | 1,58 | 0,0013 |
| <i>ymgG</i> | orf, hypothetical protein | 1,58 | 0,002933 |
| <i>aidB</i> | putative acyl coenzyme A dehydrogenase | 1,58 | 0,01428 |
| <i>yebF</i> | orf, hypothetical protein | 1,57 | 0,00351 |
| <i>yjbl</i> | orf, hypothetical protein | 1,57 | 0,01294 |
| <i>yhfG</i> | orf, hypothetical protein | 1,57 | 0,0141 |
| <i>yggB</i> | putative transport protein | 1,56 | 0,04535 |
| <i>yehV</i> | putative transcriptional regulator | 1,56 | 0,01004 |
| <i>ykgG</i> | putative transporter | 1,56 | 0,04866 |
| <i>ydiZ</i> | orf, hypothetical protein | 1,56 | 0,02934 |
| --- | intergenic region | 1,56 | 0,0118 |
| <i>tnaC // tnaL</i> | tryptophanase leader peptide | 1,55 | 0,01964 |
| c4571 | Hypothetical protein yfjX | 1,55 | 0,01718 |
| <i>ydiH</i> | orf, hypothetical protein | 1,55 | 0,0112 |
| --- | intergenic region | 1,55 | 0,004294 |
| <i>ecnB</i> | entericidin B | 1,55 | 0,006157 |
| <i>artM</i> | arginine 3rd transport system permease protein | 1,55 | 0,009819 |

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|---------------------|---|------|----------|
| <i>ycdJ</i> | orf; Unknown function | 1,55 | 0,01218 |
| <i>araD</i> | L-ribulose-5-phosphate 4-epimerase | 1,54 | 0,002439 |
| <i>yjhC</i> | putative dehydrogenase | 1,54 | 0,02711 |
| <i>emrR // mprA</i> | regulator of plasmid mcrB operon (microcin B17 synthesis) | 1,54 | 0,02265 |
| <i>yqjC</i> | orf, hypothetical protein | 1,54 | 0,01132 |
| <i>araH</i> | high-affinity L-arabinose transport system; membrane protein, fragment 2 | 1,54 | 0,005181 |
| <i>lhgO</i> | orf, hypothetical protein | 1,54 | 0,005323 |
| <i>nmpC</i> | outer membrane porin protein; locus of qsr prophage | 1,54 | 0,04243 |
| <i>fimI</i> | Fimbrin-like protein fimI precursor | 1,54 | 0,02314 |
| <i>ybaT</i> | putative amino acidamine transport protein | 1,54 | 0,03002 |
| <i>yqjK</i> | orf, hypothetical protein | 1,53 | 0,009723 |
| <i>ldcC</i> | lysine decarboxylase 2, constitutive | 1,53 | 0,02842 |
| <i>narL</i> | pleiotropic regulation of anaerobic respiration: response regulator for nar, frd, dms and tor genes | 1,52 | 0,004627 |
| <i>ggt</i> | gamma-glutamyltranspeptidase | 1,52 | 0,008883 |
| <i>gapC</i> | glyceraldehyde 3-phosphate dehydrogenase C, interrupted | 1,52 | 0,01474 |
| <i>ydgD</i> | hypothetical protein | 1,51 | 0,039 |
| --- | intergenic region | 1,51 | 0,04848 |
| <i>dkgB</i> | 2,5-diketo-D-gluconate reductase B | 1,50 | 0,0112 |
| c2371 | Hypothetical protein | 1,50 | 0,005578 |
| <i>yidX /</i> | putative replicase EC 2.7.- | 1,50 | 0,006711 |
| <i>flgA</i> | flagellar biosynthesis; assembly of basal-body periplasmic P ring | 1,50 | 0,009277 |
| --- | intergenic region | 1,50 | 0,02547 |
| <i>hisD</i> | L-histidinal:NAD+ oxidoreductase; L-histidinol:NAD+ oxidoreductase | 1,51 | 0,0141 |
| <i>rlmG // ygjO</i> | putative enzyme | 1,51 | 0,01882 |
| <i>thiM</i> | hydroxyethylthiazole kinase | 1,51 | 0,02626 |
| --- | intergenic region | 1,51 | 0,006886 |
| --- | intergenic region | 1,51 | 0,01867 |
| c0799 | Hypothetical protein | 1,51 | 0,03155 |
