Table 3. Predicted coding sequences within *Eca* SCRI1043 that have a putative role in pathogenicity

Systematic gene name	Gene name	Functional category	Putative function	Similarities shown with FASTA comparison score are the best database matches (not shown for genes previously sequenced in *E. carotovora*) and selected other database matches of note (where appropriate). Also listed are significant matches within the Eca1043 genome where applicable and PFAM scores where relevant.
ECA0800		1.I	Type I Secretion System protein	No significant database matches. *Shewanella oneidensis* outer membrane efflux family protein E(): 0.00079, 22.79% ID in 487 aa. *Escherichia coli* hypothetical outer-membrane lipoprotein YohG precursor E(): 0.0067, 22.56% ID in 483 aa.
ECA0801		1.I	Type I Secretion System protein	*Vibrio cholerae* hypothetical protein vc0913 E(): 2.3e-10, 26.29% ID in 232 aa, and to *Shewanella oneidensis* HlyD family secretion protein so3483 E(): 2.4e-09, 25.49% ID in 251 aa.
ECA0802		1.I	Type I Secretion System protein	*Vibrio cholerae* periplasmic linker protein, putative vc1756 E(): 4e-05, 27.53% ID in 247 aa.
ECA0803		1.I	Type I Secretion System protein	No significant database matches. Putative membrane protein.
ECA1096*		1.I	Type I Secretion System protein	*Pseudomonas putida* protein secretion ABC efflux system, E(): 9.1e-67, 54.23% ID in 378 aa; *Escherichia coli* O157:H7 putative membrane spanning export protein E(): 2.9e-66, 54.3% ID in 372 aa.
ECA1097*		1.I	Type I Secretion System protein	*Pseudomonas putida* protein secretion ABC efflux system, permease and ATP-binding protein E(): 5.9e-111, 46.31% ID in 691 aa; *Salmonella typhi* putative type I secretion protein, ATP-binding protein: E(): 1.4e-103, 42.34% ID in 692 aa.
ECA1098*		1.I	Type I Secretion System protein	*Escherichia coli* O157:H7 putative outer membrane export protein E(): 2.7e-75, 50.56% ID in 439 aa; *Ralstonia solanacearum* putative outer membrane efflux transmembrane protein rsp1181 E(): 1.9e-23, 29.39% ID in 398 aa.
ECA2781*	*prtF*	1.I	Type I Secretion System protein	*Erwinia chrysanthemi* proteases secretion protein PrtF precursor E(): 3.6e-123, 73.25% ID in 445 aa.
ECA2782*	*prtE*	1.I	Type I Secretion System protein	*Erwinia chrysanthemi* proteases secretion protein PrtE E(): 9.7e-110, 72.33% ID in 441 aa. ECA1535 (47.529% ID in 425 aa overlap).
ECA2783*	*prtD*	1.I	Type I Secretion System protein	*Erwinia chrysanthemi* proteases secretion ATP-binding protein PrtD E(): 1.2e-155, 74.6% ID in 575 aa.
ECA3268*		1.I	Type I Secretion System protein	*Actinobacillus pleuropneumoniae* RTX-I toxin determinant

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				B Apxib E(): 1.1e-55, 28.05% ID in 695 aa; *Pseudomonas putida* toxin secretion ATP-binding protein pp0167 E(): 1.1e-188, 69.83% ID in 706 aa.
ECA3269*		1.I	Type I Secretion System protein	*Rhizobium leguminosarum* PrsE protein E(): 4.6e-27, 29.72% ID in 434 aa; *Pseudomonas putida* HlyD family secretion protein pp0166 E(): 1.9e-103, 65.19% ID in 454 aa.
ECA3098*	*outO*	1.II	Type II Secretion System protein	
ECA3099*	*outN*	1.II	Type II Secretion System protein	
ECA3100*	*outM*	1.II	Type II Secretion System protein	
ECA3101*	*outL*	1.II	Type II Secretion System protein	
ECA3102*	*outK*	1.II	Type II Secretion System protein	
ECA3103*	*outJ*	1.II	Type II Secretion System protein	
ECA3104*	*outI*	1.II	Type II Secretion System protein	
ECA3105*	*outH*	1.II	Type II Secretion System protein	
ECA3106*	*outG*	1.II	Type II Secretion System protein	
ECA3107*	*outF*	1.II	Type II Secretion System protein	
ECA3108*	*outE*	1.II	Type II Secretion System protein	
ECA3109*	*outD*	1.II	Type II Secretion System protein	
ECA3110*	*outC*	1.II	Type II Secretion System protein	
ECA3113*	*outB*	1.II	Type II Secretion System protein	
ECA3114*	*outS*	1.II	Type II Secretion System protein	
ECA0199	*tatA*	1.II	sec-independent translocase	*Escherichia coli,* sec-independent protein translocase protein TatA E(): 2.5e-17, 64.83% ID in 91 aa.
ECA0200	*tatB*	1.II	sec-independent translocase	*Escherichia coli,* sec-independent protein translocase protein TatB E(): 4.4e-22, 52.82% ID in 195 aa.
ECA0201	*tatC*	1.II	sec-independent translocase	*Escherichia coli* sec-independent protein translocase protein TatC E(): 1.5e-78, 79.83% ID in 248 aa.
ECA2076*	*hrcU*	1.III	Type III Secretion System protein	
ECA2077*	*hrcT*	1.III	Type III Secretion System protein	
ECA2078*	*hrcS*	1.III	Type III Secretion System protein	
ECA2079*	*hrcR*	1.III	Type III Secretion System protein	
ECA2080*	*hrcQ*	1.III	Type III Secretion System protein	
ECA2081*	*hrpP*	1.III	Type III Secretion System protein	
ECA2082*	*hrpO*	1.III	Type III Secretion System protein	
ECA2083*	*hrcN*	1.III	Type III Secretion System protein	
ECA2084*	*hrpQ*	1.III	Type III Secretion System protein	
ECA2085*	*hrcV*	1.III	Type III Secretion System protein	
ECA2086*	*hrpJ*	1.III	Type III Secretion System protein	

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ECA2087*	*hrpL*	1.III	Type III Secretion System protein	
ECA2088*	*hrpX*	1.III	Type III Secretion System protein	
ECA2089*	*hrpY*	1.III	Type III Secretion System protein	
ECA2090*	*hrpS*	1.III	Type III Secretion System protein	
ECA2093*	*hrpA*	1.III	Type III Secretion System protein	
ECA2094*	*hrpB*	1.III	Type III Secretion System protein	
ECA2095*	*hrcJ*	1.III	Type III Secretion System protein	
ECA2096*	*hrpD*	1.III	Type III Secretion System protein	
ECA2097*	*hrpE*	1.III	Type III Secretion System protein	
ECA2098*	*hrpF*	1.III	Type III Secretion System protein	
ECA2099*	*hrpG*	1.III	Type III Secretion System protein	
ECA2100*	*hrcC*	1.III	Type III Secretion System protein	
ECA2101*	*hrpT*	1.III	Type III Secretion System protein	
ECA2102*	*hrpV*	1.III	Type III Secretion System protein	
ECA1613*	*virB11*	1.IV	Type IV Secretion System / conjugal transfer protein	*Escherichia coli* VirB11 protein: E(): 1e-37, 38.06% ID in 331 aa; *Actinobacillus actinomycetemcomitans* transport associated protein 9 E(): 7.1e-48, 46.01% ID in 326 aa.
ECA1614*	*virB10*	1.IV	Type IV Secretion System / conjugal transfer protein	*Escherichia coli* VirB10 protein E(): 1.2e-23, 32.41% ID in 401 aa.
ECA1615*	*virB9*	1.IV	Type IV Secretion System / conjugal transfer protein	*Escherichia coli* VirB9 protein VirB9 E(): 2.5e-15, 32.52% ID in 289 aa.
ECA1616*	*virB8*	1.IV	Type IV Secretion System / conjugal transfer protein	*Escherichia coli* VirB8 protein VirB8 E(): 2.8e-14, 29.46% ID in 224 aa.
ECA1616A*	*virB7*	1.IV	Type IV Secretion System / conjugal transfer protein	*Escherichia coli* VirB7 protein E(): 0.7, 40% ID in 40 aa.
ECA1617*	*virB6*	1.IV	Type IV Secretion System / conjugal transfer protein	*Escherichia coli* VirB6 protein E(): 9e-06, 21.12% ID in 355 aa.
ECA1619*	*virB5*	1.IV	Type IV Secretion System / conjugal transfer protein	*Escherichia coli* VirB5 protein E(): 0.00064, 22.88% ID in 236 aa.
ECA1620*	*virB4* and *virB3*	1.IV	Type IV Secretion System / conjugal transfer protein	*Escherichia coli* VirB4 protein E(): 2.4e-90, 34.71% ID in 818 aa; N-terminal portion has 30% ID in 85 aa to *Escherichia coli* Pilx3 protein.
ECA1621*	*virB2*	1.IV	Type IV Secretion System / conjugal transfer protein	*Escherichia coli* VirB2 protein E(): 0.0022, 30.66% ID in 75 aa.
ECA1622*	*virB1*	1.IV	Type IV Secretion System / conjugal transfer protein	*Escherichia coli* VirB1 protein E(): 1.1e-12, 32.27% ID in 220 aa.
ECA1099		2.I	Type I Secretion System protein; large (3615 AA) repetitive secreted protein.	*Salmonella typhi* protein sty2875 E(): 1.9e-41, 26.46% ID in 3438 aa; *Yersinia pestis* putative autotransporter protein YapH E(): 8e-31, 23.21% ID in 3584 aa.

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ECA2784*	*inh*	2.I	Type I Secretion System protein; protease inhibitor	
ECA2785*	*prtW*	2.I	Type I Secretion System protein; protease	
ECA3266 *		2.I	Type I Secretion System protein; large (4588AA) secreted RTX-toxin family protein.	*Ralstonia solanacearum* putative hemagglutinin/hemolysin-related protein rsp1180 E(): 3.1e-134, 29.53% ID in 4320 aa.
ECA3267*		2.I	Type I Secretion System protein; secreted protein	*Pseudomonas putida* agglutination protein precursor AggA E(): 4e-73, 47.27% ID in 440 aa.
ECA0107*	*pmeB*	2.II	plant cell wall degrading enzyme; pectin methylesterase	
ECA0804*	*rhiE*	2.II	plant cell wall degrading enzyme; rhamnogalacturonate lyase	*Erwinia chrysanthemi* rhamnogalacturonase precursor RhiE: E(): 1.3e-133, 60.1% ID in 554 aa. The only other significant database matches are eukaryotic.
ECA0852*		2.II	plant cell wall degrading enzyme; arabinogalactan endo-1,4-betagalactosidase or proteoglycan hydrolyase	Similar to *Pseudomonas fluorescens* arabinogalactan endo-1,4-beta-galactosidase precursor gGalaA or GanA E(): 1.2e-16 33.53% ID in 325 aa.
ECA0931*		2.II	secreted virulence / avirulence associated protein.	*Xanthomonas campestris* avirulence protein E(): 3.9e-141, 57.42% ID in 613aa. Previously partially sequenced in EcaSCRI1039.
ECA1094*	*pelB (pel3)*	2.II	plant cell wall degrading enzyme; pectate lyase	
ECA1095*	*pehA*	2.II	plant cell wall degrading enzyme; endopolygalacturonase	
ECA1190*	*pehN*	2.II	plant cell wall degrading enzyme; endopolygalacturonase	*Erwinia chrysanthemi* putative polygalacturonase precursor PehN 9.4e-151, 80.13% ID in 458 aa.
ECA1499*	*pnl*	2.II	plant cell wall degrading enzyme; pectin lyase	
ECA1981*	*celV*	2.II	plant cell wall degrading enzyme; cellulase	
ECA2220*		2.II	plant cell wall degrading enzyme; cellulase	*Bacillus subtilis* YoaJ E(): 4.2e-47, 53.61% ID in 235 aa; also similar to the C-terminal region of *Clavibacter michiganensis* subsp. *sepedonicus* cellulase CelA E(): 2.6e-09, 30.52% ID in 190 aa.
ECA2331*	*expL (rssA)*	2.II	secreted phospholipase	Previously sequenced in *E. carotovora.* Has patatin-like phospholipase PFAM domain (score 2.4e-56).
ECA2408*	*paeX*	2.II	plant cell wall degrading enzyme; pectin acetylesterase	*Erwinia chrysanthemi* pectin acetylesterase 78% ID in 310 aa, *Xanthomonas campestris* xylanase XynB E(): 3.3e-61, 56.08% ID in 296 aa.

