同性を有していた (Fig. 6 (A))．近年，TcpAタンパク質のうち，ある5つの残基が，線維状の構造を構築するために高度に保存されているという報告があり(17,18) pEntYN10のCofAもこれらの残基が保存されていることが分かった(Fig. 6B)．したがってCS8としての機能も保持されていると考えられる．しかし，CS8抗体を用いたドットブロットテストでは陰性であった(11)．アミノ酸配列の違いから抗体が反応しなかった可能性が考えられるが，電子顕微鏡観察でもCS8様の線毛は観察されておらず(6)，0169のCS8は発現していないのかもしれない．RT-PCRなどによりmRNAの転写が起きているのか今後検討すべきと考える．

pEntYN10のK88-like遺伝子群は，主要線毛サブユニットをコードする*faeG*と相同性のある配列が2つ保有されていた (Fig. 3)．*faeG*配列の系統発生樹によると，2つの*faeG*遺伝子は，ブタから分離された大腸菌の*faeG*よりも，ヒトから分離された*Salmonella enterica* serovar Infantisの*faeG*と近いことが分かった (Fig. 5)．このことから，pEntYN10のK88-likeがヒトへの感染のために働いている可能性も考えられる．*S.* Infantisが0169と同様の細胞接着性を示すのかどうかも今後観察してみる価値はあるだろう．

0169の特異な付着に関係するのは，これらの3つの推定定着因子のどれかだと考えられる．今後はこれらの3つの遺伝子のクローニングを行い，どの遺伝子群が本菌の特異な付着に関与するか検討する．

ETECはヒトのみならずブタやウシの下痢症原因ともなる．そのエンテロトキシンLTとSTの毒性は家畜とヒトに共通のものが多い．しかし，腸粘膜への定着因子が異なるため，家畜のETECは家畜の間で，ヒトのETECはヒトの間だけで感染を循環させており相互の行き来はないとされている(3)．しかしながら，pEntYN10のようにin vitroでは脱落しやすいプラスミドが0169に保たれていると言う事実は，本菌が常に効率よく感染を繰り返しin vivoで保たれていることを示唆する．本プラスミド上にコードされた3種の定着因子遺伝子を使い分けることによって0169が多様な宿主に感染する能力を得ているとすれば，脱落しやすいプラスミドが保持され続けるのも理解できる．K88はもともとブタETECの定着因子であり，ヒトに感染するためのCS6やCS8などと宿主に合わせた使い分けを0169がしているとすれば，ETEC感染症対策について考えを改める必要も生じる．ヒトETECの汚染源が本当にヒトだけなのか，新しい視点で調べ直す必要もありそうだ．

E. 結論

ETEC O169:H41 の病原プラスミドの全塩基配列を決定したところ，本菌には CS6, CS8-like, K88-like, 以上３種類の腸管定着因子がコードされていることが明らかとなった．極めて不安定で脱落しやすいプラスミドであるにもかかわらず維持されている理由として，異なる宿主に対応できる定着因子をコードし，O169 の適応力増強に本プラスミドが寄与しているためかもしれない．ETEC の宿主特異性について固定観念を取り払って考え直す価値がありそうだ．

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G. 健康危険情報

なし

H. 研究発表

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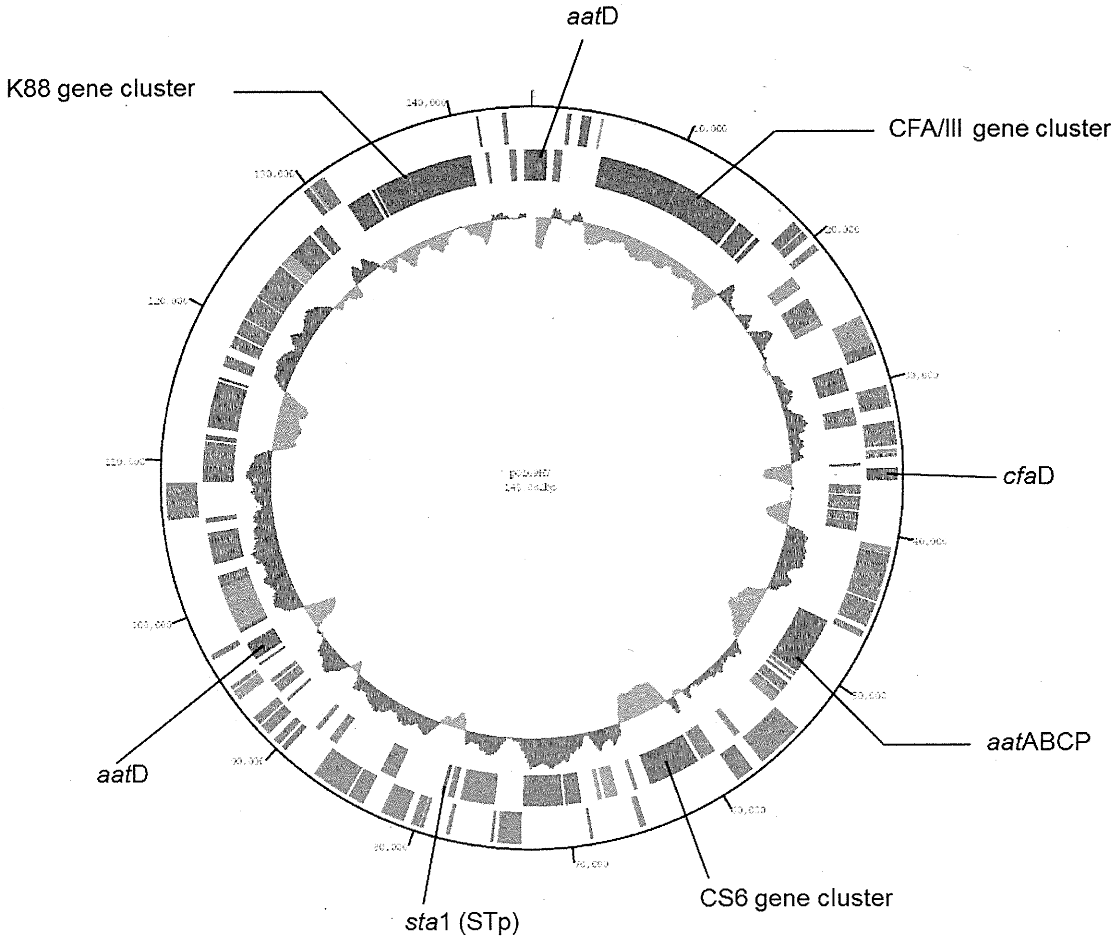