| <i>htrC // yjaZ</i> | heat shock protein C | 1,51 | 0,01649 |
| <i>ylaC</i> | orf, hypothetical protein | 1,52 | 0,000516 |
| <i>trpE</i> | anthranilate synthase component I | 1,52 | 0,02039 |
| <i>glpE</i> | rhodanese (thiosulfate:cyanide sulfurtransferase) | 1,52 | 0,0268 |
| --- | intergenic region | 1,52 | 0,012 |
| --- | intergenic region | 1,52 | 0,005 |
| <i>cycA</i> | transport of D-alanine, D-serine, and glycine | 1,52 | 0,04254 |
| ECs4710 | orf, hypothetical protein | 1,52 | 0,04612 |
| <i>deoB</i> | phosphopentomutase | 1,53 | 0,02681 |
| --- | intergenic region | 1,53 | 0,02756 |
| c0902 | Hypothetical protein | 1,53 | 0,009123 |
| c3917 | Hypothetical protein | 1,53 | 0,02027 |
| <i>yhbE</i> | orf, hypothetical protein | 1,53 | 0,0112 |
| --- | intergenic region | 1,53 | 0,01221 |
| --- | intergenic region | 1,54 | 0,005 |
| --- | intergenic region | 1,54 | 0,01154 |

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|---------------------|--|------|----------|
| <i>recF</i> | ssDNA and dsDNA binding, ATP binding | 1,54 | 0,01293 |
| --- | intergenic region | 1,54 | 0,0272 |
| --- | intergenic region | 1,54 | 0,01304 |
| <i>exuT</i> | transport of hexuronates | 1,55 | 0,007687 |
| --- | intergenic region | 1,55 | 0,01474 |
| c1089 | Hypothetical protein | 1,55 | 0,01163 |
| c0182 | Hypothetical protein | 1,55 | 0,0203 |
| --- | intergenic region | 1,56 | 0,03734 |
| ECs5383 | intergenic region | 1,56 | 0,02456 |
| c4882 | Hypothetical protein | 1,56 | 0,02027 |
| --- | intergenic region | 1,56 | 0,01911 |
| <i>thrL</i> | thr operon leader peptide | 1,56 | 0,03497 |
| <i>celB // chbC</i> | PTS system, cellobiose-specific IIC component | 1,56 | 0,006466 |
| <i>fepC</i> | ATP-binding component of ferric enterobactin transport | 1,56 | 0,003 |
| --- | intergenic region | 1,57 | 0,04986 |
| <i>ecnA</i> | entericidin A | 1,57 | 0,003647 |
| <i>fadI</i> | putative acyltransferase | 1,57 | 0,01623 |
| c3925 | Hypothetical protein | 1,57 | 0,005484 |
| <i>ycjM</i> | orf, hypothetical protein | 1,57 | 0,02481 |
| <i>murP</i> | putative PTS enzyme II | 1,58 | 0,01019 |
| --- | intergenic region | 1,58 | 0,01058 |
| <i>panF</i> | sodiumpantothenate symporter | 1,58 | 0,01723 |
| --- | intergenic region | 1,58 | 0,01557 |
| c3988 | Hypothetical protein | 1,58 | 0,04224 |
| <i>sdaC</i> | probable serine transporter | 1,59 | 0,004627 |
| <i>leuA</i> | 2-isopropylmalate synthase | 1,60 | 0,04288 |
| <i>yojI</i> | putative ATP-binding component of a transport system | 1,60 | 0,02265 |
| --- | Hypothetical protein | 1,60 | 0,0112 |
| --- | intergenic region | 1,60 | 0,01474 |
| <i>obgE</i> | putative GTP-binding factor | 1,60 | 0,000617 |
| <i>fliG</i> | flagellar biosynthesis, component of motor switching and energizing, enabling rotation and determining its direction | 1,60 | 0,02592 |
| --- | intergenic region | 1,60 | 0,02466 |
| <i>yjgX</i> | orf, hypothetical protein | 1,60 | 0,02265 |
| --- | intergenic region | 1,61 | 0,02269 |
| <i>rsd // yjaE</i> | putative transcriptional regulator | 1,61 | 0,000644 |