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ECA2553*		2.II	plant cell wall degrading enzyme; pectate lyase	*Erwinia chrysanthemi* pectate lyase L precursor PelL E(): 9.3e-21, 39.57% ID in 422 aa.
ECA2827*	*celB (celS)*	2.II	plant cell wall degrading enzyme; cellulase.	
ECA3111*	*pehX*	2.II	plant cell wall degrading enzyme; polygalacturonase	*Erwinia chrysanthemi* exo-poly-alpha-D-galacturonosase precursor PehX E(): 1e-59, 48.5% ID in 635 aa.
ECA3112*		2.II	plant cell wall degrading enzyme; pectate lyase	*Bacillus* sp. pectate lyase PelK E(): 2.7e-35, 35.16% ID in 472 aa; *Erwinia chrysanthemi* pectate lyase a precursor PelA E(): 1.1e-27, 31.9% ID in 442 aa.
ECA3252*	*paeY*	2.II	plant cell wall degrading enzyme; pectin acetylesterase	*Erwinia chrysanthemi* pectin acetylesterase PaeY E(): 8.8e-135, 61.07% ID in 542 aa.
ECA3253*	*pemA*	2.II	plant cell wall degrading enzyme; pectin methylesterase	*Erwinia chrysanthemi* pectinesterase a precursor PemA E(): 3.5e-98, 70.47% ID in 359 aa.
ECA3552*		2.II	plant cell wall degrading enzyme; possible endopolygalacturonase	*Prevotella ruminicola* polygalacturonase E(): 3.9e-17, 23.87% ID in 423 aa; *Agrobacterium tumefaciens* polygalacturonase atu4560 E(): 2.8e-56, 36.03% ID in 444 aa.
ECA4067*	*pelA/pel1*	2.II	plant cell wall degrading enzyme; pectate lyase	Similar to ECA4068 (88.503% ID in 374 aa overlap), and to ECA4069 (83.110% ID in 373 aa overlap).
ECA4068*	*pelB/pel2*	2.II	plant cell wall degrading enzyme; pectate lyase	Similar to ECA4067 (88.503% ID in 374 aa overlap), and to ECA4069 (82% ID in 373 aa overlap).
ECA4069*	*pelC/pel3*	2.II	plant cell wall degrading enzyme; pectate lyase	Similar to ECA4067 (83.110% ID in 374 aa overlap), and to ECA4068 (82.038% ID in 373 aa overlap).
ECA4070*	*pelZ*	2.II	plant cell wall degrading enzyme; pectate lyase	*Erwinia chrysanthemi* pectate lyase precursor PelZ E(): 5.1e-120, 72.53% ID in 426 aa.
ECA4510*	*pelX (Ech)*	2.II	plant cell wall degrading enzyme; exopolygalacturonate lyase	*Erwinia chrysanthemi* exopolygalacturonate lyase PelX E(): 1.9e-206, 73.8% ID in 733 aa.
ECA0257	*cah*	2.II	carbonic anhydrase.	Previously sequenced only in *E. carotovora*. Has eukaryotic-type carbonic anhydrase PFAM domain (score 1.5e-22) and Prosite signature.
ECA0421		2.II	secreted lipase.	*Zymomonas mobilis* hypothetical protein E(): 2.9e-49, 41.3% ID in 368aa. Has secretory lipase PFAM domain (4.7e-07).
ECA0925		2.II	secreted phospholipase.	*Mus musculus* schwannoma-associated protein pld3 E(): 6e-08, 29.31% ID in 382aa. Has two PFAM phospholipase D active site motifs (scores 0.23 and 0.00084).
ECA1873		2.II	plant cell wall degrading enzyme; possible xylanase	*Escherichia coli* O6 hypothetical protein YieL E(): 4.7e-106, 70.57% ID in 401 aa; *Shigella flexneri* putative xylanase YieL E(): 5.9e-105, 70.07% ID in 401 aa.
ECA3087		2.II	necrosis inducing protein	*Vibrio* sp. CH-291 hypothetical protein E(): 9.1e-59,

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				55.98% ID in 259aa; *Phytophthora parasitica* necrosis-inducing protein Npp1 E(): 1.9e-07, 31.1% ID in 209aa.
ECA4373	*BscZ (cel8Y)*	2.II	plant cell wall degrading enzyme; endoglucanase	*Escherichia coli* endoglucanase precursor BcsZ E(): 1.1e-87, 60.49% ID in 367 aa, *Erwinia chrysanthemi* endo-1,4-beta-D-glucanase precursor Cel8Y E(): 7e-18, 29.11% ID in 340 aa.
ECA2103*	*hrpN*	2.III	Type III Secretion System secreted harpin	
ECA2112*	*hrpW*	2.III	Type III Secretion System secreted harpin	*Erwinia amylovora* HrpW protein E(): 2.7e-36, 50.67% ID in 448 aa.
ECA2113*	*dspE*	2.III	Type III Secretion System effector protein	*Erwinia amylovora* DspE or DspA E(): 1.7e-101, 39.38% ID in 1658 aa.
ECA2114*	*dspF*	2.III	Type III Secretion System chaperone	*Erwinia amylovora* DspF or DspB E(): 1.8e-19, 42.85% ID in 133 aa.
ECA2217*		2.III	Type III Secretion System associated protein	*Salmonella typhimurium* SrfC E(): 4.2e-23, 30.06% ID in 795 aa; *Yersinia pestis* putative virulence factor y2123 FASTA scores: E(): 2.9e-65, 55.12% ID in 849 aa; *Pseudomonas syringae* pv. *tomato* str.DC3000 HopPtoL 37% ID.
ECA2218*		2.III	Type III Secretion System associated protein	*Salmonella typhimurium* SrfB E(): 0, 57.47% ID in 997 aa; *Yersinia pestis* putative virulence factor ypo2290 E(): 2.1e-214, 73.8% ID in 1027 aa.
ECA2219*		2.III	Type III Secretion System associated protein	*Salmonella typhimurium* and *Salmonella typhi* SrfA E(): 2.4e-16, 41.06% ID in 431 aa; *Yersinia pestis* putative virulence factor y2121 E(): 4.2e-29, 51.02% ID in 488 aa.
ECA2111	*hrpW chaperone*	2.III	Type III Secretion System chaperone	*Erwinia amylovora* potential HrpW-specific chaperone E(): 2e-10, 38.46% ID in 104 aa.
ECA0980*		2.V	secreted serine protease	*Pseudomonas fluorescens* serine protease homologue PspB E(): 1.6e-25, 28.66% ID in 1106 aa; *Serratia marcescens* extracellular serine protease precursor E(): 1.1e-16, 25.6% ID in 1082 aa.
ECA2163*		2.V	Type V secretion system protein autotransporter	*Pseudomonas aeruginosa* PapB protein E(): 9.1e-146, 57.05% ID in 652 aa; *Escherichia coli* alkaline phosphatase isozyme conversion protein precursor Iap E(): 4e-24, 35.67% ID in 342 aa. Has a PFAM autotransporter beta-domain, score 2.1e-25.
ECA0799		2.V	large (3288AA) secreted protein.	*Bradyrhizobium japonicum* Bll3563 protein E(): 8.9e-20, 22.46% ID in 3387 aa; *Brucella suis* outer membrane autotransporter bra1148 E(): 6.1e-08, 22.91% ID in 3217 aa.

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ECA0391*	*hecB*	2.VI	Two Partner Secretion System activator / transporter protein for possible adhesin.	*Erwinia chrysanthemi* HecB precursor E(): 9.6e-40, 29.33% ID in 559 aa; *Yersinia pestis* putative hemolysin activator protein ypo2491 E(): 8.5e-141, 63.86% ID in 559 aa.
ECA0392*	*hecA*	2.VI	Two Partner Secretion System secreted adhesin; possible pseudogene.	*Yersinia pestis* putative hemolysin E(): 7.4e-93, 41.25% ID in 2390 aa, *Ralstonia solanacearum* probable hemagglutinin-related protein E(): 1.5e-92, 30.39% ID in 3145 aa; *Erwinia chrysanthemi* hemolysin/hemagglutinin-like protein HecA E(): 2.6e-91, 31.08% ID in 2474 aa.
ECA2116*	*hecB*	2.VI	Two Partner Secretion System activator / transporter protein for possible adhesin.	*Erwinia chrysanthemi* HecB E(): 9.6e-40, 29.33% ID in 559 aa; *Yersinia pestis* putative hemolysin activator protein E(): 8.5e-141, 63.86% ID in 559 aa.
ECA2117*	*hecA*	2.VI	Two Partner Secretion System secreted adhesin; possible pseudogene.	*Erwinia chrysanthemi* hemolysin/hemagglutinin-like protein HecA precursor E(): 3.6e-110, 43.11% ID in 1148 aa.
ECA2118*	*hecA*	2.VI	Two Partner Secretion System extracellular adhesin; possible pseudogene.	*Erwinia chrysanthemi* hemolysin/hemagglutinin-like protein HecA p E(): 7.2e-116, 36.39% ID in 4407 aa.
ECA2135*	*pelB*	2.VII	plant cell wall degrading enzyme; periplasmic pectate lyase	
ECA2402*	*pelW/kdgC*	2.VII	plant cell wall degrading enzyme; pectate disaccharide lyase	*Erwinia chrysanthemi* pectate disaccharide-lyase PelW E(): 1.8e-175, 73.97% ID in 538 aa.
ECA2426*	*ogl*	2.VII	plant cell wall degrading enzyme; oligogalacturonate lyase	
ECA0722		2.VII	protease	*Proteus mirabilis* STM-protease A E(): 3.6e-114, 82.03% ID in 334 aa.
ECA3211	*prt1*	2.VII	secreted protease	
ECA2399	*kdgF*	2.VII	pectin degradation and transport	*Erwinia chrysanthemi* pectin degradation KdgF E(): 3.3e-38, 89.09% ID in 110 aa.
ECA2407	*kdgM*	2.VII	pectin degradation and transport	*Erwinia chrysanthemi* oligogalacturonate-specific porin KdgM E(): 7.1e-64, 67.22% ID in 238 aa.
ECA4124	*kgdT*	2.VII	pectin degradation and transport	*Erwinia carotovora* 2-keto-3-deoxygluconate permease KdgT E(): 1.4e-108, 95.91% ID in 318 aa.
ECA4360	*kdgK*	2.VII	pectin degradation and transport	*Erwinia chrysanthemi* 2-dehydro-3-deoxygluconokinase KdgK E(): 1.4e-100, 82.25% ID in 310 aa.
ECA2400	*kduI1*	2.VII	pectin degradation and transport	*Erwinia chrysanthemi* 4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase KduI E(): 8e-99, 85.61% ID in 278 aa.
ECA2401	*kduD*	2.VII	pectin degradation and transport	*Erwinia carotovora* subsp. *atroseptica* 2-keto-3-