Fig. 1
pEntYN10 の環状図．一番内側の環状は GC 含量を表わしている．それぞれ，50%以上は紫色，50%以下は緑色で示されている．外側の円は，遺伝子の方向を表わしている（外側が forward，内側が reverse）．推定される遺伝子の機能によって色分けがされている．赤，病原性に関連するタンパク質；緑，プラスミドの複製または維持機能；ピンク，挿入配列関連または トランスポゼース断片；青，推定遺伝子

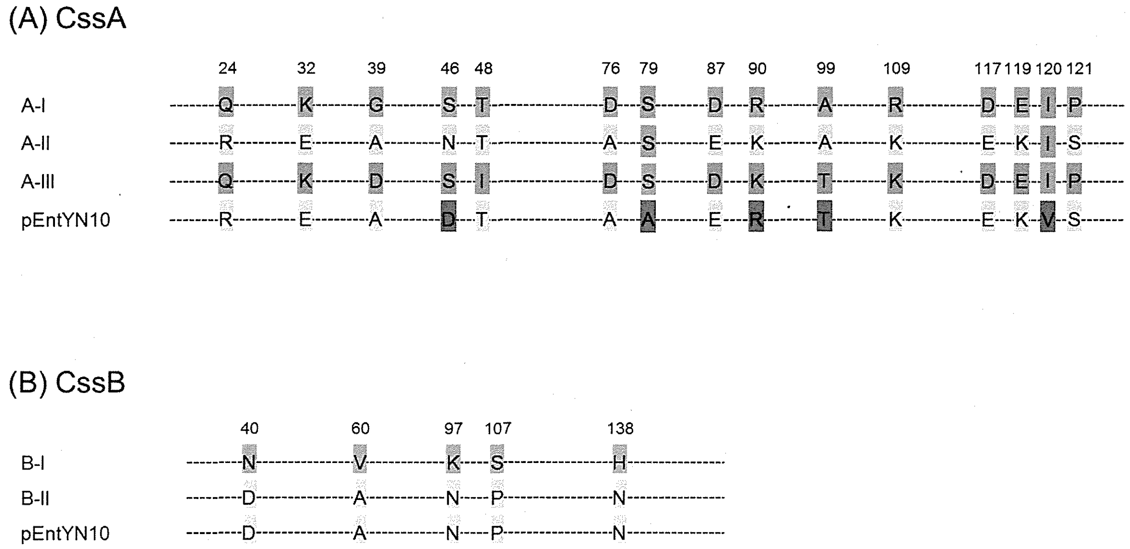
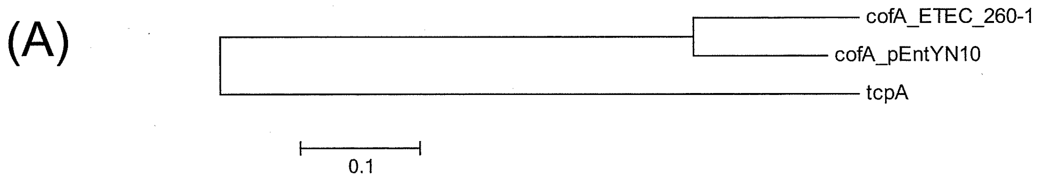


Fig. 2
CS6 の CssA および CssB のバリエーション.



(B)

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                         10        20        30        40        50        60        70        80        90       100
                 ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
cofA_260-1       MLSVYNRTQKMKEEARKKLAKYHELRK--QRGMSLLEVIIVLGIIGTIAAGVVILAQRAFDSRTVSELVTNTNTIRVAMKDAYQRDGKYPDYQAPLSLTA
cofA_pEntYN10    MLSVYNKTQKMKEEARKKLAKYHELRK--QRGMSLLEVIIVLGIIGTIAAGVVVLAQRAFDSRAITELVSNTNTIRVAMKDAYQRNGVYPDYQSPISLTA
tcpA             -------MQLLKQLFKKKFVKEEHDKKTGQEGMTLLEVIIVLGIMGVVSAGVVTLAQRAIDSQNMTKAAQNLNSVQIAMTQTYRSLGNYPATANANAATQ
                         * :*:  :**:.* .. :*  *.**:**********:*.::**** *****:**: ::: . * *::::**.::*:  * **   .  : *

                        110       120       130       140       150       160       170       180       190       200
                 ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
cofA_260-1       DSIKTDSTGI-AVAQLVQLGKLTPDEARNGISGDYIGIGGAITSSGSTINKGFAMELNGLSQEQCRSILGQVGDNWEYVAVGTSPSGSYDALSAGAVNML
cofA_pEntYN10    DTIKNPGTNLPAIAQLVQLGKLTADEGRNNISGDFVGVAGIVTSDNVTAKKAFAIELNGLSQDQCRSILGQVGNNWEYVEVGTSASGQYN-LGT-ARNMS
tcpA             LANG-----------LVSLGKVSADEAKNPFTGTAMGIFSFPR--NSAANKAFAITVGGLTQAQCKTLVTSVGDMFPFINVKEGAFAAVADLGDFETSVA
                  :             **.***::.**.:* ::*  :*: .     . : :*.**: :.**:* **:::: .**: : :: *  .. .    *.    .:

                        210       220       230       240
                 ....|....|....|....|....|....|....|....|....|..
cofA_260-1       AATDNTTILRSLAANGQ-----VSLTAEKILKTCTATVNSITLASR-
cofA_pEntYN10    SEVSN-TILRSLADGGQ-----DALTADKILGTCTATTNSIILGSR-
tcpA             DAATGAGVIKSIAPGSANLNLTNITHVEKL---CTGTAPFTVAFGNS
                   . .  :::*:* ..          ::*:   **.*.      ..
```

Fig. 3
pEntYN10 と *V. cholerae* 01 および ETEC 260-1 との CofA の比較．(A) Neighbour Joining method に基づく系統発生樹．(B) CLUSTAL 2.1 による 3 つのタンパク質のアミノ酸配列アレイメント．高度に保存された，*V. cholerae* の線毛構造の安定化に重要な残基をグレーで示している．

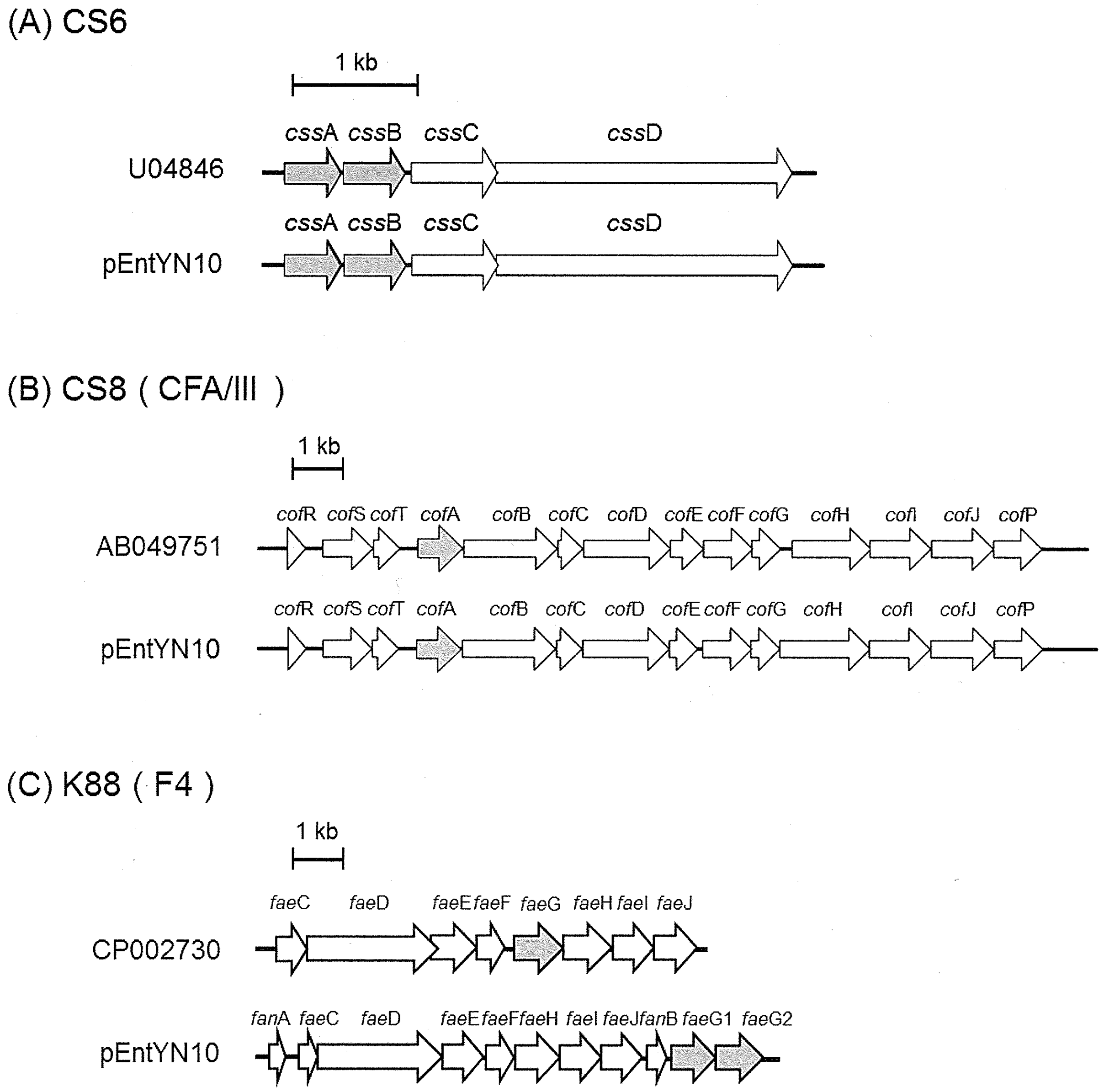

Fig. 4

pEntYN10と以前に報告されているETECプラスミド間の，付着関連遺伝子群の比較. (A) CS6[Accession ID:U04846] (B) CS8(CFA/III) CS6[Accession ID:AB049751] (C) K88(F4)-likeは，pUMNK88プラスミドの全塩基配列から抜粋したものと比較した [Accession ID:U04846]. 繊毛構造タンパク質をコードしている遺伝子は，グレーで示されている.

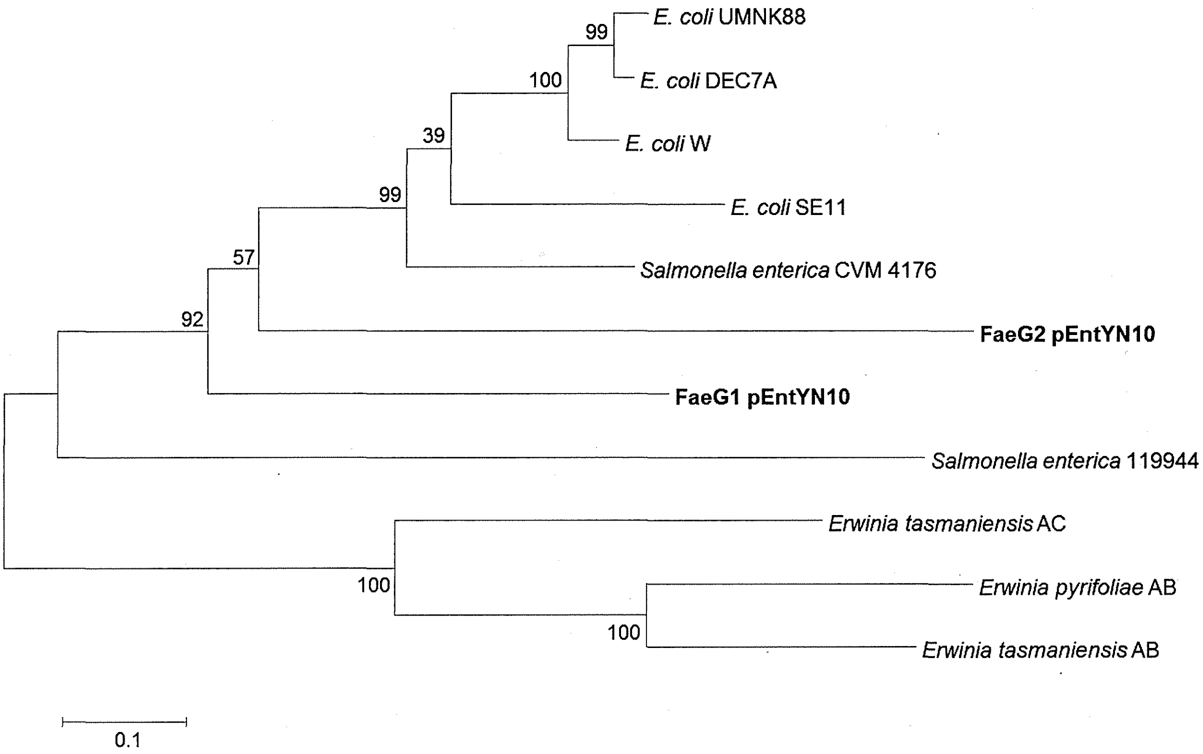

Fig. 5
faeG のアミノ酸配列を元に作成した系統発生樹．系統発生樹の分かれ目に記載されている数字は，ブートストラップバリューを表わす．

Table 3 細胞付着に関係することが予想される pEntYN10 上の推定 CDS

Gene				Products				
Cluster	Name	Length (bp)	GC content (%)	Length (AAs)	Size of AAs (kDa)	Predicted function	Putative ortholog (accession no.)	Identity (no. of AA, %)
CS6	*css* D	2409	32.30	802	90.21	Outer membrane usher	AAC45096	776/819 (94.7)
	css C	699	28.04	232	26.74	Periplasmic chaperone	AAC45095	224/232 (96.6)
	css B	504	37.50	167	17.94	Pilus subunit	AAC45094	159/167 (95.2)
	css A	465	36.34	154	16.97	Pilus subunit	AAC45093	141/154 (91.6)
CS8 (CFA/III)	*cof* P	825	33.81	274	30.52	Peptide-processing of prepilin	BAB62907	169/274 (61.7)
	cof J	1065	35.40	354	40.88	Unknown	BAB62906	191/363 (52.6)
	cof I	1026	38.30	341	38.11	Type II secretion system	BAB62905	293/341 (85.9)
	cof H	1530	38.69	509	57.85	Type II secretion system	BAB62904	397/510 (77.8)
	cof G	489	35.17	162	17.89	Unknown	BAB62903	93/162 (57.4)
	cof F	828	34.42	275	31.06	Pilus biosynthesis	BAB62902	159/275 (54.5)
	cof E	477	35.22	158	18.43	Pilus transmembrane anchor	BAB62901	99/186 (53.2)
	cof D	1458	36.21	485	54.22	Pilus biosynthesis	BAB62900	412/485 (84.9)
	cof C	420	39.52	139	15.66	Pilus biosynthesis	BAB62899	86/140 (61.4)
	cof B	1569	35.81	522	58.27	Pilus biosynthesis	BAB62898	336/527 (63.8)
	cof A	711	40.37	236	25.27	Pilus subunit	BAB62897	175/239 (73.2)
	cof T	444	43.47	147	16.62	Unknown	BAB62896	106/147 (72.1)
	cof S	834	36.21	277	31.53	Transcriptional regulator	BAB62895	160/285 (56.1)
	cof R	300	35.00	99	11.73	Transcriptional regulator	BAB62894	66/100 (66.0)
K88 (F4)	*fae* G2	873	38.83	290	31.04	Fimbrial major subunit	YP_006131672.1	115/308 (37.3)
	fae G1	831	44.40	276	28.88	Fimbrial major subunit	YP_006131672.1	129/291 (44.3)
	fae J	744	37.90	247	28.00	Minor fimbrial subunit	YP_006131675.1	73/265 (27.5)
	fae I	765	42.09	254	27.99	Minor fimbrial subunit	YP_006131674.1	113/258 (43.8)
	fae H	837	39.67	278	30.73	Minor fimbrial subunit	YP_006131673.1	152/309 (49.2)
	fae F	504	35.52	167	18.33	Minor fimbrial subunit	YP_006131671.1	72/167 (43.1)
	fae E	735	38.78	244	26.88	Periplasmic chaperone	YP_006131670.1	166/295 (56.3)
	fae D	2400	42.88	799	85.36	Outer membrane usher	YP_006131669.1	522/816 (64.0)
	fae C	633	35.87	210	23:01	Minor fimbrial subunit	YP_006131668.1	105/211 (49.8)

Table 1. ETEC O169:H41 の病原プラスミド pEntYN10 上の全タンパク質コード配列

No. of CDS	Strand orientation	Gene	Left end	Right end	Size (amino acids)	Putative description	The closest homology		
							Accession No.	Amino acid Identity	Description
