

Upregulated genes of <i>E. coli</i> O157:H7 during adherence to CCD CoN 841 cells			
Symbol	FC on CCD CoN 841	FC on RAJ	Biological Function
<i>aidB</i>	2.97	-2.05	cellular response to DNA damage stimulus
<i>dctR</i>	6.11	-1.69	acidic PH
<i>gadA</i>	2.10	-1.37	carboxylic acid metabolic process
<i>hutW</i>	7.97	-7.80	Unknown
<i>hutX</i>	11.87	-19.59	Unknown
<i>iha_1</i>	1.97	-6.37	Unknown
<i>iha_2</i>	1.85	-7.69	Unknown
<i>mntH</i>	4.25	-2.74	cadmium ion transmembrane transport
<i>nrdE</i>	4.61	-4.96	deoxyribonucleotide biosynthetic process
<i>nrdF</i>	5.11	-10.06	deoxyribonucleotide biosynthetic process
<i>nrdI</i>	5.40	-5.80	protein modification process
<i>pqqL</i>	5.24	-2.54	Proteolysis
<i>shiA</i>	4.12	-1.85	shikimate transport
<i>sufB</i>	2.07	-2.03	iron-sulfur cluster assembly
<i>sufC</i>	2.40	-2.28	iron-sulfur cluster assembly
<i>tdcB</i>	7.26	-1.97	L-serine catabolic process
<i>wzz(fepE)</i>	3.41	-6.85	Unknown
<i>yddA</i>	5.13	-2.93	transmembrane transport
<i>yddB</i>	4.42	-2.46	iron coordination entity transport
<i>yegP</i>	4.50	-1.94	double-strand break repair
<i>yjjZ</i>	6.23	-4.09	Unknown
<i>yncE</i>	5.95	-5.49	DNA binding proten (outer membrane)
Uniquely expressed genes of <i>E. coli</i> O157:H7 during adherence to CCD CoN 841 cells			
<i>adhE</i>	9.10	0.00	Glycolysis
<i>cpdB</i>	2.03	0.00	cellular response to DNA damage stimulus
<i>fsa_1</i>	9.02	0.00	Unknown
<i>gcvT</i>	1.80	0.00	glycine catabolic process
<i>glgS</i>	3.10	0.00	negative regulation of bacterial-type flagellum-dependent cell motility/negative regulation of biofilm formation
<i>gpmA</i>	5.51	0.00	Glycolysis
<i>kch</i>	1.88	0.00	ion transport
<i>metE</i>	6.89	0.00	cellular amino acid biosynthetic process
<i>minD</i>	1.85	0.00	barrier septum assembly
<i>nrdH</i>	5.04	0.00	cell redox homeostasis
<i>raiA</i>	2.05	0.00	dormancy process
<i>rmf</i>	2.04	0.00	dormancy process
<i>tdcA</i>	6.84	0.00	L-threonine catabolic process to propionate
<i>uspF</i>	3.95	0.00	cell adhesion
<i>ybaT</i>	2.42	0.00	response to pH
<i>ybiI</i>	4.24	0.00	positive regulation of secondary metabolite biosynthetic process
<i>yciI</i>	3.26	0.00	Unknown
<i>yeaG</i>	2.47	0.00	cellular response to nitrogen starvation
<i>yeaH</i>	2.66	0.00	Unknown
<i>ygeV</i>	3.06	0.00	Unknown
<i>yobF</i>	1.82	0.00	cellular response to cell envelope stress
<i>ytfT</i>	3.94	0.00	carbohydrate transport
Upregulated genes of <i>E. coli</i> O157:H7 during adherence to RAJ cells			
<i>eutS</i>	-1.29	8.29	ethanolamine catabolic process
<i>sodB</i>	-1.09	6.66	cellular response to chemical stimulus
<i>pta_2</i>	-1.20	5.06	Unknown
<i>emrK</i>	-1.00	4.91	drug transmembrane export/ response to antibiotic