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				deoxygluconate oxidoreductase KduD E(): 6.3e-94, 98.41% ID in 253 aa.
ECA2125	*kduI2*	2.VII	pectin degradation and transport	*Erwinia carotovora* KduI E(): 2e-112, 96.4% ID in 278 aa, and *Erwinia chrysanthemi* 4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase KduI E(): 7.7e-77, 64.38% ID in 278 aa.
ECA0817	*togT*	2.VII	pectin degradation and transport	*Erwinia chrysanthemi* oligogalacturonide transporter TogT E(): 5.8e-176, 84.81% ID in 507 aa.
ECA2403	*togM*	2.VII	pectin degradation and transport	*Erwinia chrysanthemi* inner membrane protein TogM E(): 1.2e-115, 97.63% ID in 296 aa.
ECA2404	*togN*	2.VII	pectin degradation and transport	*Erwinia chrysanthemi* inner membrane protein TogN E(): 1.7e-108, 90.03% ID in 301 aa.
ECA2405	*togA*	2.VII	pectin degradation and transport	*Erwinia chrysanthemi* ABC ATPase TogA E(): 8e-119, 85.6% ID in 375 aa.
ECA2406	*togB*	2.VII	pectin degradation and transport	*Erwinia chrysanthemi* periplasmic binding protein precursor TogB E(): 3.3e-143, 84.84% ID in 429 aa.
ECA0644	*exuT*	2.VII	pectin degradation and transport	*Erwinia chrysanthemi* ExuT E(): 6.4e-122, 88.78% ID in 330 aa. *Ralstonia solanacearum* ExuT E():2.8e-99, 56.39% ID in 422 aa.
ECA0532	*pilL*	3	Type IV pilus (fimbrial) protein	*Salmonella dublin* and *Salmonella typhi* PilL E(): 8.9e-32, 44.98% ID in 449 aa.
ECA0533	*pilM*	3	Type IV pilus (fimbrial) protein	*Escherichia coli* and *Salmonella typhimurium* PilM E(): 2.4e-05, 29.45% ID in 146 aa.
ECA0534	*pilN*	3	Type IV pilus (fimbrial) protein	*Escherichia coli* and *Salmonella typhimurium* lipoprotein PilN E(): 8.1e-61, 40.71% ID in 560 aa.
ECA0535	*pilO*	3	Type IV pilus (fimbrial) protein; probable pseudogene.	*Escherichia coli* PilO E(): 1.1e-13, 22.22% ID in 441 aa.
ECA0537	*pilP*	3	Type IV pilus (fimbrial) protein	*Escherichia coli* PilP E(): 0.12, 23.75% ID in 160 aa,
ECA0538	*pilQ*	3	Type IV pilus (fimbrial) protein	*Escherichia coli* and *Salmonella typhimurium* nucleotide-binding protein PilQ E(): 2.7e-42, 32.67% ID in 508 aa.
ECA0540	*pilR*	3	Type IV pilus (fimbrial) protein	*Escherichia coli* and *Salmonella typhimurium* integral membrane protein PilR E(): 7.1e-24, 29.68% ID in 347 aa.
ECA0541	*pilS*	3	Type IV pilus (fimbrial) protein	*Yersinia pseudotuberculosis* type IV prepilin PilS E(): 1.2e-05, 31.84% ID in 179 aa.
ECA0542	*pilT*	3	Type IV pilus (fimbrial) protein	*Salmonella typhi* and *Salmonella dublin* PilT E(): 2.3e-28, 55.07% ID in 138 aa.
ECA0543	*pilU*	3	Type IV pilus (fimbrial) protein	*Shigella sonnei* prepilin peptase PilU E(): 0.029, 26.33% ID in 224 aa.
ECA0544	*pilV*	3	Type IV pilus (fimbrial) protein	*Escherichia coli* PilV E(): 8.8e-12, 32.47% ID in 428 aa.
ECA0787		3	Type IV pilus (fimbrial) protein	*Rhizobium loti* type IV prepilin peptase, CpaA E(): 3.7e-05,

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				30.53% ID in 167 aa; *Rhizobium meliloti* probable CpaA2 pilus assembly protein E(): 6.4e-05, 28.48% ID in 172 aa.
ECA0788		3	Type IV pilus (fimbrial) protein	*Bradyrhizobium japonicum* CtpC protein E(): 2.7e-09, 30.96% ID in 281 aa; *Vibrio vulnificus* flp pilus assembly protein CpaB vv12330 E(): 8.4e-09, 28.94% ID in 304 aa.
ECA0789		3	Type IV pilus (fimbrial) protein	*Actinobacillus actinomycetemcomitans* rough colony protein A RcpA; *Escherichia coli* protein transport protein HofQ precursor E(): 2.9e-10, 24.71% ID in 433 aa; *Salmonella typhi* Type II Secretion System protein HofQ E(): 7e-10, 27.27% ID in 253 aa.
ECA0790		3	Type IV pilus (fimbrial) protein	*Agrobacterium tumefaciens* components of type IV pilus CtpE E(): 0.0024, 23.63% ID in 220 aa; *Rhizobium meliloti* hypothetical protein FASTA scores: E(): 0.81, 21.62% ID in 222 aa.
ECA0791		3	Type IV pilus (fimbrial) protein	*Bradyrhizobium japonicum* protein blr3493 E(): 1.7e-20, 26.68% ID in 371 aa; *Caulobacter crescentus* pilus assembly protein CpaE 7.2e-16, 27.76% ID in 371 aa; *Agrobacterium tumefaciens* components of type IV pilus CtpF E(): 5.2e-13, 29.79% ID in 292 aa.
ECA0792		3	Type IV pilus (fimbrial) protein	*Caulobacter crescentus* CpaF E(): 6.1e-65, 45.13% ID in 452 aa; *Bradyrhizobium japonicum* component of type IV pilus blr3494 E(): 1.7e-74, 55.01% ID in 429 aa; *Vibrio vulnificus* flp pilus assembly protein E(): 6.7e-66, 44.73% ID in 465 aa.
ECA0793		3	Type IV pilus (fimbrial) protein	*Vibrio vulnificus* flp pilus assembly protein TadB E(): 7.9e-20, 28.38% ID in 310 aa; *Actinobacillus actinomycetemcomitans* TadB E(): 7.7e-14, 27.57% ID in 243 aa.
ECA0794		3	Type IV pilus (fimbrial) protein	*Vibrio vulnificus* flp pilus assembly protein TadC 2.7e-25, 31.34% ID in 319 aa; *Agrobacterium tumefaciens* components of type IV pilus CtpI E(): 2.7e-24, 34.12% ID in 296 aa.
ECA0939		3	fimbrial protein	*Xenorhabdus nematophilus* fimbrial major subunit MrxA 9.2e-13, 35% ID in 180 aa; *Salmonella typhimurium* fimbrial subunit BcfA E(): 7.3e-10, 30.68% ID in 176 aa; *Escherichia coli* adhesion protein PapA E(): 4.8e-07, 26.66% ID in 150 aa.
ECA0940		3	fimbrial protein	*Escherichia coli* O6 hypothetical protein c3794 E(): 8.4e-14, 27.55% ID in 352 aa.
ECA0941		3	fimbrial protein	*Proteus mirabilis* chaperone protein PmfD E(): 8.9e-43,

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				46.72% ID in 229 aa, *Escherichia coli* chaperone protein PapD E(): 2e-36, 42.98% ID in 228 aa; *Escherichia coli* PrfD E(): 2e-36, 42.98% ID in 228 aa.
ECA0942		3	fimbrial protein	*Photorhabdus luminescens* MrfC E(): 6.4e-137, 43.95% ID in 810 aa; *Proteus mirabilis* outer membrane usher protein PmfC E(): 3e-132, 42.75% ID in 807 aa; *Escherichia coli* outer membrane usher protein PapC E 1.6e-126, 43.34% ID in 849 aa.
ECA0943		3	fimbrial protein	*Escherichia coli* f15 P-fimbriae major subunit precursor FfiA E(): 2.8e-17, 38.5% ID in 174 aa; *Serratia marcescens* fimbria A protein precursor SmfA E(): 1.3e-16, 39.34% ID in 183 aa.
ECA3075		3	fimbrial protein	*Pseudomonas aeruginosa* probable pili assembly chaperone pa4651 E(): 1.3e-45, 49.78% ID in 237 aa; *Pseudomonas putida* type 1 pili usher pathway chaperone CsuC or pp2361 E(): 8.6e-40, 45.6% ID in 239 aa.
ECA3076		3	fimbrial protein	*Pseudomonas aeruginosa* hypothetical protein Pa4652 E(): 1.3e-148, 51.74% ID in 775 aa; *Pseudomonas putida* type 1 pili usher protein CsuD or pp2362 E(): 1.6e-125, 43.44% ID in 778 aa.
ECA3222		3	fimbrial protein	*Pseudomonas aeruginosa* PilF protein E(): 4.5e-07, 28.4% ID in 169 aa; *Yersinia pestis* putative fimbrial biogenesis protein ypo2881 or y1351 E(): 4.2e-62, 71.91% ID in 235 aa.
ECA1685	*flhD*	3	flagellar protein	*Escherichia coli* flagellar transcriptional activator FlhD E(): 6.7e-32, 76.47% ID in 119 aa.
ECA1686	*flhC*	3	flagellar protein	
ECA1696	*flhB*	3	flagellar protein	*Escherichia coli* flagellar biosynthetic protein FlhB E(): 6.9e-93, 61.15% ID in 381 aa.
ECA1697	*flhA*	3	flagellar protein	*Escherichia coli* flagellar biosynthesis protein FlhA E(): 2.2e-214, 83.35% ID in 691 aa.
ECA1698	*flhE*	3	flagellar protein	*Escherichia coli* flagellar protein FlhE E(): 1.2e-12, 38.68% ID in 137 aa.
ECA1699	*flgN*	3	flagellar protein	*Salmonella typhimurium* flagella synthesis protein FlgN E(): 2.4e-14, 38.88% ID in 144 aa.
ECA1700	*flgM*	3	flagellar protein	*Escherichia coli* negative regulator of flagellin synthesis FlgM E(): 4.5e-14, 59.18% ID in 98 aa.
ECA1701	*flgA*	3	flagellar protein	*Salmonella typhimurium* flagella basal body P-ring formation protein FlgA E(): 2.5e-36, 48.05% ID in 206 aa.
ECA1702	*flgB*	3	flagellar protein	*Salmonella typhimurium* flagellar basal-body rod protein