1	-	*aat*D2	407	1057	216	Putative apolipoprotein N-acyltransferase AatD	WP_024171405.1	100%	apolipoprotein acyltransferase [Escherichia coli]
2	-		1609	1938	109	Transposase	WP_001595087.1	99%	hypothetical protein [Escherichia coli]
3	-		1987	2151	54	IS21 ORF2	EZB22434.1	100%	hypothetical protein BY55_18530 [Escherichia coli O169:H41 str. F9792]
4	+		2280	2492	70	IS1294 transposase	WP_001717486.1	100%	putative transposase [Escherichia coli]
5	+	*yaf*B	3178	3786	202	Putative unknown function protein YafB	WP_024191425.1	99%	hypothetical protein [Escherichia coli]
6	+		4441	4587	48	IS91 ORF	EMW29464.1	100%	putative transposase [Escherichia coli 2845650]
7	-	*cof*P	4945	5769	274	Type 4 prepilin-like proteins leader peptide-processing enzyme CofP	WP_001595093.1	100%	hypothetical protein [Escherichia coli]
8	-	*cof*J	5775	6839	354	Putative uncharacterized protein CofJ	WP_001595094.1	100%	hypothetical protein [Escherichia coli]
9	-	*cof*I	6854	7879	341	Type II secretion system F domain-containing protein CofI	WP_001595096.1	99%	hypothetical protein [Escherichia coli]
10	-	*cof*H	7866	9395	509	Type II secretion system protein CofH	WP_001595097.1	99%	hypothetical protein [Escherichia coli]
11	-	*cof*G	9395	9883	162	Putative uncharacterized protein CofG	WP_001595098.1	100%	hypothetical protein [Escherichia coli]
12	-	*cof*F	9871	10698	275	Putative pilus biosynthesis protein CofF	WP_001595099.1	100%	hypothetical protein [Escherichia coli]
13	-	*cof*E	10783	11259	158	Putative pilus biosynthesis transmembrane anchor protein CofE	WP_001595100.1	100%	hypothetical protein [Escherichia coli]
14	-	*cof*D	11262	12719	485	Putative exported pilus biosynthesis protein CofD	WP_001717441.1	100%	bacterial type II and III secretion system family protein [Escherichia coli]
15	-	*cof*C	12736	13155	139	Toxin co-regulated pilus biosynthesis protein CofC	WP_024171393.1	100%	pilus assembly protein [Escherichia coli]
16	-	*cof*B	13174	14742	522	Putative pilus biosynthesis protein CofB	WP_024171394.1	100%	N-terminal cleavage protein [Escherichia coli]
17	-	*cof*A	14803	15513	236	Toxin-coregulated pilus subunit CofA	WP_001717445.1	100%	toxin-coregulated pilus subunit TcpA family protein [Escherichia coli]
17.1	-	*cof*T	15817	16260	147	Putative hypothetical protein CofT	WP_001595106.1	100%	hypothetical protein [Escherichia coli]
18	-	*cof*S	16268	17101	277	Putative transcriptional regulator CofS	WP_001717447.1	100%	bacterial regulatory helix-turn-helix s, AraC family protein [Escherichia coli]
19	-	*cof*R	17385	17684	99	Major pilus subunit operon regulatory protein CofR	WP_024171395.1	100%	transcriptional regulator [Escherichia coli]
20	+		18421	19161	246	Site-specific recombinase	WP_001717448.1	100%	phage integrase family protein [Escherichia coli]
21	+		19251	19532	93	Putative uncharacterized protein	ELG41993.1	100%	hypothetical protein A1WM_04622 [Escherichia coli KTE101]
22	+		19581	19748	55	Transposase	WP_032189942.1	98%	transposase [Escherichia coli]
23	+		20329	20772	147	Integrase catalytic subunit	ELG41673.1	100%	hypothetical protein A1WM_04646 [Escherichia coli KTE101]
24	-	*rep*B	21130	22107	325	Initiator protein RepB	WP_023486339.1	99%	RepFIB replication protein A [Escherichia coli]
25	-		22980	23240	86	IS91 ORF	EGX22082.1	100%	putative transposase [Escherichia coli TX1999]
26	-		23234	24157	307	IS91 ORF	WP_032206866.1	98%	transposase [Escherichia coli]
27	-		24157	24522	121	IS91 ORF2	WP_001353648.1	100%	transposase [Escherichia coli]