| <i>ebgC</i> | evolved beta-D-galactosidase, beta subunit; cryptic gene | 1,61 | 0,01294 |
| c4007 | Hypothetical protein | 1,61 | 0,005031 |
| <i>fadJ</i> | putative enzyme | 1,61 | 0,02152 |
| --- | intergenic region | 1,61 | 0,0118 |
| <i>kefG // yheR</i> | putative NAD(P)H oxidoreductase | 1,61 | 0,003573 |
| <i>mall</i> | maltose regulon regulatory protein | 1,61 | 0,006478 |
| <i>ygjI</i> | orf, hypothetical protein | 1,61 | 0,006466 |
| --- | intergenic region | 1,61 | 0,005315 |
| --- | intergenic region | 1,62 | 0,005741 |
| <i>ydaG</i> | orf, hypothetical protein | 1,62 | 0,02389 |

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|---------------------|---|------|----------|
| <i>psrN</i> | MG1655_sraF_b4448 /SEG=NC_000913:+3236015,3236203 /LEN=188 | 1,62 | 0,01833 |
| --- | intergenic region | 1,62 | 0,001049 |
| c2356 | Hypothetical protein | 1,63 | 0,006524 |
| <i>pheL</i> | leader peptide of chorismate mutase-P-prephenate dehydratase | 1,63 | 0,0426 |
| <i>sibA</i> | MG1655_ryeC_b4436 /SEG=NC_000913:+2151297,2151445 /LEN=148 | 1,63 | 0,03531 |
| <i>mgo // yojH</i> | hypothetical protein | 1,63 | 0,04629 |
| <i>fliA</i> | flagellar biosynthesis; alternative sigma factor 28; regulation of flagellar operons | 1,63 | 0,02148 |
| <i>fliZ</i> | orf, hypothetical protein | 1,63 | 0,0134 |
| --- | intergenic region | 1,64 | 0,006585 |
| --- | intergenic region | 1,64 | 0,01058 |
| <i>entF</i> | ATP-dependent serine activating enzyme (may be part of enterobactin synthase as component F) | 1,64 | 0,007848 |
| <i>fliF</i> | flagellar biosynthesis; basal-body MS(membrane and supramembrane)-ring and collar protein | 1,64 | 0,03963 |
| --- | intergenic region | 1,64 | 0,01625 |
| <i>ybaA</i> | orf, hypothetical protein | 1,64 | 0,01474 |
| --- | intergenic region | 1,65 | 0,00724 |
| <i>trpB</i> | tryptophan synthase, beta protein | 1,65 | 0,03783 |
| --- | intergenic region | 1,65 | 0,01019 |
| <i>fepG</i> | ferric enterobactin transport protein | 1,66 | 0,005199 |
| <i>proW</i> | high-affinity transport system for glycine betaine and proline | 1,66 | 0,01568 |
| --- | intergenic region | 1,66 | 0,04026 |
| <i>cstA</i> | carbon starvation protein | 1,66 | 0,002942 |
| <i>yhhQ</i> | orf, hypothetical protein | 1,66 | 0,0133 |
| <i>fliM</i> | flagellar biosynthesis, component of motor switch and energizing, enabling rotation and determining its direction | 1,66 | 0,00975 |
| <i>yhaO</i> | putative transport system permease protein | 1,66 | 0,004294 |
| <i>entA</i> | 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase, enterochelin biosynthesis | 1,67 | 0,01603 |
| <i>fliO</i> | flagellar biosynthesis | 1,67 | 0,00951 |
| <i>yhdL</i> | Putative regulator | 1,67 | 0,04243 |
| Z5814 | orf; Unknown function | 1,67 | 0,004294 |
| --- | intergenic region | 1,67 | 0,001288 |
| --- | intergenic region | 1,67 | 0,00726 |
| --- | intergenic region | 1,68 | 0,002933 |
| <i>sdaB</i> | L-serine dehydratase (deaminase), L-SD2 | 1,68 | 0,006107 |