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				FlgB E(): 2.6e-37, 77.37% ID in 137 aa.
ECA1703	*flgC*	3	flagellar protein	*Salmonella typhimurium* and *Salmonella typhi* flagellar basal-body rod protein FlgC E(): 7.9e-37, 81.34% ID in 134 aa.
ECA1704	*flgD*	3	flagellar protein	*Salmonella typhimurium* and *Salmonella typhi* basal-body rod modification protein FlgD E(): 1.2e-43, 54.31% ID in 232 aa.
ECA1705	*flgE*	3	flagellar protein	*Salmonella typhimurium* and *Salmonella typhi* flagellar hook protein FlgE E(): 9.2e-78, 58.43% ID in 409 aa.
ECA1706	*flgF*	3	flagellar protein	*Salmonella typhimurium* flagellar basal-body rod protein FlgF E(): 3.9e-62, 70.4% ID in 250 aa.
ECA1707	*flgG*	3	flagellar protein	*Salmonella typhimurium* and *Salmonella typhi* flagellar basal-body rod protein FlgG E(): 1.3e-77, 82.3% ID in 260 aa.
ECA1708	*flgH*	3	flagellar protein	*Salmonella typhimurium* and *Salmonella typhi* flagellar L-ring protein precursor FlgH E(): 2.4e-60, 76.44% ID in 225 aa.
ECA1709	*flgI*	3	flagellar protein	*Salmonella typhimurium* flagellar P-ring protein precursor FlgI E(): 2.5e-98, 79.6% ID in 358 aa.
ECA1710	*flgJ*	3	flagellar protein	*Salmonella typhimurium* peptoglycan hydrolase FlgJ E(): 8.9e-65, 61.49% ID in 322 aa.
ECA1711	*flgK*	3	flagellar protein	*Salmonella typhimurium* and *Salmonella typhi* flagellar hook-associated protein 1 FlgK E(): 4.8e-81, 55.53% ID in 569 aa.
ECA1712	*flgL*	3	flagellar protein	*Salmonella typhimurium* flagellar hook-associated protein 3 FlgL E(): 3.7e-61, 55.34% ID in 318 aa.
ECA1714	*fliR*	3	flagellar protein	
ECA1715	*fliQ*	3	flagellar protein	
ECA1716	*fliP*	3	flagellar protein	
ECA1717	*fliO*	3	flagellar protein	
ECA1718	*fliN*	3	flagellar protein	
ECA1719	*fliM*	3	flagellar protein	*Salmonella typhimurium* flagellar motor switch protein FliM E(): 5e-113, 84.77% ID in 335 aa.
ECA1720	*fliL*	3	flagellar protein	*Escherichia coli* flagellar FliL protein E(): 5e-28, 57.23% ID in 159 aa.
ECA1721	*fliK*	3	flagellar protein	*Salmonella typhimurium* flagellar hook-length control protein FliK E(): 1.9e-22, 35.3% ID in 405 aa.
ECA1722	*fliJ*	3	flagellar protein	*Salmonella typhimurium* and *Salmonella typhi* flagellar FliJ protein E(): 8.3e-26, 55.78% ID in 147 aa.
ECA1723	*fliI*	3	flagellar protein	*Salmonella typhimurium* flagellum-specific ATP synthase

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				FliI E(): 1.5e-139, 85.24% ID in 454 aa.
ECA1724	*fliH*	3	flagellar protein	*Salmonella typhimurium* flagellar assembly protein FliH E(): 1.6e-43, 58.36% ID in 245 aa.
ECA1725	*fliG*	3	flagellar protein	*Escherichia coli* flagellar motor switch protein FliG E(): 1.1e-95, 85.71% ID in 329 aa.
ECA1726	*fliF*	3	flagellar protein	*Escherichia coli* flagellar M-ring protein FliF (): 9.2e-77, 62.63% ID in 570 aa.
ECA1727	*fliE*	3	flagellar protein	*Escherichia coli* flagellar hook-basal body complex protein FliE (): 1.8e-20, 63.46% ID in 104 aa.
ECA1728	*fliT*	3	flagellar protein	*Escherichia coli* flagellar protein FliT (): 9.7e-11, 44.14% ID in 111 aa; *Erwinia chrysanthemi* FliT protein E(): 3.1e-15, 49.16% ID in 120 aa.
ECA1729	*fliS*	3	flagellar protein	*Salmonella typhimurium* flagellar protein FliS E(): 1.4e-30, 69.85% ID in 136 aa; *Erwinia chrysanthemi* FliS protein FliS E(): 4.4e-33, 73.52% ID in 136 aa.
ECA1730	*fliD*	3	flagellar protein	*Salmonella typhimurium* flagellar hook-associated protein 2 FliD (): 3.9e-44, 43.82% ID in 486 aa; *Erwinia chrysanthemi* flagellar hook associated protein 2 FliD E(): 2.2e-48, 39.25% ID in 484 aa.
ECA1731	*fliC*	3	flagellar protein	*Erwinia chrysanthemi* flagellin FliC (): 3.2e-36, 65.29% ID in 291 aa.
ECA1739	*fliA*	3	flagellar protein; RNA polymerase sigma factor	*Escherichia coli* RNA polymerase sigma factor for flagellar operon FliA E(): 1.1e-68, 82.62% ID in 236 aa.
ECA1740	*fliZ*	3	flagellar protein; alternative sigma factor regulatory protein for flagellar genes.	*Escherichia coli* FliZ protein E(): 1.7e-24, 44.93% ID in 158 aa.
ECA1741	*fliC*	3	flagellar protein	*Salmonella rubislaw* flagellin FliC (): 6.3e-28, 34% ID in 497 aa; *Escherichia coli* flagellin E(): 1.9e-30, 34.86% ID in 499 aa.
ECA0149		4	lipopolysaccharide biosynthesis protein	*Yersinia pestis* putative sugar transferase RafQ E(): 8.7e-82, 60.06% ID in 323 aa; *Serratia marcescens* putative heptosyl transferase III WaaQ E(): 7.2e-12, 26.23% ID in 343 aa.
ECA0150		4	lipopolysaccharide biosynthesis protein	*Escherichia coli* CoaD (): 4.1e-45, 74.05% ID in 158 aa.
ECA0151		4	lipopolysaccharide biosynthesis protein	*Escherichia coli* 3-deoxy-D-manno-octulosonic-acid transferase KdtA or WaaA E(): 2.7e-134, 78.11% ID in 425 aa.
ECA0152		4	lipopolysaccharide biosynthesis protein	*Paracoccidioides brasiliensis* putative mannosyltransferase (): 0.00027, 26.86% ID in 201 aa; *Pasteurella piscicida*

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				capsular polysaccharide FASTA scores: E(): 1, 22.46% ID in 187 aa.
ECA0153		4	lipopolysaccharide biosynthesis protein	*Serratia marcescens* lipopolysaccharide core biosynthesis glycosyl transferase KdtX E(): 3.5e-66, 65.72% ID in 248 aa.
ECA0154		4	lipopolysaccharide biosynthesis protein	*Edwardsiella tarda* putative beta1,4-galactosyltransferase WaaX E(): 9.1e-32, 40.96% ID in 249 aa.
ECA0155		4	part of lipopolysaccharide biosynthesis cluster but role unknown; doubtful CDS.	No significant database matches
ECA0156		4	part of LPS biosynthesis cluster but role unknown.	No significant database matches
ECA0157		4	lipopolysaccharide biosynthesis protein	*Escherichia coli* lipopolysaccharide 1,2-glucosyltransferase RfaJ or WaaJ 4.4e-63, 49.69% ID in 330 aa.
ECA0158		4	lipopolysaccharide biosynthesis protein	*Escherichia coli* lipopolysaccharide 1,3-galactosyltransferase RfaI or WaaI E(): 7.7e-60, 44.21% ID in 337 aa
ECA0159		4	lipopolysaccharide biosynthesis protein	*Escherichia coli* lipopolysaccharide core biosynthesis protein Rfag or WaaG E(): 1.2e-87, 58.69% ID in 368 aa
ECA0160		4	lipopolysaccharide biosynthesis protein	*Escherichia coli* lipopolysaccharide core biosynthesis glycosyl transferase RfaQ or WaaQ E(): 1.3e-65, 52.69% ID in 334 aa.
ECA0161		4	lipopolysaccharide biosynthesis protein	*Escherichia coli* O-antigen ligase RfaL or WaaL E(): 2.7e-28, 30.54% ID in 406 aa.
ECA0162		4	lipopolysaccharide biosynthesis protein	*Escherichia coli* O-antigen ligase RfaL or WaaL E(): 1.2e-28, 29.22% ID in 414 aa.
ECA0163		4	lipopolysaccharide biosynthesis protein	*Escherichia coli* lipopolysaccharide heptosyltransferase 1 RfaC or WaaC E(): 6.6e-89, 71.47% ID in 319 aa.
ECA0164		4	lipopolysaccharide biosynthesis protein	*Escherichia coli* ADP-heptose--LPS heptosyltransferase II RfaF or WaaF E(): 6.2e-108, 74.41% ID in 344 aa.
ECA0165		4	lipopolysaccharide biosynthesis protein	*Escherichia coli* and *Escherichia coli* O157:H7 ADP-L-glycero-D-manno-heptose-6-epimerase RfaD or HtrM E(): 2.1e-106, 84.41% ID in 308 aa.
ECA0499	*wcaJ*	4	capsular polysaccharide biosynthesis protein	*Escherichia coli* putative colanic biosynthesis UDP-glucose lipid carrier transferase WcaJ E(): 6.8e-69, 43.62% ID in 463 aa; *Klebsiella pneumoniae* probable CPS biosynthesis glycosyltransferase E(): 1e-69, 43.95% ID in 455 aa.
ECA0500		4	capsular polysaccharide biosynthesis protein	*Methylobacillus* sp. 12S EpsL E(): 4, 20.86% ID in 393 aa; *Vibrio vulnificus* conserved hypothetical protein vv12303 E(): 4e-82, 46.98% ID in 415 aa.

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ECA0501		4	capsular polysaccharide biosynthesis protein	*Vibrio vulnificus* polysaccharide export-related protein vv12304 E(): 5.2e-31, 53.61% ID in 166 aa; *Brucella suis* capsule polysaccharide export protein E(): 5.5e-18, 37.91% ID in 182 aa.
ECA0502		4	capsular polysaccharide biosynthesis protein	*Rhizobium leguminosarum* exopolysaccharide polymerization protein PssP E(): 8.1e-10, 23.42% ID in 730 aa; *Vibrio cholerae* exopolysaccharide biosynthesis protein, putative vc0937 E(): 1.4e-44, 28.87% ID in 717 aa.
ECA0503		4	capsular polysaccharide biosynthesis protein	*Rhizobium meliloti* succinoglycan biosynthesis transport protein ExoT E(): 0.042, 19.1% ID in 335 aa; *Vibrio vulnificus* hypothetical protein vv12306 E(): 1e-94, 57.56% ID in 403 aa; *Staphylococcus aureus* Cap8K E(): 2.9e-09, 19.75% ID in 400 aa.
ECA0504		4	capsular polysaccharide biosynthesis protein	*Streptococcus agalactiae* CpsH E(): 0.76, 18.88% ID in 360 aa; *Vibrio vulnificus* hypothetical protein vv12307 E(): 7.4e-117, 61.31% ID in 455 aa.
ECA0505		4	capsular polysaccharide biosynthesis protein	*Vibrio vulnificus* putative glycosyltransferase protein vv12308 E(): 7.6e-86, 64.81% ID in 324 aa; *Rhizobium meliloti* putative glycosyltransferase protein rb1330 E(): 5.2e-37, 37.42% ID in 326 aa.
ECA0506		4	capsular polysaccharide biosynthesis protein	*Klebsiella pneumoniae* WbdC (): 8.9e-10, 28.04% ID in 246 aa; *Vibrio vulnificus* putative glycosyltransferase protein vv12309 E(): 5e-95, 60% ID in 400 aa.
ECA0507		4	capsular polysaccharide biosynthesis protein	*Shigella boydii* putative glycosyl transferase wbdS E(): 7.8e-11, 23.69% ID in 363 aa; *Vibrio vulnificus* putative glycosyltransferase protein vv12310 E(): 3.5e-94, 66.85% ID in 362 aa.
ECA0508		4	capsular polysaccharide biosynthesis protein	*Vibrio vulnificus* hypothetical protein vv12311 E(): 1e-16, 45.92% ID in 135 aa.
ECA0509		4	capsular polysaccharide biosynthesis protein	*Vibrio vulnificus* hypothetical protein E(): 5.5e-105, 53.91% ID in 447 aa.
ECA0510		4	capsular polysaccharide biosynthesis protein	*Escherichia coli* k30 capsule biosynthesis cluster, partial sequence E(): 2.1e-15, 36.74% ID in 166 aa; *Escherichia coli* putative colanic acid biosynthesis acetyltransferase WcaB E(): 1.8e-14, 40% ID in 150 aa.
ECA1416	*wecA*	4	exopolysaccharide / O antigen biosynthesis protein	*Escherichia coli* undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase WecA or Rfe E(): 3e-70, 52.18% ID in 343 aa.
ECA1417	*wza*	4	exopolysaccharide / O antigen biosynthesis protein	*Escherichia coli* putative polysaccharide export protein Wza precursor E(): 3.3e-105, 68.86% ID in 379 aa.