28	-	*rel*E	24557	24883	108	Toxin-antitoxin system, toxin component, RelE family	WP_001595119.1	100%	RelE/StbE family addiction module toxin [Escherichia coli]
29	-		24880	25131	83	Toxin-antitoxin system, antitoxin component, PHD family	WP_001595120.1	100%	hypothetical protein [Escherichia coli]
30	+	*par*A	25685	26551	288	Partitioning protein ParA	WP_001595122.1	100%	hypothetical protein [Escherichia coli]
31	+	*par*B	26551	27582	343	Partitioning protein ParB	WP_001595123.1	100%	ParB-like partition protein [Escherichia coli]

32	+		27579	28019	146	Putative uncharacterized protein	ELG41659.1	99%	hypothetical protein A1WM_04659 [Escherichia coli KTE101]
33	+		28016	28339	107	Putative uncharacterized protein	WP_000143877.1	100%	MULTISPECIES: hypothetical protein [Enterobacteriaceae]
34	-	*umu*C	28378	29652	424	UV protection protein UmuC	WP_001595125.1	100%	protein samB [Escherichia coli]
35	-	*imp*A	29652	30074	140	UV protection protein UmuD	WP_001595126.1	100%	protein samA [Escherichia coli]
35.1	+		30377	31744	455	Transposase	EMW13368.1	99%	transposase family protein [Escherichia coli 2845650]
36	-		31329	31742	137	IS66 family element, transposase	WP_024171605.1	100%	transposase [Escherichia coli]
37	-		31792	32139	115	IS66 family ORF2	WP_001595131.1	100%	transposase [Escherichia coli]
38	-		32136	32537	133	IS66 family ORF1	WP_000536900.1	99%	transposase [Escherichia coli]
39	+		32676	33020	114	IS600 ORF2	WP_001719400.1	100%	integrase core domain protein [Escherichia coli]
40	+		33064	34176	370	IS186/IS421 transposase	WP_001300563.1	99%	MULTISPECIES: IS186 transposase [Bacteria]
41	+		34412	34720	102	IncFII RepA family protein	WP_032159711.1	100%	hypothetical protein [Escherichia coli]
42	+		34773	34919	48	IS91 ORF	ELG41999.1	100%	hypothetical protein A1WM_04628 [Escherichia coli KTE101]
43	-		35233	35430	65	Putative uncharacterized protein	WP_001413878.1	100%	hypothetical protein [Escherichia coli]
44	+	*cfa*D2	35627	36424	265	Transcriptional activator CfaD	WP_001595134.1	100%	transcriptional activator AggR [Escherichia coli]
45	-		36792	36938	48	IS91 ORF	ELG41999.1	100%	hypothetical protein A1WM_04628 [Escherichia coli KTE101]
46	-		36913	37416	167	Transposase	ELG41642.1	98%	hypothetical protein A1WM_04677 [Escherichia coli KTE101]
47	-		37574	38317	247	Transposase	ESS90459.1	99%	Mobile element protein [Escherichia coli CE516]
48	-		38311	38538	75	Transposase	WP_001595148.1	100%	hypothetical protein [Escherichia coli]
49	-		38674	39303	209	Putative uncharacterized protein	EMW26924.1	100%	hypothetical protein EC2845650_5230 [Escherichia coli 2845650]
50	-		39365	39601	78	Putative uncharacterized protein	WP_032348502.1	97%	AAA domain protein [Escherichia coli]
51	-		39619	40026	135	Putative uncharacterized protein	ELG41646.1	100%	hypothetical protein A1WM_04681 [Escherichia coli KTE101]
52	+		40698	41258	186	Resolvase domain-containing protein	WP_001595151.1	99%	transposons resolvase [Escherichia coli]
53	+		41261	43351	696	Transposase Tn3 family protein	WP_001717584.1	100%	tn3 transposase DDE domain protein [Escherichia coli]
54	+		43378	44229	283	Transposase for transposon Tn1721	WP_021557736.1	99%	transposase for transposon Tn501 [Escherichia coli]
55	+		44374	44739	121	IS91 ORF2	WP_001353648.1	100%	transposase [Escherichia coli]
56	+		44739	45662	307	IS91 ORF	WP_032206866.1	98%	transposase [Escherichia coli]
57	+		45656	45916	86	IS91 ORF	EGX22082.1	100%	putative transposase [Escherichia coli TX1999]
58	+		46272	46472	66	Iso-IS1 ORF2	WP_001717490.1	100%	transposase, IS1 family [Escherichia coli]