<i>eutE</i>	-1.99	4.04	Unknown
<i>eutQ</i>	-1.24	3.86	ethanolamine catabolic process
<i>narK</i>	-1.19	3.82	nitrate assimilation / transmembrane transport
<i>yfcC</i>	-1.08	3.78	transmembrane transport
<i>eutM</i>	-2.32	3.53	ethanolamine catabolic process
<i>ynfH</i>	-1.42	3.05	anaerobic electron transport chain
<i>napF</i>	-1.02	2.99	response to oxidative stress
<i>eutG</i>	-1.53	2.97	alcohol dehydrogenase (NAD) activity
<i>eutC</i>	-1.20	2.92	ethanolamine catabolic process
<i>cesD</i>	-1.22	2.74	Unknown
<i>ynjE</i>	-1.24	2.65	Unknown
<i>eutB</i>	-1.49	2.54	ethanolamine catabolic process
<i>eutK</i>	-1.34	2.40	ethanolamine catabolic process
<i>eutL</i>	-1.36	2.40	ethanolamine catabolic process
<i>fldA</i>	-1.02	2.34	electron transport chain
<i>eutT</i>	-2.31	2.33	ethanolamine catabolic process
<i>suhB</i>	-1.49	2.33	inositol metabolic process/ phosphatidylinositol phosphorylation
<i>cesD2</i>	-1.22	2.31	Unknown
<i>nrfE</i>	-1.01	2.31	cytochrome c-heme linkage via heme-L-cysteine
<i>eutH</i>	-1.13	2.27	ethanolamine catabolic process
<i>fumB_2</i>	-1.44	2.25	Unknown
<i>nrfG</i>	-1.21	2.14	cytochrome c-heme linkage via heme-L-cysteine

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**Uniquely expressed genes of *E. coli* O157:H7 during adherence to RAJ cells**

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<i>abrB</i>	0.00	2.18	regulation of gene expression
<i>accA</i>	0.00	1.46	fatty acid biosynthetic process
<i>accD</i>	0.00	1.99	fatty acid biosynthetic process
<i>acrA</i>	0.00	1.53	response to toxic substance
<i>adiA</i>	0.00	3.09	arginine catabolic process
<i>aegA</i>	0.00	2.67	urate catabolic process
<i>allR</i>	0.00	1.73	cellular response to DNA damage stimulus
<i>amiD</i>	0.00	1.61	cell wall organization/peptidoglycan catabolic process )
<i>apbE</i>	0.00	1.53	protein flavinylation
<i>cpoB</i>	0.00	1.62	FtsZ-dependent cytokinesis
<i>cueO</i>	0.00	1.57	detoxification of copper ion
<i>cvpA</i>	0.00	2.16	toxin biosynthetic process
<i>cyaY</i>	0.00	3.26	iron-sulfur cluster assembly
<i>cybB</i>	0.00	1.49	removal of superoxide radicals
<i>dinF</i>	0.00	1.45	transmembrane transport /xenobiotic transport
<i>dmsB_1</i>	0.00	6.25	Unknown
<i>dmsB_2</i>	0.00	9.29	Unknown
<i>dtpD</i>	0.00	1.80	dipeptide transmembrane transport
<i>ecpR</i>	0.00	2.37	regulation of bacterial-type flagellum-dependent cell motility
<i>elaA</i>	0.00	2.18	UDP-N-acetylglucosamine biosynthetic process
<i>emrA</i>	0.00	1.55	drug transmembrane export/response to toxic substance
<i>emrK</i>	0.00	4.91	drug transmembrane export/response to toxic substance
<i>emrR</i>	0.00	1.60	Unknown
<i>epmA</i>	0.00	2.97	cellular response to acidic pH
<i>eutA</i>	0.00	2.49	ethanolamine catabolic process
<i>eutE</i>	0.00	4.04	ethanolamine catabolic process
<i>eutJ</i>	0.00	10.93	ethanolamine catabolic process
<i>eutP</i>	0.00	9.11	ethanolamine catabolic process
<i>fetA</i>	0.00	2.40	cellular iron ion homeostasis
<i>fetB</i>	0.00	2.71	cellular iron ion homeostasis