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ECA1418	*wzb*	4	exopolysaccharide / O antigen biosynthesis protein	*Salmonella typhimurium* low molecular weight protein-tyrosine-phosphatase Wzb E(): 1.5e-34, 65.73% ID in 143 aa; *Erwinia amylovora* probable low molecular weight protein-tyrosine-phosphatase AmsI E(): 5.8e-37, 69.44% ID in 144 aa.
ECA1419	*wzc*	4	exopolysaccharide / O antigen biosynthesis protein	*Escherichia coli* tyrosine-protein kinase Wzc E(): 7.9e-146, 57.67% ID in 723 aa; *Erwinia amylovora* putative tyrosine-protein kinase AmsA E(): 1e-145, 55.18% ID in 723 aa.
ECA1420	*rfbP*	4	exopolysaccharide / O antigen biosynthesis protein	*Salmonella typhimurium* undecaprenyl-phosphate galactosephosphotransferase RfbP E(): 3e-129, 64.65% ID in 464 aa; *Erwinia amylovora* UDP-galactose-lipid carrier transferase amsG E(): 2.8e-131, 66.3% ID in 466 aa.
ECA1421	*rfbI*	4	exopolysaccharide / O antigen biosynthesis protein	*Yersinia pestis*CDP-6-deoxy-L-threo-D-glycero-4-hexulose-3-dehydrase reductase AscD or RfbI E(): 2.8e-45, 45.7% ID in 326 aa.
ECA1422	*rfbF*	4	exopolysaccharide / O antigen biosynthesis protein	*Yersinia pestis* glucose-1-phosphate cytidylyltransferase DdhA E(): 1.9e-88, 80.54% ID in 257 aa.
ECA1423	*rfbG*	4	exopolysaccharide / O antigen biosynthesis protein	*Salmonella typhimurium* CDP-glucose 4,6-dehydratase RfbG E(): 5e-105, 68.92% ID in 354 aa.
ECA1424	*rfbH*	4	exopolysaccharide / O antigen biosynthesis protein	*Salmonella typhimurium* lipopolysaccharide biosynthesis protein RfbH E(): 3.5e-143, 78.94% ID in 437 aa.
ECA1425		4	exopolysaccharide / O antigen biosynthesis protein	*Escherichia coli* 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase HpcH or HpaI E(): 4.9e-22, 32.4% ID in 250 aa.
ECA1426		4	exopolysaccharide / O antigen biosynthesis protein	*Bacillus subtilis* acetolactate synthase large subunit IlvB E(): 5.9e-45, 32.32% ID in 563 aa.
ECA1427		4	exopolysaccharide / O antigen biosynthesis protein	*Leptospira interrogans* dTDP-glucose 4,6-dehydratase RfbB1 E(): 0.0023, 23.05% ID in 321 aa; *Pyrococcus horikoshii* 306aa long hypothetical UDP-glucose 4-epimerase E(): 0.011, 28.63% ID in 213 aa.
ECA1428		4	exopolysaccharide / O antigen biosynthesis protein	*Pseudomonas fluorescens* and *Pseudomonas putida* acetaldehyde dehydrogenase NahO E(): 5e-45, 44.17% ID in 292 aa.
ECA1429		4	exopolysaccharide / O antigen biosynthesis protein	*Pseudomonas putida* 4-hydroxy-2-oxovalerate aldolase NahM E(): 8.3e-48, 43.86% ID in 342 aa.
ECA1430		4	exopolysaccharide / O antigen biosynthesis protein	*Cicer arietinum* dTDP-glucose 4-6-dehydratase E(): 1.7e-10, 28.52% ID in 284 aa; *Leptospira interrogans* dTDP-glucose 4,6-dehydratase RfbB4 E(): 1.2e-09, 28.67% ID in 279 aa.
ECA1431		4	exopolysaccharide / O antigen biosynthesis protein	*Salmonella typhi* putative O-antigen transporter RfbX E(): 2.3e-41, 33.25% ID in 418 aa.

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ECA1432		4	exopolysaccharide / O antigen biosynthesis protein	*Streptococcus agalactiae* CpsI E(): 2.4e-08, 26.76% ID in 213 aa; *Chlorobium tepidum* glycosyl transferase ct0919 E(): 7.9e-13, 29.48% ID in 251 aa.
ECA1433		4	exopolysaccharide / O antigen biosynthesis protein	*Ralstonia solanacearum* putative acyl transferase rsp1012 E(): 4.2e-11, 36.7% ID in 188 aa; *Methanococcus jannaschii* hypothetical protein Mj1064 E(): 5.1e-10, 31.75% ID in 211 aa.
ECA1434		4	exopolysaccharide / O antigen biosynthesis protein	*Vibrio cholerae* WblE protein E(): 2.9e-09, 26.18% ID in 317 aa; *Streptococcus thermophilus* EpsG E(): 1.1e-08, 26.85% ID in 324 aa.
ECA1435	*rfc*	4	exopolysaccharide / O antigen biosynthesis protein	*Salmonella typhimurium* and *Salmonella typhi* O-antigen polymerase Rfc E(): 1.4e-54, 39.58% ID in 389 aa.
ECA1436	*rfbU*	4	exopolysaccharide / O antigen biosynthesis protein	*Salmonella typhimurium* RfbU E(): 2.8e-40, 45.65% ID in 357 aa.
ECA1437	*rfbN*	4	exopolysaccharide / O antigen biosynthesis protein	*Salmonella typhimurium* O antigen biosynthesis rhamnosyltransferase RfbN E(): 2.1e-53, 45.24% ID in 305 aa.
ECA1438	*rfbM*	4	exopolysaccharide / O antigen biosynthesis protein	*Escherichia coli* mannose-1-phosphate guanylyltransferase ManC or CpsB or RfbM E(): 2.1e-114, 60.88% ID in 473 aa.
ECA1439	*rfbK*	4	exopolysaccharide / O antigen biosynthesis protein	*Escherichia coli* phosphomannomutase ManB or RfbK or RfbK2 E(): 8.5e-137, 74.34% ID in 456 aa.
ECA1440	*rmlD*	4	exopolysaccharide / O antigen biosynthesis protein	*Escherichia coli* dTDP-4-dehydrorhamnose reductase RfbD or RmlD E(): 8.3e-36, 41.72% ID in 290 aa.
ECA1441	*rmlC*	4	exopolysaccharide / O antigen biosynthesis protein	*Escherichia coli* dTDP-6-deoxy-D-glucose-3,5 epimerase RmlC E(): 5.4e-40, 59.06% ID in 171 aa.
ECA1442	*rffH*	4	exopolysaccharide / O antigen biosynthesis protein	*Escherichia coli* and *Shigella flexneri* glucose-1-phosphate thymidylyltransferase RffH E(): 7.2e-85, 76.22% ID in 286 aa.
ECA1443	*galF*	4	exopolysaccharide / O antigen biosynthesis protein	*Escherichia coli* UTP-glucose-1-phosphate uridylyltransferase GalF or WcaN E(): 7.1e-74, 65.43% ID in 298 aa.
ECA1777	*opgG*	4	periplasmic glucans biosynthesis protein	*Erwinia chrysanthemi* OpgG protein E(): 1.1e-182, 84.48% ID in 522 aa; *Escherichia coli* periplasmic glucans biosynthesis protein MdoG E(): 8.1e-166, 76.96% ID in 508 aa.
ECA1778	*opgH*	4	periplasmic glucans biosynthesis protein	*Erwinia chrysanthemi* OpgH protein E(): 0, 83.15% ID in 855 aa; *Escherichia coli* MdoH E(): 0, 75.67% ID in 847 aa.
ECA4200	*wecG/ ffM*	4	enterobacterial common antigen	*Escherichia coli* probable UDP-N-acetyl-D-

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			synthesis protein	mannosaminuronic acid transferase WecG or RffM E(): 9.8e-68, 72.76% ID in 246 aa.
ECA4201	*WzyE*	4	enterobacterial common antigen synthesis protein	*Escherichia coli* putative ECA polymerase WzyE E(): 4.4e-142, 77.77% ID in 441 aa.
ECA4202	*wecF /rffT*	4	enterobacterial common antigen synthesis protein	*Escherichia coli* 4-alpha-L-fucosyltransferase WecF or RffT E(): 7.7e-97, 65.45% ID in 359 aa.
ECA4203	*wzxE*	4	enterobacterial common antigen synthesis protein	*Escherichia coli* and *Shigella flexneri* WzxE (): 6.6e-111, 72.11% ID in 416 aa.
ECA4204	*rffA / wecE*	4	enterobacterial common antigen synthesis protein	*Escherichia coli* lipopolysaccharide biosynthesis protein RffA or WecE E(): 7.4e-130, 83.77% ID in 376 aa.
ECA4205	*rffC / wecD*	4	enterobacterial common antigen synthesis protein	*Escherichia coli* lipopolysaccharide biosynthesis protein RffC or WecD E(): 1e-33, 55.78% ID in 190 aa.
ECA4206	*rffG*	4	enterobacterial common antigen synthesis protein	*Escherichia coli* dTDP-glucose 4,6-dehydratase RffG E(): 6.4e-119, 83% ID in 353 aa.
ECA4207	*wecC / rffD*	4	enterobacterial common antigen synthesis protein	*Escherichia coli* UDP-N-acetyl-D-mannosamine dehydrogenase WecC or RffD E(): 3.6e-130, 81.19% ID in 420 aa.
ECA4208	*wecB / rffE*	4	enterobacterial common antigen synthesis protein	*Escherichia coli* UDP-N-acetylglucosamine 2-epimerase WecB or RffE E(): 8.5e-116, 77.21% ID in 373 aa.
ECA4209	*wzzE*	4	enterobacterial common antigen synthesis protein	*Escherichia coli* lipopolysaccharide biosynthesis protein WzzE E(): 1.4e-94, 72.07% ID in 333 aa.
ECA4210	*wecA / rfe*	4	enterobacterial common antigen synthesis protein	*Escherichia coli* undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase WecA or Rfe E(): 7.4e-112, 75.97% ID in 358 aa.
ECA0602*	*cfa7*	5	phytotoxic polyketide synthesis protein	*Pseudomonas syringae* type I polyketide synthase Cfa7 E(): 0, 52.6% ID in 2091 aa; *Streptomyces coelicolor* putative type I polyketide synthase sco6275 E(): 3e-183, 44.33% ID in 1845 aa.
ECA0603*	*cfa6*	5	phytotoxic polyketide synthesis protein	*Pseudomonas syringae* type I polyketide synthase Cfa6 E(): 0, 60.14% ID in 2725 aa; *Polyangium cellulosum* soraphen polyketide synthase A SorA E(): 0, 43.21% ID in 2277 aa.
ECA0604*		5	phytotoxic polyketide synthesis protein	*Oceanobacillus iheyensis* O-succinylbenzoate-CoA ligase MenE E(): 7e-13, 22.99% ID in 448 aa; *Pseudomonas putida* non-ribosomal peptide synthetase domain protein pp4220 E(): 6.1e-09, 25.58% ID in 426 aa.
ECA0606*	*cfa3*	5	phytotoxic polyketide synthesis protein	*Pseudomonas syringae* cfa-beta-ketoacylsynthase Cfa3 E(): 2.7e-75, 56.15% ID in 374 aa; *Streptomyces coelicolor* putative 3-oxoacyl-(acyl-carrier-protein) synthase E(): 3.6e-25, 34.45% ID in 415 aa.
ECA0607*	*cfa2*	5	phytotoxic polyketide synthesis	*Pseudomonas syringae* coronafacic acid dehydratase Cfa2