59	+		46488	46667	59	Iso-IS1 ORF2	WP_001472221.1	100%	transposase, IS1 family [Escherichia coli]
60	-	*css*D	46681	49089	802	CS6 outer membrane usher protein CssD	WP_001717499.1	100%	type VII secretion system (T7SS), usher family protein [Escherichia coli]
61	-	*css*C	49073	49771	232	CS6 subunits chaperone CssC	WP_001595139.1	100%	chaperone CssC [Escherichia coli]
62	-	*css*B	49820	50323	167	CS6 structural subunit CssB	WP_001595140.1	100%	hypothetical protein [Escherichia coli]
63	-	*css*A	50341	50805	154	CS6 structural subunit CssA	WP_024171410.1	100%	Cro/Cl family transcriptional regulator [Escherichia coli]
64	-		50951	51184	77	ISSfl4 ORF1	WP_032159698.1	100%	transposase [Escherichia coli]
65	-		51403	51576	57	Putative uncharacterized protein	EMW28502.1	98%	hypothetical protein EC2845650_5111 [Escherichia coli 2845650]
66	-		51877	52182	101	IS91 ORF	WP_001595218.1	100%	hypothetical protein [Escherichia coli]
67	-		52158	52532	124	IS91 ORF	ELG40995.1	100%	hypothetical protein A1WM_04745 [Escherichia coli KTE101]

68	-		52701	52973	90	Arylsulfatase regulatory protein	WP_000566440.1	100%	arylsulfatase regulatory protein [Escherichia coli]
69	-		52966	53544	192	Resolvase domain-containing protein	WP_001400936.1	100%	resolvase, N terminal domain protein [Escherichia coli]
70	+		53694	56741	1015	Transposase	WP_001717496.1	100%	tn3 transposase DDE domain protein [Escherichia coli]
71	-		56727	57128	133	IS91 ORF2	ELG40991.1	99%	hypothetical protein A1WM_04741 [Escherichia coli KTE101]
72	+	*sbm*A	57530	58717	395	Microcin B17 transporter SbmA	WP_024191434.1	100%	microcin B17 transporter [Escherichia coli]
72.1	-		58891	59469	192	Transposase	EZB21051.1	99%	transposase [Escherichia coli O169:H41 str. F9792]
73	-		59526	59807	93	Integrase catalytic subunit	WP_001595212.1	100%	transposase insF for insertion sequence IS3C [Escherichia coli]
74	-		59804	59962	52	Transposase insN for insertion sequence element IS911A	WP_001427614.1	100%	transposase [Escherichia coli]
75	-	*aat*C	60283	60909	208	ABC transporter ATP-binding protein AatC	WP_001595210.1	100%	hypothetical protein [Escherichia coli]
76	-	*aat*B	60902	61600	232	ABC transporter protein AatB	WP_001404563.1	100%	hypothetical protein [Escherichia coli]
77	-	*aat*A	61632	62834	400	ABC transporter membrane protein AatA	WP_001595205.1	100%	hypothetical protein [Escherichia coli]
78	-	*aat*P	62831	63970	379	ABC transporter membrane protein AatP	WP_024171554.1	100%	ABC transporter permease [Escherichia coli]
79	-		64966	65196	76	IS630 ORF	ELG40984.1	100%	hypothetical protein A1WM_04734 [Escherichia coli KTE101]
80	+		65203	65571	122	IS91 ORF	WP_001456881.1	99%	transposase family protein [Escherichia coli]
81	-	*rep*A1	66431	67300	289	IncFII family protein plasmid replication initiator RepA	EGB69767.1	99%	incFII family protein plasmid replication initiator RepA [Escherichia coli TW10509]
82	-	*rep*A2	67581	67841	86	Replication regulatory protein RepA2	WP_000083817.1	100%	replication protein [Escherichia coli]
83	+		68623	68805	60	Putative uncharacterized protein	WP_001393357.1	100%	hypothetical protein [Escherichia coli]
84	-	*tra*X	69029	69760	243	Type-F conjugative transfer system pilin acetylase TraX	WP_001717613.1	100%	type-F conjugative transfer system pilin acetylase TraX [Escherichia coli]
85	-		69757	70146	129	Superfamily I DNA and RNA helicases and helicase subunits (hypothetical)	WP_032201473.1	100%	hypothetical protein [Escherichia coli]