<i>ftnA</i>	0.00	8.45	cellular iron ion homeostasis
<i>fur</i>	0.00	1.53	negative regulation of siderophore biosynthetic process
<i>glxR</i>	0.00	3.81	allantoin assimilation pathway
<i>grlA</i>	0.00	2.30	Unknown
<i>grlR</i>	0.00	3.07	Unknown
<i>grxA</i>	0.00	8.87	cellular response to oxidative stress
<i>grxD</i>	0.00	2.56	cellular response to oxidative stress
<i>gsiD</i>	0.00	1.51	dipeptide transmembrane transport
<i>gspL</i>	0.00	1.46	protein secretion by the type II secretion system
<i>gstA</i>	0.00	1.61	response to hydrogen peroxide
<i>hslJ</i>	0.00	2.33	response to heat
<i>iraD</i>	0.00	13.90	cellular response to oxidative stress
<i>kdpC</i>	0.00	3.25	potassium ion transport
<i>lacY</i>	0.00	2.17	carbohydrate transmembrane transport
<i>lolB</i>	0.00	1.75	lipoprotein localization to outer membrane
<i>lpxA</i>	0.00	1.87	lipid A biosynthetic process
<i>lpxC</i>	0.00	1.57	lipid A biosynthetic process
<i>lpxD</i>	0.00	1.47	lipid A biosynthetic process
<i>marB</i>	0.00	3.34	OMP/cellular response to antibiotics
<i>marR</i>	0.00	1.83	OMP/cellular response to antibiotics
<i>menB</i>	0.00	2.65	menaquinone biosynthetic process
<i>menC</i>	0.00	2.38	menaquinone biosynthetic process
<i>menD</i>	0.00	1.53	menaquinone biosynthetic process
<i>menE</i>	0.00	1.64	menaquinone biosynthetic process
<i>menI</i>	0.00	1.78	menaquinone biosynthetic process
<i>mipA</i>	0.00	2.18	peptidoglycan biosynthetic process
<i>mlaA</i>	0.00	1.55	phospholipid transport
<i>mlaB</i>	0.00	1.55	phospholipid transport
<i>mlaC</i>	0.00	1.53	phospholipid transport
<i>modE</i>	0.00	1.76	molybdate ion transport
<i>mrcB</i>	0.00	1.54	cell wall organization /cell wall repair
<i>murA</i>	0.00	1.47	UDP-N-acetylgalactosamine biosynthetic process
<i>murI</i>	0.00	1.90	cell wall organization
<i>narH_1</i>	0.00	3.04	unknown
<i>narI_1</i>	0.00	4.17	unknown
<i>narJ</i>	0.00	3.17	chaperone-mediated protein complex assembly / nitrate assimilation
<i>narK</i>	0.00	3.82	nitrate assimilation
<i>nikB</i>	0.00	2.40	dipeptide transmembrane transport
<i>nikC</i>	0.00	2.08	dipeptide transmembrane transport
<i>nikD</i>	0.00	4.06	dipeptide transmembrane transport
<i>nikE</i>	0.00	2.00	nickel cation transport
<i>ompA</i>	0.00	1.87	ion transmembrane transport
<i>ompR</i>	0.00	1.73	phosphorelay signal transduction system
<i>oppA</i>	0.00	1.54	oligopeptide transport
<i>oppC</i>	0.00	1.49	oligopeptide transport
<i>oppD</i>	0.00	1.71	oligopeptide transport
<i>oppF</i>	0.00	1.81	oligopeptide transport
<i>pgaD</i>	0.00	2.08	cell adhesion involved in biofilm formation
<i>pgsA</i>	0.00	1.60	glycerophospholipid biosynthetic process
<i>potD</i>	0.00	1.59	polyamine transport
<i>potE</i>	0.00	8.92	L-ornithine transmembrane transport
<i>preA</i>	0.00	2.00	bacterial-type flagellum-dependent swarming motility
<i>pta_2</i>	0.00	5.06	unknown