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			protein	E(): 3.3e-49, 76.97% ID in 165 aa.
ECA0608*	*cfa1*	5	phytotoxic polyketide synthesis protein	*Pseudomonas syringae* cfa-acyl carrier protein Cfa1 E(): 6.8e-17, 60% ID in 80 aa.
ECA0609*	*cfl*	5	phytotoxic polyketide synthesis protein	*Pseudomonas syringae* coronafacate ligase Cfl E(): 1.4e-71, 37.3% ID in 512 aa.
ECA0600		5	phytotoxic polyketide synthesis protein	*Pseudomonas syringae* oxidoreductase Cfa8 E(): 6.5e-122, 74.05% ID in 397 aa; *Streptomyces lavendulae* hypothetical 45.2 kDa protein (414 aa) FASTA scores: E(): 2.2e-82, 52.39% ID in 397 aa.
ECA0601		5	phytotoxic polyketide synthesis protein	*Pseudomonas syringae* oxidoreductase Cfa8 E(): 8.2e-20, 45.11% ID in 133 aa.
ECA0605		5	phytotoxic polyketide synthesis protein	No significant database matches.
ECA1486		5	non-ribosomal peptide transporter	*Pseudomonas syringae* ATP-binding protein SyrD E(): 1.2e-54, 34.27% ID in 566 aa.
ECA1487		5	non-ribosomal peptide synthetase	*Pseudomonas syringae* syringomycin synthetase SyrE E(): 0, 43.13% ID in 6600 aa.
ECA1488		5	non-ribosomal peptide synthetase	*Pseudomonas syringae* syringomycin synthetase syrE E(): 0, 42.92% ID in 7655 aa
ECA0056		6	iron acquisition; TonB-dependent heme receptor	*Bordetella avium* BhuR E(): 8.3e-14, 23.68% ID in 874 aa; *Pasteurella multocida* HemR E(): 1.5e-143, 51.04% ID in 717 aa.
ECA0474	*entD*	6	iron acquisition; enterobactin synthetase component	*Escherichia coli* 4'-phosphopantetheinyl transferase EntD E(): 4.1e-09, 31.49% ID in 181 aa.
ECA0475		6	iron acquisition; TonB-dependent siderophore receptor protein	*Escherichia coli* colicin i receptor precursor CirA or FeuA E(): 9.5e-57, 36.61% ID in 661 aa; *Vibrio cholerae* iron-regulated outer membrane virulence protein precursor IrgA E(): 1.1e-48, 29.73% ID in 676 aa.
ECA0476		6	iron acquisition; transporter	*Stigmatella aurantiaca* MxcK E(): 2.9e-29, 32.74% ID in 394 aa.
ECA0477	*entC*	6	iron acquisition; enterobactin synthetase component C	*Escherichia coli* isochorismate synthase EntC E(): 6.1e-66, 46.31% ID in 393 aa.
ECA0478	*entE*	6	iron acquisition; enterobactin synthetase component E	*Escherichia coli* enterobactin synthetase component E EntE E(): 1.1e-129, 64.63% ID in 540 aa.
ECA0479	*entB*	6	iron acquisition; enterobactin synthetase component B	*Escherichia coli*, EntB or EntG E(): 1.1e-69, 63.63% ID in 286 aa.
ECA0480	*entF*	6	iron acquisition; enterobactin synthetase component F	*Escherichia coli* enterobactin synthetase component F EntF E(): 2.4e-63, 30.4% ID in 1069 aa.
ECA0481	*entA*	6	iron acquisition; enterobactin synthetase component A	*Escherichia coli* 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase EntA E(): 6.7e-54, 59.92% ID in 252 aa.

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ECA0731	*fcuA*	6	iron acquisition; ferric siderophore TonB-dependent receptor	*Yersinia enterocolitica* ferrichrome receptor FcuA E(): 2.6e-175, 59.78% ID in 756 aa; *Bordetella bronchiseptica* putative ferric siderophore receptor BfrB E(): 1.2e-99, 39.86% ID in 725 aa.
ECA0811		6	iron acquisition; TonB-dependent ferrichrome receptor	*Vibrio cholerae* ferrichrome outer membrane receptor FhuA E(): 2.8e-96, 40.61% ID in 687 aa; *Bradyrhizobium japonicum* FegA E(): 1.5e-78, 35.22% ID in 738 aa.
ECA0876	*iutA*	6	iron acquisition;TonB-dependent ferric aerobactin receptor	*Escherichia coli* ferric aerobactin receptor precursor iutA E(): 0, 75.85% ID in 733 aa; *Shigella boydii* IutA E(): 0, 75.44% ID in 733 aa.
ECA0927		6	iron acquisition; putative TonB-dependent receptor	*Escherichia coli* probable TonB-dependent receptor yncd precursor E(): 9e-12, 22.77% ID in 751 aa; *Caulobacter crescentus* TonB-dependent receptor cc3436 E(): 4.1e-16, 25.64% ID in 772 aa.
ECA0935	*fhuE*	6	iron acquisition; TonB-dependent ferric receptor	*Escherichia coli* FhuE receptor precursor E(): 1.9e-162, 55.86% ID in 725 aa.
ECA1073	*fecE*	6	iron acquisition; ferric citrate transport ATP-binding protein	*Escherichia coli* FecE E(): 8.2e-64, 67.84% ID in 255 aa.
ECA1074	*fecD*	6	iron acquisition; ferric citrate transport system permease protein	*Escherichia coli* FecD E(): 1.6e-85, 69.3% ID in 316 aa.
ECA1075	*fecC*	6	iron acquisition; ferric citrate transport system permease protein	*Escherichia coli* FecC E(): 2.5e-94, 74.09% ID in 332 aa.
ECA1076	*fecB*	6	iron acquisition; ferric citrate binding periplasmic protein	*Escherichia coli* FecB E(): 1.1e-80, 70.66% ID in 300 aa.
ECA1077	*fecA*	6	iron acquisition; ferric citrate transport protein	*Escherichia coli* FecA 0, 80.56% ID in 782 aa.
ECA1078	*fecR*	6	iron acquisition; ferric citrate sensor protein	*Escherichia coli* protein FecR E(): 7.6e-87, 69.55% ID in 312 aa.
ECA1079	*fecI*	6	iron acquisition; RNA polymerase sigma factor	*Escherichia coli* probable RNA polymerase sigma factor FecI E(): 1.1e-48, 78.61% ID in 173 aa.
ECA1275		6	iron acquisition; TonB-dependent ferrichrome-iron receptor	*Anabaena* sp. ferrichrome-iron receptor all2610 E(): 3.4e-38, 27.33% ID in 684 aa; *Pseudomonas putida* putative outer membrane ferric siderophore receptor pp3155 E(): 2.2e-29, 27.35% ID in 691 aa.
ECA1534	*hasF*	6	iron acquisition; Type I Secretion System protein for heme-binding protein	*Pseudomonas fluorescens* outer membrane protein HasF E(): 1.5e-85, 54.96% ID in 433 aa.
ECA1535	*hasE*	6	iron acquisition; Type I Secretion	*Pseudomonas fluorescens* membrane fusion protein HasE

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			System protein for heme-binding protein	E(): 2.5e-67, 52.28% ID in 438 aa.
ECA1536	*hasD*	6	iron acquisition; Type I Secretion System protein for heme-binding protein	*Pseudomonas fluorescens* ABC protein HasD E(): 2.6e-129, 65.58% ID in 584 aa; *Erwinia chrysanthemi* proteases secretion ATP-binding protein PrtD E(): 5.2e-113, 59.47% ID in 570 aa. ECA2783 58.719% ID in 562 aa overlap
ECA1537	*hasA*	6	iron acquisition; extracellular heme-binding protein	*Serratia marcescens* hemophore HasA E(): 6.1e-27, 50.27% ID in 183 aa; *Pseudomonas aeruginosa* HasaP E(): 8.3e-25, 45.71% ID in 210 aa.
ECA1538	*hasR*	6	iron acquisition; TonB-dependent heme receptor	*Serratia marcescens* HasR protein E(): 2.1e-176, 62.03% ID in 893 aa.
ECA2315	*tonB*	6	iron acquisition	*Erwinia chrysanthemi* TonB protein E(): 2.8e-41, 70.42% ID in 257 aa.
ECA2392	*yfeA*	6	iron acquisition; chelated iron transporter	*Yersinia pestis* periplasmic chelated iron-binding protein YfeA E(): 1.6e-89, 78.85% ID in 298 aa.
ECA2393	*yfeB*	6	iron acquisition; chelated iron transporter	*Yersinia pestis* chelated iron transport system membrane protein YfeB E(): 1.6e-83, 80.14% ID in 277 aa.
ECA2394	*yfeC*	6	iron acquisition; chelated iron transporter	*Yersinia pestis* chelated iron transport system membrane protein YfeC E(): 2.1e-93, 90.03% ID in 281 aa.
ECA2395	*yfeD*	6	iron acquisition; chelated iron transporter	*Yersinia pestis* chelated iron transport system membrane protein YfeD E(): 3.6e-84, 76.67% ID in 283 aa.
ECA2722		6	iron acquisition; exogenous ferric siderophore TonB-dependent receptor	*Vibrio cholerae* iron-regulated outer membrane virulence protein precursor E(): 9.1e-29, 35.05% ID in 716 aa; *Escherichia coli* exogenous ferric siderophore receptor R4 E(): 2e-148, 55.45% ID in 678 aa.
ECA2806	*cbrD*	6	iron acquisition; achromobactin transport ATP-binding protein	*Erwinia chrysanthemi* achromobactin transport ATP-binding protein CbrD E(): 3.9e-64, 70.75% ID in 253 aa.
ECA2807	*cbrC*	6	iron acquisition; achromobactin transport system permease protein	*Erwinia chrysanthemi* achromobactin transport system permease protein CbrC E(): 4.9e-69, 61.91% ID in 344 aa.
ECA2808	*cbrB*	6	iron acquisition; achromobactin transport system permease protein	*Erwinia chrysanthemi* achromobactin transport system permease protein CbrB E(): 8.6e-66, 58.15% ID in 325 aa.
ECA2809	*cbrA*	6	iron acquisition; achromobactin-binding periplasmic protein	*Erwinia chrysanthemi* achromobactin-binding periplasmic protein precursor CbrA E(): 1.5e-62, 63.74% ID in 262 aa.
ECA2810	*acr*	6	iron acquisition; TonB-dependent ferric achromobactin receptor	*Erwinia chrysanthemi* Acr E(): 2.5e-108, 57.76% ID in 483 aa.
ECA3137	*sfuA*	6	iron acquisition; transporter	*Serratia marcescens* iron(III)-binding periplasmic protein precursor SfuA E(): 1.3e-102, 82.84% ID in 338 aa; *Yersinia enterocolitica* YfuA E(): 4.7e-99, 80.17% ID in