86	-	*tra*I	70321	73155	944	Conjugative transfer relaxase protein TraI	ESS98353.1	99%	IncF plasmid conjugative transfer DNA-nicking and unwinding protein TraI [Escherichia coli CE516]
87	+		73220	73588	122	IS600 ORF1	WP_000088325.1	100%	MULTISPECIES: transposase [Enterobacteriaceae]
88	+		73545	74696	383	Integrase	WP_001702847.1	100%	Mobile element protein [Escherichia coli]
89	+	*ybl*166	74981	75154	57	Ybl166	ELG40973.1	100%	hypothetical protein A1WM_04723 [Escherichia coli KTE101]
90	-		75181	76773	530	IS66 family element, transposase	WP_021514829.1	99%	transposase [Escherichia coli]
91	-		76804	77154	116	ISCro1 transposase B	WP_000624718.1	100%	MULTISPECIES: isocitrate lyase [Enterobacteriaceae]
92	-		77151	77576	141	Transposase OrfA	WP_013279332.1	100%	IS66 transposase [Escherichia coli]
93	+		77785	78003	72	Transposase	EMW17544.1	100%	transposase domain protein [Escherichia coli 2845650]
94	-		78065	78484	139	ISCro1 transposase C	WP_000381331.1	100%	hypothetical protein [Escherichia coli]
95	-	*est*	78778	78996	72	Heat-stable enterotoxin st-ia/st-p precursor	ELG40970.1	100%	heat-stable enterotoxin ST-IA/ST-P [Escherichia coli KTE101]
96	+		79501	79689	62	Transposase	WP_000598243.1	100%	transposase [Escherichia coli]
97	+		79774	80097	107	Transposase	ELG42021.1	95%	hypothetical protein A1WM_04608 [Escherichia coli KTE101]
98	+		80094	80276	60	Insertion element DNA-binding protein	WP_032228510.1	100%	transposase [Escherichia coli]
99	+		80806	81240	144	Transposase	WP_011076572.1	100%	transposase [Escherichia coli]
100	+		81237	81587	116	ISCro1 transposase B	WP_024171399.1	100%	transposase [Escherichia coli]
101	+		81618	82292	224	IS66 family element, transposase	WP_032306392.1	99%	transposase [Escherichia coli]
102	-		82403	83515	370	IS186/IS421 transposase	ENF96990.1	99%	transposase DDE domain protein [Escherichia coli P0305260.3]

103	+		83585	84580	331	IS66 family element, transposase	WP_032257626.1	99%	transposase [Escherichia coli]
104	+		84778	85203	141	Transposase OrfA from plasmid origin	WP_013279332.1	100%	IS66 transposase [Escherichia coli]
105	+		85200	85550	116	ISCro1 transposase B	WP_000624718.1	100%	MULTISPECIES: isocitrate lyase [Enterobacteriaceae]
106	+		85581	87173	530	IS66 family element, transposase	WP_021514829.1	99%	transposase [Escherichia coli]
107	-		87200	87745	181	Transposase	EMW28471.1	100%	integrase core domain protein [Escherichia coli 2845650]
108	-		88718	89014	98	IS91 ORF	EMW28019.1	99%	putative iS91 transposase [Escherichia coli 2845650]
109	+	*cex*E	89508	89864	118	Putative uncharacterized protein CexE (CfaD-dependent expression extracytoplasmic protein)	WP_013188496.1	95%	putative protein CexE precursor (CfaD-dependent expression extracytoplasmic protein) [Escherichia coli]
110	+		90078	90506	142	IS2 repressor TnpA	EGI19584.1	96%	transposase InsC for insertion element IS2A/D/F/H/I/K [Escherichia coli M718]
111	+		91017	91679	220	ISCro1 transposase C	WP_001410326.1	93%	isocitrate lyase [Escherichia coli]
112	-		91696	91890	64	Putative uncharacterized protein	EMW21114.1	100%	hypothetical protein EC2845650_1873 [Escherichia coli 2845650]
113	+		91855	92403	182	IS66 family element, transposase	EMW21113.1	99%	transposase IS66 family protein [Escherichia coli 2845650]
114	-		92545	93225	226	Protein encoded within IS	WP_021512953.1	98%	transposase [Escherichia coli]
115	-		93405	93638	77	IS2 ORF1	EMW13461.1	100%	transposase family protein [Escherichia coli 2845650]