| <i>rybA</i> | MG1655_rybA_b4416 /SEG=NC_000913:-852175,852263 /LEN=88 | 1,68 | 0,04535 |
| --- | intergenic region | 1,68 | 0,01425 |
| <i>ygeQ</i> | orf, hypothetical protein | 1,68 | 0,005181 |
| <i>sstT // ygjU</i> | putative transport protein | 1,68 | 0,006107 |
| <i>rpiB</i> | ribose 5-phosphate isomerase B | 1,68 | 0,01676 |
| <i>chbF</i> | phospho-beta-glucosidase; cryptic | 1,69 | 0,004294 |
| c3363 | Hypothetical protein | 1,69 | 0,002979 |
| <i>yjfl</i> | orf, hypothetical protein | 1,69 | 0,00351 |
| --- | intergenic region | 1,70 | 0,0118 |
| <i>deaD</i> | inducible ATP-independent RNA helicase | 1,70 | 0,006055 |
| ECs5584 | orf; Unknown function | 1,70 | 0,002572 |

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|---------------------|---|------|----------|
| <i>ycgF</i> | orf, hypothetical protein | 1,70 | 0,03055 |
| <i>ykgL</i> | orf, hypothetical protein | 1,70 | 0,02711 |
| --- | intergenic region | 1,70 | 0,004627 |
| --- | phenylalanyl-tRNA synthetase (pheST) operon leader peptide | 1,71 | 0,03175 |
| --- | intergenic region | 1,71 | 0,01608 |
| <i>ydiE</i> | orf, hypothetical protein | 1,71 | 0,04298 |
| <i>argD // astC</i> | acetylornithine delta-aminotransferase | 1,71 | 0,04751 |
| <i>yohG</i> | orf, hypothetical protein | 1,71 | 0,0149 |
| --- | intergenic region | 1,72 | 0,01127 |
| --- | intergenic region | 1,72 | 0,03453 |
| <i>argT</i> | lysine-, arginine-, ornithine-binding periplasmic protein | 1,72 | 0,03798 |
| <i>yjaZ</i> | heat shock protein htrC | 1,72 | 0,002925 |
| --- | intergenic region | 1,72 | 0,03342 |
| <i>entH // ybdb</i> | orf, hypothetical protein | 1,73 | 0,01685 |
| <i>entB</i> | 2,3-dihydro-2,3-dihydroxybenzoate synthetase, isochroismatase | 1,74 | 0,009999 |
| --- | intergenic region | 1,75 | 0,02251 |
| <i>ebgA</i> | evolved beta-D-galactosidase, alpha subunit; cryptic gene | 1,75 | 0,000972 |
| <i>fliP</i> | flagellar biosynthesis | 1,75 | 0,002072 |
| --- | intergenic region | 1,75 | 0,01882 |
| <i>dsrA</i> | anti-sense RNA, silencer of rcsA gene, interacts with rpoS translation | 1,75 | 0,0357 |
| c3554 | Hypothetical protein | 1,76 | 0,03783 |
| <i>yqiJ</i> | putative oxidoreductase | 1,76 | 0,03445 |
| <i>isrC</i> | MG1655_IS102_b4435 /SEG=NC_000913:+2069337,2069540 /LEN=203 | 1,76 | 0,003568 |
| c4243 | Hypothetical protein | 1,76 | 0,007944 |
| --- | intergenic region | 1,77 | 0,04243 |
| <i>ebgA</i> | evolved beta-D-galactosidase, alpha subunit; cryptic gene | 1,77 | 0,002973 |
| <i>fliN</i> | flagellar biosynthesis, component of motor switch and energizing, enabling rotation and determining its direction | 1,78 | 0,004727 |
| c1776 | Hypothetical protein | 1,78 | 0,005181 |
| <i>ybdZ</i> | orf; Unknown function | 1,79 | 0,003573 |
| <i>flgB</i> | flagellar biosynthesis, cell-proximal portion of basal-body rod | 1,80 | 0,0133 |
| --- | intergenic region | 1,80 | 0,0149 |
| <i>sibD</i> | MG1655_rygD_b4447 /SEG=NC_000913:-3192767,3192916 /LEN=149 | 1,81 | 0,04923 |
| --- | intergenic region | 1,81 | 0,006107 |
| --- | intergenic region | 1,82 | 0,03074 |