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				338 aa.
ECA3138	*sfuB*	6	iron acquisition; transporter	*Serratia marcescens* iron(III)-transport system permease protein SfuB E(): 7.3e-141, 71.29% ID in 526 aa; *Yersinia pestis* iron(III)-transport system permease protein SfuB E(): 2.2e-139, 70.61% ID in 524 aa.
ECA3139	*sfuC*	6	iron acquisition; transporter	*Serratia marcescens* iron(III)-transport ATP-binding protein SfuC E(): 3.5e-64, 59.59% ID in 344 aa; *Yersinia pestis* iron(III)-transport ATP-binding protein SfuC E(): 8.4e-65, 57.92% ID in 347 aa.
ECA3241		6	iron acquisition; transporter	*Yersinia pestis* putative solute-binding periplasmic protein of ABC transporter E(): 6.7e-37, 35.22% ID in 335 aa; *Agrobacterium tumefaciens* ABC transporter, substrate binding protein E(): 2.4e-36, 32.24% ID in 366 aa.
ECA3242		6	iron acquisition; transporter	*Yersinia pestis* putative FecD-family membrane transport protein E(): 2.2e-108, 81.66% ID in 360 aa; *Salmonella typhimurium* putative ABC transport protein E(): 2.2e-94, 72.06% ID in 358 aa.
ECA3243		6	iron acquisition; transporter	*Escherichia coli* ferric-enterobactin-transport protein E(): 7.9e-59, 67.05% ID in 255 aa; *Yersinia pestis* putative siderophore ABC transporter, ATP-binding subunit E(): 1.4e-74, 81.15% ID in 260 aa.
ECA3380	*pvcB*	6	iron acquisition; possible novel siderophore synthesis protein	*Pseudomonas aeruginosa* pyoverdine biosynthesis protein PvcB E(): 7.7e-50, 49.43% ID in 263 aa.
ECA3381	*pvcA*	6	iron acquisition; possible novel siderophore synthesis protein	*Pseudomonas aeruginosa* pyoverdine biosynthesis protein PvcA E(): 2.3e-70, 61.38% ID in 303 aa.
ECA3564		6	iron acquisition; iron-chelating periplasmic-binding protein	*Escherichia coli* iron-chelating periplasmic-binding protein E(): 7.3e-53, 47.19% ID in 303 aa; *Methanosarcina acetivorans* iron ma1222 E(): 1.2e-30, 33.72% ID in 338 aa.
ECA3565		6	iron acquisition; TonB dependant ferrichrome receptor	*Yersinia enterocolitica* ferrichrome receptor FcuA E(): 2.8e-42, 29.09% ID in 787 aa; *Escherichia coli* O6 hypothetical protein E(): 1.5e-160, 57.22% ID in 720 aa.
ECA3781		6	iron acquisition; TonB dependent siderophore receptor	*Escherichia coli* ferrienterobactin receptor precursor FepA E(): 1.6e-186, 63.68% ID in 738 aa.
ECA3781	*fepA*	6	iron acquisition; TonB dependent siderophore receptor	*Escherichia coli* ferrienterobactin receptor precursor FepA E(): 1.6e-186, 63.68% ID in 738 aa; *Pseudomonas aeruginosa* ferric enterobactin receptor precursor pfea E(): 1.1e-187, 66.1% ID in 717 aa.
ECA4115		6	iron acquisition; TonB-dependent siderophore receptor	*Ralstonia solanacearum* probable ferric siderophore receptor protein E(): 2.3e-136, 51.09% ID in 734 aa; *Vibrio*

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				anguillarum ferric anguibactin receptor precursor fatA E(): 3.5e-79, 35.45% ID in 722 aa.
ECA4116		6	iron acquisition; possible siderophore (aerobactin) synthesis gene	*Escherichia coli* aerobactin siderophore biosynthesis protein IucC E(): 9.5e-19, 29.59% ID in 321 aa.
ECA4198		6	iron or phosphate acquisition; phytase	*Pseudomonas syringae* phytase PhyM E(): 3.4e-77, 48.73% ID in 433 aa; Escherichia coli glucose-1-phosphatase precursor Agp or E(): 1.5e-31, 31.08% ID in 415 aa.
ECA4254		6	iron acquisition; transporter	*Escherichia coli* ferrichrome transport ATP-binding protein FhuC E(): 1.2e-25, 37.5% ID in 256 aa; *Brucella melitensis* iron(III) dicitrate transport ATP-binding protein bmeii0537 E(): 6e-28, 42.21% ID in 244 aa.
ECA4255		6	iron acquisition; transporter	*Rhizobium loti* iron(III) ABC transporter, periplasmic-binding protein mlr8228 E(): 8e-77, 62.38% ID in 319 aa; *Pseudomonas aeruginosa* hypothetical protein Pa2913 E(): 1.3e-50, 45.57% ID in 316 aa.
ECA4256		6	iron acquisition; transporter	*Bordetella avium B*huU E(): 1.1e-33, 38.8% ID in 317 aa; *Rhizobium loti* ABC transporter, permease protein mlr8229 E(): 1.3e-61, 54.4% ID in 329 aa.
ECA4302	*sftP*	6	iron acquisition; TonB-dependent receptor	*Pseudomonas putida* SftP SWALL:Q9R9W7 E(): 5e-33, 37.71% ID in 753 aa; *Xanthomonas axonopodis* TonB-dependent receptor FyuA E(): 1.7e-22, 23.65% ID in 782 aa.
ECA4451	*hmsS*	6	iron acquisition and storage; hemin storage protein	*Yersinia pestis* HmsS E(): 8.8e-07, 28.77% ID in 139 aa.
ECA4452	*hmsR*	6	iron acquisition and storage; hemin storage protein	*Yersinia pestis* HmsR E(): 3.8e-136, 73.24% ID in 441 aa.
ECA4453	*hmsF*	6	iron acquisition and storage; hemin storage protein	*Yersinia pestis* HmsF E(): 8.5e-166, 58.42% ID in 671 aa.
ECA4454	*hmsH*	6	iron acquisition and storage; hemin storage protein	*Yersinia pestis* HmsF E(): 8.5e-166, 58.42% ID in 671 aa.
ECA3251*	*hmpX*	7	defence against oxidative burst	*Erwinia chrysanthemi* flavohemoprotein HmpX E(): 1.3e-112, 70.52% ID in 397 aa.
ECA3597*	*msrA*	7	defence against oxidative burst	*Erwinia chrysanthemi* peptide methionine sulfoxide reductase MsrA E(): 2.6e-72, 80.95% ID in 210 aa.
ECA0092	*sodA*	7	defence against oxidative burst	*Erwinia chrysanthemi* manganese superoxide dismutase SodA E(): 3.7e-73, 87.98% ID in 208 aa.
ECA0330	*tolC*	7	plant antimicrobial compound resistance protein	*Escherichia coli* outer membrane protein TolC precursor E(): 4.1e-124, 75.32% ID in 466 aa, *Erwinia chrysanthemi* outer membrane protein TolC E(): 2.3e-128, 77.89% ID in

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				466 aa.
ECA1859	*sufA*	7	defence against oxidative burst	*Erwinia chrysanthemi* SufA protein E(): 2.9e-33, 68.29% ID in 123 aa; *Escherichia coli* SufA E(): 3e-30, 67.52% ID in 117 aa.
ECA1860	*sufB*	7	defence against oxidative burst	*Erwinia chrysanthemi* SufB protein SufB E(): 1.6e-185, 88.6% ID in 500 aa; Escherichia coli SufB E(): 2.1e-176, 84.4% ID in 500 aa.
ECA1861	*sufC*	7	defence against oxidative burst	*Escherichia coli* probable ATP-dependent transporter SufC E(): 2.7e-71, 85.08% ID in 248 aa; *Erwinia chrysanthemi* SufC E(): 6.7e-72, 85.88% ID in 248 aa.
ECA1862	*sufD*	7	defence against oxidative burst	*Escherichia coli* SufD E(): 1e-99, 61.5% ID in 413 aa; *Erwinia chrysanthemi* SufD protein 1.6e-114, 69.78% ID in 417 aa.
ECA1863	*sufS*	7	defence against oxidative burst	*Escherichia coli* selenocysteine lyase CsdB or SufS E(): 3e-113, 70.69% ID in 406 aa; and to *Erwinia chrysanthemi* cysteine desulfurase sufS E(): 4.6e-123, 77.72% ID in 404 aa.
ECA1864	*sufE*	7	defence against oxidative burst	*Escherichia coli* SufE E(): 1.9e-35, 70.07% ID in 137 aa; *Erwinia chrysanthemi* SufE protein E(): 7.4e-39, 73.91% ID in 138 aa.
ECA1909	*katB*	7	defence against oxidative burst; catalase peroxidase	*Legionella pneumophila* catalase-peroxidase KatB E(): 0, 78.28% ID in 723 aa.
ECA1973	*sapF*	7	plant antimicrobial peptide resistance protein	*Erwinia chrysanthemi* SapF E(): 5.2e-80, 88.8% ID in 268 aa; *Salmonella typhimurium* peptide transport system ATP-binding protein SapF E(): 9e-75, 80.89% ID in 267 aa.
ECA1974	*sapD*	7	plant antimicrobial peptide resistance protein	*Erwinia chrysanthemi* SapD E(): 1.6e-113, 86.32% ID in 329 aa; *Salmonella typhimurium* peptide transport system ATP-binding protein SapD E(): 6.3e-111, 85.36% ID in 328 aa.
ECA1975	*sapC*	7	plant antimicrobial peptide resistance protein	*Erwinia chrysanthemi* SapC protein E(): 1.5e-89, 78.37% ID in 296 aa; *Salmonella typhi* peptide transport system permease protein SapC E(): 2.5e-87, 75.33% ID in 296 aa.
ECA1976	*sapB*	7	plant antimicrobial peptide resistance protein	*Erwinia chrysanthemi* SapB protein S E(): 2.2e-84, 71.65% ID in 321 aa, *Salmonella typhi* SapB 9.2e-94, 73.2% ID in 321 aa.
ECA1977	*sapA*	7	plant antimicrobial peptide resistance protein	*Erwinia chrysanthemi* SapA protein E(): 1.5e-178, 80.92% ID in 540 aa; *Salmonella typhimurium* SapA E(): 6.1e-161, 71.4% ID in 535 aa.
ECA2532	*pqiB*	7	defence against oxidative burst; paraquat inducible protein	*Escherichia coli* paraquat-inducible protein B PqiB E(): 3.8e-141, 66.72% ID in 544 aa.