<i>rclA</i>	0.00	3.35	response to hypochlorite
<i>rcnB</i>	0.00	1.66	cellular response to DNA damage stimulus
<i>rcsB</i>	0.00	1.49	cellular stress response to acidic pH
<i>rfaC</i>	0.00	1.63	lipopolysaccharide biosynthetic process
<i>rfaD</i>	0.00	2.14	lipopolysaccharide biosynthetic process
<i>rfaF</i>	0.00	1.78	lipopolysaccharide biosynthetic process
<i>rfaL</i>	0.00	1.78	lipopolysaccharide biosynthetic process
<i>rfaY</i>	0.00	1.50	lipopolysaccharide biosynthetic process
<i>skp</i>	0.00	2.10	Gram-negative-bacterium-type cell outer membrane assembly
<i>slmA</i>	0.00	1.46	barrier septum site selection
<i>slyB</i>	0.00	1.48	Outer membrane lipoprotein
<i>sodB</i>	0.00	6.66	removal of superoxide radicals
<i>sodC_3</i>	0.00	2.05	unknown
<i>sorE</i>	0.00	2.32	unknown
<i>stpA</i>	0.00	10.12	negative regulation of transcription
<i>tatA</i>	0.00	1.54	protein transport by the Tat complex
<i>tatE</i>	0.00	2.26	protein transport by the Tat complex
<i>tolB</i>	0.00	1.61	bacteriocin transport
<i>trkA</i>	0.00	1.46	ion transport
<i>trxA</i>	0.00	2.65	cell redox homeostasis
<i>trxB</i>	0.00	2.38	cell redox homeostasis
<i>tyrP</i>	0.00	3.14	amino acid transmembrane transport
<i>ubiG</i>	0.00	1.69	hyperosmotic salinity response
<i>ureC_1</i>	0.00	1.57	unknown
<i>ureC_2</i>	0.00	1.53	unknown
<i>ureE_2</i>	0.00	1.60	unknown
<i>ureG_1</i>	0.00	2.39	unknown
<i>uvrD</i>	0.00	2.67	unknown
<i>wecG</i>	0.00	1.51	enterobacterial common antigen biosynthetic process
<i>wzy</i>	0.00	1.54	unknown
<i>wzzB</i>	0.00	1.72	lipopolysaccharide biosynthetic process
<i>xanP</i>	0.00	3.45	transmembrane transport
<i>yaaA</i>	0.00	1.70	response to hydroperoxide
<i>yajC</i>	0.00	1.53	protein insertion into membrane from inner side
<i>ybdG</i>	0.00	1.71	cellular response to osmotic stress
<i>ybhS</i>	0.00	1.78	drug transmembrane export
<i>ycdX</i>	0.00	1.86	bacterial-type flagellum-dependent swarming motility
<i>ychF</i>	0.00	2.36	response to oxidative stress
<i>yddG</i>	0.00	3.12	amino acid export
<i>ydgA</i>	0.00	1.45	bacterial-type flagellum-dependent swarming motility
<i>ydhL</i>	0.00	2.40	response to hydrogen peroxide
<i>ydiV</i>	0.00	1.53	negative regulation of bacterial-type flagellum-dependent cell motility
<i>ydiY</i>	0.00	4.61	unknown
<i>yeaR</i>	0.00	4.18	unknown
<i>yebB</i>	0.00	3.25	unknown
<i>yecC</i>	0.00	2.09	unknown
<i>yecD</i>	0.00	2.09	unknown
<i>yedD</i>	0.00	2.48	unknown
<i>yfcC</i>	0.00	3.78	transmembrane transport
<i>yfeH</i>	0.00	1.79	transmembrane transport
<i>yfeX</i>	0.00	2.74	cellular oxidant detoxification
<i>yhcC</i>	0.00	3.69	4 iron, 4 sulfur cluster binding
<i>yhcN</i>	0.00	2.71	cellular response to acidic pH

<i>yiaF</i>	0.00	1.55	symbiosis, encompassing mutualism through parasitism
<i>yijE</i>	0.00	2.20	amino acid transmembrane transport
<i>yjbH</i>	0.00	3.13	extracellular polysaccharide biosynthetic process
<i>yjdP</i>	0.00	3.52	unknown
<i>yjiX</i>	0.00	3.60	cellular response to DNA damage stimulus
<i>ynjD</i>	0.00	1.94	transmembrane transport
<i>yoaB</i>	0.00	1.92	single-species biofilm formation
<i>ypdA</i>	0.00	1.83	cell wall organization
<i>ytfB</i>	0.00	1.66	FtsZ-dependent cytokinesis
<i>ytfE</i>	0.00	1.71	iron incorporation into metallo-sulfur cluster

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