| <i>fliH</i> | Flagellar assembly protein fliH | 1,82 | 0,002663 |
| <i>flgJ</i> | flagellar biosynthesis | 1,84 | 0,00356 |
| <i>yhcG</i> | orf, hypothetical protein | 1,84 | 0,008684 |
| <i>glcC</i> | transcriptional activator for glc operon | 1,85 | 0,01957 |
| <i>ybfN</i> | orf, hypothetical protein | 1,85 | 0,004294 |
| --- | intergenic region | 1,85 | 0,000505 |
| <i>dctA</i> | uptake of C4-dicarboxylic acids | 1,86 | 0,01568 |
| <i>fliL</i> | flagellar biosynthesis | 1,86 | 0,01489 |
| <i>flgC</i> | flagellar biosynthesis, cell-proximal portion of basal-body rod | 1,87 | 0,006532 |
| --- | intergenic region | 1,87 | 0,000936 |
| <i>pheL</i> | Phe leader peptide | 1,88 | 0,02075 |

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|---------|---|------|----------|
| c1624 | Hypothetical protein | 1,89 | 0,005988 |
| fhuF | orf, hypothetical protein | 1,89 | 0,01319 |
| fepD | ferric enterobactin (enterochelin) transport | 1,89 | 0,002072 |
| --- | intergenic region | 1,91 | 0,01293 |
| flgD | flagellar biosynthesis, initiation of hook assembly | 1,92 | 0,005315 |
| ECs3543 | orf, hypothetical protein | 1,92 | 0,01012 |
| --- | intergenic region | 1,94 | 0,004977 |
| dsdA | D-serine dehydratase (deaminase) | 1,94 | 0,04243 |
| ybfM | orf, hypothetical protein | 1,94 | 0,004043 |
| flgE | flagellar biosynthesis, hook protein | 1,95 | 0,00394 |
| fliI | flagellum-specific ATP synthase | 1,96 | 0,000553 |
| fhuF | orf, hypothetical protein | 1,96 | 0,01074 |
| mgtA | Mg ²⁺ transport ATPase, P-type 1 | 1,97 | 0,007227 |
| flgH | flagellar biosynthesis, basal-body outer-membrane L (lipopolysaccharide layer) ring protein | 1,98 | 0,004751 |
| betI | probably transcriptional repressor of bet genes | 1,98 | 0,000644 |
| betA | choline dehydrogenase, a flavoprotein | 1,99 | 0,006863 |
| flgE | flagellar biosynthesis, hook protein | 1,99 | 0,002351 |
| --- | intergenic region | 2,00 | 0,006107 |
| ivbL | ilvB operon leader peptide | 2,01 | 0,003229 |
| fliQ | flagellar biosynthesis | 2,01 | 0,001178 |
| fliK | flagellar hook-length control protein | 2,02 | 0,003717 |
| --- | intergenic region | 2,03 | 0,000553 |
| --- | intergenic region | 2,03 | 0,000936 |
| fhuE | outer membrane receptor for ferric iron uptake | 2,04 | 0,0118 |
| --- | orf, hypothetical protein | 2,04 | 0,00495 |
| fliJ | flagellar fliJ protein | 2,05 | 0,002132 |
| entE | 2,3-dihydroxybenzoate-AMP ligase | 2,05 | 0,01455 |
| --- | intergenic region | 2,06 | 0,04388 |
| flgF | flagellar biosynthesis, cell-proximal portion of basal-body rod | 2,07 | 0,004294 |
| sokC | antisense RNA blocking mokC (orf69) and hokC (gef) translation | 2,07 | 0,03299 |
| --- | intergenic region | 2,09 | 0,007441 |
| yhdU | orf, hypothetical protein | 2,09 | 0,01665 |
| ybdA | putative transport | 2,10 | 0,005686 |
| flgG | flagellar biosynthesis, cell-distal portion of basal-body rod | 2,10 | 0,000472 |
| betT | high-affinity choline transport | 2,10 | 0,006052 |
| c4645 | Hypothetical protein | 2,11 | 0,002892 |
| --- | intergenic region | 2,12 | 0,001035 |