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ECA2533	*pqiA*	7	defence against oxidative burst; paraquat inducible protein	*Escherichia coli* paraquat-inducible protein PqiA E(): 3.7e-111, 66.42% ID in 411 aa.
ECA2984	*xenA*	7	defence against oxidative burst; flavoprotein reductase	*Pseudomonas putida* xenobiotic reductase a XenA E(): 2.4e-114, 75.96% ID in 362 aa; *Xanthomonas campestris* xenobiotic flavin oxidoreductase A frp E(): 2.5e-104, 70.44% ID in 362 aa.
ECA3167	*ohr*	7	defence against oxidative burst; peroxide resistance protein	*Xanthomonas axonopodis* organic hydroperoxide resistance protein Ohr E(): 7.1e-36, 71.94% ID in 139 aa; *Ralstonia solanacearum* probable organic hydroperoxide resistance protein Ohr E(): 2.7e-40, 77.3% ID in 141 aa.
ECA3168	*ohrR*	7	defence against oxidative burst; peroxide resistance protein	*Xanthomonas campestris* transcriptional regulator OhrR E(): 1.2e-34, 69.06% ID in 139 aa.
ECA3942	*ahpC*	7	defence against oxidative burst; peroxide resistance protein	*Escherichia coli* and *Shigella flexneri* alkyl hydroperoxide reductase C22 protein AhpC E(): 1.3e-63, 83.87% ID in 186 aa.
ECA2521*	*mviN*	8	putative virulence factor	*Escherichia coli* and *Escherichia coli* O157:H7 virulence factor MviN homolog E(): 1.2e-160, 81.99% ID in 511 aa; *Yersinia pestis* putative membrane protein mvin E(): 5.1e-165, 84.51% ID in 510 aa.
ECA2522*	*mviM*	8	putative virulence factor	*Salmonella typhimurium* virulence factor MviM E(): 2.9e-71, 63.3% ID in 297 aa; *Escherichia coli* virulence factor MviM E(): 1.2e-67, 60% ID in 300 aa
ECA3559*	*rhiN*	8	plant inducible protein	*Erwinia chrysanthemi* RhiN E(): 9e-146, 87.07% ID in 379 aa; *Salmonella typhimurium* putative cytoplasmic protein E(): 1.5e-128, 75.72% ID in 379 aa.
ECA3749*		8	plant inducible protein	*Erwinia chrysanthemi* RhiN E(): 1.8e-53, 45.01% ID in 311 aa; *Agrobacterium tumefaciens* hypothetical protein atu4561 E(): 4.9e-74, 53.46% ID in 361 aa. ECA3559 43.810% ID in 315 aa overlap.
ECA0274		8	hypothetical protein only matching proteins from plant pathogens.	*Xanthomonas campestris* hypothetical protein Xcc1623 E(): 1.7e-15, 38.65% ID in 194 aa. No other significant database matches.
ECA0766		8	hypothetical protein only matching proteins from plant pathogens	*Xanthomonas campestris* hypothetical protein xcc3622 E(): 5.2e-16, 36.15% ID in 177 aa; *Xanthomonas axonopodis* hypothetical protein xac0573 E(): 7.7e-15, 35.02% ID in 177 aa. Note that the only significant database matches are to *Xanthomonas* spp.
ECA0767		8	hypothetical protein only matching proteins from plant pathogens	*Xanthomonas campestris* hypothetical protein xcc3298 E(): 3e-10, 33.33% ID in 174 aa; *Xanthomonas campestris* hypothetical protein xcc3128 E(): 3.2e-10, 34.44% ID in

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				180 aa. Note that the only significant database matches are to *Xanthomonas* spp.
ECA3083	*vacJ*	8	putative virulence factor	*Shigella flexneri* VacJ lipoprotein 1.2e-75, 71.71% ID in 251 aa; Yersinia pestis VacJ E(): 3.3e-80, 76.68% ID in 253 aa.
ECA0482		8	non-ribosomal peptide biosynthesis protein	*Bacillus subtilis* fengycin synthetase FenE E(): 1.3e-104, 31.95% ID in 1546 aa; *Pseudomonas putida* non-ribosomal peptide synthetase domain protein, E(): 1.1e-112, 31.67% ID in 2033 aa.
ECA0483		8	non-ribosomal peptide biosynthesis protein	*Tolypothrix* sp. PCC 7601/1 peptide synthetase TpsA E(): 4.5e-41, 30.3% ID in 561 aa; *Pseudomonas syringae* syringomycin biosynthesis enzyme 1 SyrB1 E(): 1e-40, 32.3% ID in 517 aa.
ECA0045		8	resistance to complement killing	*Salmonella typhimurium* resistance to complement killing Rck or pslt009 E(): 7.9e-27, 44.68% id in 188 aa. *Salmonella typhimurium* virulence membrane protein PagC precursor or stm1246 E(): 3.5e-26, 45.05% ID in 182 aa.
ECA0008	*qseB*	9	regulator; may link quorum sensing to flagellar motility	*Escherichia coli* transcriptional regulatory protein QseB S E(): 3.1e-59, 68.34% ID in 218 aa.
ECA0007	*qseC*	9	regulator; may link quorum sensing to flagellar motility	*Escherichia coli* sensor protein QseC E(): 7.4e-94, 56.15% ID in 447 aa.
ECA0030	*typA* (bipA)	9	pathogenicity regulator	*Escherichia coli* GTP-binding protein TypA or BipA E(): 1.1e-189, 90.18% ID in 591 aa.
ECA0105	*expI (carI, hslI)*	9	pathogenicity regulator; autoinducer synthesis protein	
ECA0106	*expR*	9	pathogenicity regulator; transcriptional activator protein	Similar to ECA1561 (67.839%% ID in 199 aa overlap).
ECA0643	*exuR*	9	pathogenicity regulator; exu regulon transcriptional regulator	
ECA0809	*hexY*	9	pathogenicity regulator; LysR-family	
ECA0917	*rspA*	9	regulator; may link quorum sensing to starvation sensing	*Escherichia coli* starvation sensing protein RspA E(): 5.7e-163, 92.57% ID in 404 aa.
ECA0918	*rspB*	9	regulator; may link quorum sensing to starvation sensing	*Escherichia coli* starvation sensing protein RspB E(): 5.6e-94, 73.45% ID in 339 aa.
ECA1022	*aepA*	9	pathogenicity regulator	
ECA1202	*rcsC*	9	pathogenicity regulator; capsule synthesis	*Escherichia coli* sensor protein RcsC E(): 1.6e-216, 58.97% ID in 953 aa.
ECA1203	*rcsB*	9	pathogenicity regulator; capsule synthesis	*Escherichia coli* capsular synthesis regulator component B RcsB E(): 1.2e-66, 92.52% ID in 214 aa.

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ECA1561		9	pathogenicity regulator; quorum sensing LuxR homologue	*Erwinia chrysanthemi* transcriptional activator protein EchR E(): 5e-67, 72.35% ID in 246 aa; *Erwinia carotovora* transcriptional activator protein ExpR E(): 1.3e-57, 59.5% ID in 242 aa. Similar to Eca0106 ExpR 67.839% ID in 199 aa overlap.
ECA1665	*hns*	9	pathogenicity regulator; global regulator	*Escherichia coli*, DNA-binding protein H-NS E(): 3.4e-22, 61.19% ID in 134 aa; *Erwinia chrysanthemi* regulatory protein hnS E(): 1.5e-22, 61.65% ID in 133 aa. Also similar to ECA2893 (87.970% ID in 133 aa overlap) ECA2328 (61.654% ID in 133 aa overlap).
ECA1931	*hor*	9	pathogenicity regulator; gobal regulator	
ECA1971	*aidA*	9	quorum sensing regulator	*Ralstonia solanacearum* AidA E(): 2.2e-11, 32.75% ID in 174 aa.
ECA1989	*tyrR*	9	pathogenicity regulator	*Erwinia herbicola* transcriptional regulatory protein TyrR E(): 1.8e-138, 71.12% ID in 523 aa.
ECA2035	*pecM*	9	pathogenicity regulator	*Erwinia chrysanthemi* PecM protein E(): 4e-39, 42.75% ID in 276 aa
ECA2036	*pecS*	9	pathogenicity regulator	*Erwinia chrysanthemi* regulatory protein PecS E(): 5.5e-25, 48.76% ID in 162 aa
ECA2328	*hns*	9	pathogenicity regulator; global regulator	*Erwinia chrysanthemi* Hns regulatory protein E(): 1.2e-39, 91.11% ID in 135 aa; *Escherichia coli*, DNA-binding protein H-NS E(): 8.1e-36, 84.32% ID in 134 aa. Also similar to ECA2893 (62.406% ID in 133 aa overlap) and to ECA1665 (61.654% ID in 133 aa overlap).
ECA2330	*expM*	9	pathogenicity regulator	
ECA2425	*kdgR*	9	pectin degradation repressor	
ECA2435	*rdgA*	9	regulator of pectin lyase production	
ECA2437	*rdgB*	9	regulator of pectin lyase production	
ECA2445	*pehR*	9	two-component response regulator of virulence determinants	
ECA2446	*pehS*	9	two-component response regulator of virulence determinants	
ECA2724	*rscR*	9	pathogenicity regulator; LysR-family	*Yersinia enterocolitica* RscR E(): 4.4e-91, 78.62% ID in 290 aa; *Escherichia coli* hypothetical transcriptional regulator yeie E(): 1.1e-90, 76.57% ID in 286 aa

Systematic gene name	Gene name	Functional category	Putative function	Similarities shown with FASTA comparison score are the best database matches (not shown for genes previously sequenced in *E. carotovora*) and selected other database matches of note (where appropriate). Also listed are significant matches within the Eca1043 genome where applicable and PFAM scores where relevant.
ECA2893	*hns*	9	pathogenicity regulator; global regulator	*Escherichia coli* DNA-binding protein h-ns E(): 4.1e-23, 62.68% ID in 134 aa; *Erwinia chrysanthemi* Hns regulatory protein 3.1e-23, 63.15% ID in 133 aa. Also similar to ECA1665 (87.970% ID in 133 aa overlap) and to ECA2328 (62.406% ID in 133 aa overlap)
ECA3030	*hexA*	9	pathogenicity regulator; LysR-family	Identical to ECA3032
ECA3032	*hexA*	9	pathogenicity regulator; LysR-family	Identical to ECA3030
ECA3366	*rsmA / csrA*	9	carbon storage regulator	
ECA3695		9	pathogenicity regulator	*Erwinia carotovora* DNA-binding protein RdgB E(): 1.8e-22, 60.19% ID in 103 aa; *Salmonella typhi* putative bacteriophage transcriptional regulator sty1591 SE(): 5.5e-35, 67.44% ID in 129 aa. Also similar to ECA2437, 59.259% ID in 108 aa overlap.
ECA4123	*rexZ*	9	pathogenicity regulator; exoenzymes	
ECA4259	*cytR*	9	pathogenicity regulator	

*Included as a pathogenicity gene in the comparative analyses based on feature class qualifier 5.1.5 (see GenBank/EMBL accession no. BX950851 for feature class qualifiers).

CDSs are grouped by putative functional categories: 1, protein secretion machinery (and associated regulators); 1.I, type I secretion; 1.II, type II secretion; 1.III, type III secretion; 1.IV, type IV secretion; 2, secreted proteins (and their chaperones) and plant cell-wall degrading enzymes; 2.I, type I secretion; 2.II, type II secretion; 2.III, type III secretion; 2.IV, type IV secretion; 2.V, type V secretion; 2.VI, two-partner secretion system; 2.VII, nonsecreted cell-wall degrading enzymes and proteins of unknown secretion mechanism; 3, surface appendages; 4, other cell envelope components (extracellular polysaccharide/lipopolysaccharide/osmoregulated periplasmic glucans); 5, phytotoxin-associated; 6, iron acquisition and storage; 7, protection against plant defense mechanisms; 8, miscellaneous; 9, regulators of pathogenicity.