| --- | intergenic region | 2,12 | 0,000147 |
| yahM | orf; Unknown function | 2,14 | 0,02251 |
| betB | NAD ⁺ -dependent betaine aldehyde dehydrogenase | 2,14 | 0,001497 |
| fes | enterochelin esterase | 2,14 | 0,008029 |
| --- | intergenic region | 2,15 | 0,000553 |
| --- | intergenic region | 2,15 | 0,00034 |
| ryhA | MG1655_ryhA_b4450 /SEG=NC_000913:+3348218,3348325 /LEN=107 | 2,17 | 0,000637 |
| flgF | Flagellar basal-body rod protein flgF | 2,17 | 0,004943 |

| | | | |
|-------------|--|-------|----------|
| <i>sibC</i> | MG1655_rygC_b4446 /SEG=NC_000913:+3054835,3054985 /LEN=150 | 2,20 | 0,02249 |
| <i>efeU</i> | high-affinity iron permease | 2,21 | 0,02246 |
| <i>flgK</i> | flagellar biosynthesis, hook-filament junction protein 1 | 2,21 | 0,001156 |
| --- | intergenic region | 2,21 | 0,000593 |
| <i>fepA</i> | outer membrane receptor for ferric enterobactin (enterochelin) and colicins B and D | 2,22 | 0,002979 |
| <i>flgI</i> | homolog of Salmonella P-ring of flagella basal body | 2,24 | 0,001495 |
| c3379 | Hypothetical protein | 2,25 | 0,000766 |
| --- | intergenic region | 2,28 | 0,02393 |
| --- | intergenic region | 2,28 | 0,004077 |
| c3233 | Hypothetical protein | 2,29 | 0,004224 |
| <i>sibB</i> | MG1655_ryeD_b4437 /SEG=NC_000913:+2151632,2151774 /LEN=142 | 2,31 | 0,004614 |
| <i>rttR</i> | rtT RNA; may modulate the stringent response | 2,32 | 0,006466 |
| <i>yobB</i> | orf, hypothetical protein | 2,33 | 9,06E-02 |
| --- | intergenic region | 2,34 | 0,002106 |
| <i>ryeA</i> | MG1655_ryeA_b4432 /SEG=NC_000913:+1921090,1921338 /LEN=248 | 2,36 | 0,01401 |
| <i>entC</i> | isochorismate hydroxymutase 2, enterochelin biosynthesis | 2,36 | 0,005988 |
| <i>cirA</i> | outer membrane receptor for iron-regulated colicin I receptor; porin; requires tonB gene product | 2,40 | 0,0082 |
| <i>yjch</i> | orf, hypothetical protein | 2,41 | 0,03781 |
| <i>efeU</i> | orf, hypothetical protein | 2,42 | 0,003647 |
| --- | intergenic region | 2,43 | 0,007026 |
| --- | intergenic region | 2,56 | 0,004294 |
| <i>paaA</i> | hypothetical protein | 2,61 | 0,03155 |
| c3248 | Hypothetical protein | 2,64 | 0,001156 |
| <i>yjiX</i> | orf, hypothetical protein | 2,81 | 6,42E-02 |
| <i>oxyS</i> | global regulatory RNA OxyS | 2,82 | 0,002839 |
| <i>yjaA</i> | orf, hypothetical protein | 2,88 | 0,003647 |
| <i>yjiA</i> | orf, hypothetical protein | 2,91 | 4,50E-02 |
| --- | intergenic region | 2,94 | 0,002324 |
| <i>entD</i> | enterochelin synthetase, component D | 2,94 | 0,004648 |
| <i>lldR</i> | transcriptional regulator | 3,00 | 0,007687 |
| <i>fiu</i> | putative outer membrane receptor for iron transport | 3,05 | 0,005017 |
| <i>ybiX</i> | putative enzyme | 3,11 | 0,000731 |
| c0670 | Hypothetical protein | 3,47 | 0,000553 |
| --- | intergenic region | 3,51 | 0,00034 |
| --- | intergenic region | 3,68 | 0,000509 |
| <i>yjiY</i> | putative carbon starvation protein | 4,50 | 0,000553 |
| <i>lldP</i> | L-lactate permease | 4,51 | 0,001446 |
| <i>holE</i> | DNA polymerase III, theta subunit | 47,70 | 1,53E-07 |