116	+		93854	94531	225	Resolvase domain protein	WP_001719375.1	100%	resolvase, N terminal domain protein [Escherichia coli]
117	+		94632	94850	72	Putative mobile element protein	WP_001595176.1	100%	hypothetical protein [Escherichia coli]
118	-		94916	95065	49	Conserved hypothetical protein	ELG41031.1	100%	hypothetical protein A1WM_04707 [Escherichia coli KTE101]
119	-	*aat*D1	95435	96679	414	Putative apolipoprotein N-acyltransferase AatD	WP_024171601.1	100%	acyltransferase [Escherichia coli]
120	+		96887	97213	108	IS629 transposase OrfA	WP_001595174.1	100%	transposase [Escherichia coli]
121	-		97581	97895	104	Threonine dehydrogenase	WP_000348480.1	100%	MULTISPECIES: threonine dehydrogenase [Enterobacteriaceae]
122	-	*psi*A	97892	98566	224	Plasmid SOS inhibition protein A	WP_001719371.1	100%	psiA family protein [Escherichia coli]
123	-	*psi*B	98563	98997	144	Plasmid SOS inhibition protein B	WP_001719370.1	100%	protein psiB [Escherichia coli]
124	-		99052	101019	655	ParB/RepB/Spo0J family partition domain protein	WP_032201451.1	100%	hypothetical protein [Escherichia coli]
125	-	*yde*A	101080	101313	77	Putative unknown function protein YdeA	WP_001297827.1	100%	hypothetical protein [Escherichia coli]
126	-	*ssb*	101370	101891	173	Single-stranded DNA-binding protein Ssb	WP_032201449.1	100%	single-stranded DNA-binding protein [Escherichia coli]
127	-	*ydc*A	102744	103307	187	Putative unknown function protein YdcA	WP_032201448.1	100%	ribosomal RNA adenine dimethylase family protein [Escherichia coli]
128	-	*ydb*A	103354	104715	453	Putative unknown function protein YdbA	WP_032201446.1	100%	hydrolase [Escherichia coli]
129	-	*yda*B	104767	104997	76	Putative unknown function protein YdaB	WP_000218642.1	100%	MULTISPECIES: hypothetical protein [Bacteria]
130	-		105718	106071	117	Predicted protein	WP_001717516.1	100%	hypothetical protein [Escherichia coli]
131	+		106230	106592	120	ISSfl4 ORF1	WP_000436083.1	100%	transposase [Escherichia coli]
132	+		106589	106939	116	ISCro1 transposase B	WP_000624718.1	100%	MULTISPECIES: isocitrate lyase [Enterobacteriaceae]
133	+		106970	108583	537	IS66 family element, transposase	WP_013279331.1	99%	IS66 transposase [Escherichia coli]
134	-	*ych*A	108587	109177	196	Putative unknown function protein YchA	ELG41011.1	100%	hypothetical protein A1WM_04687 [Escherichia coli KTE101]
135	-		109222	109656	144	Hypothetical protein	WP_001595158.1	100%	hypothetical protein [Escherichia coli]
136	-		109670	110059	129	IS66 family element, transposase	WP_024171402.1	100%	hypothetical protein [Escherichia coli]
137	-		110095	110655	186	IS66 family element, transposase	WP_001410354.1	94%	hypothetical protein [Escherichia coli]
138	-		110686	111036	116	ISCro1 transposase B	WP_001464094.1	100%	putative transposase [Escherichia coli]

139	-		111033	111452	139	Transposase OrfA, ISEc8	WP_001595160.1	100%	transposase [Escherichia coli]
140	-		111592	111954	120	Putative uncharacterized protein	WP_032213589.1	100%	hypothetical protein [Escherichia coli]
141	-		112486	114582	698	Putative uncharacterized protein	WP_001717881.1	100%	ABC transporter family protein [Escherichia coli]
142	-	*hly*D	114579	115790	403	Secretion protein HlyD	WP_001717882.1	100%	biotin-lipoyl like family protein [Escherichia coli]
143	-		115938	116126	62	Putative uncharacterized protein	WP_001595165.1	100%	hypothetical protein [Escherichia coli]
144	-		116929	117684	251	Transposase subunit	WP_001282653.1	100%	MULTISPECIES: ATPase AAA [Enterobacteriaceae]
145	-		118347	119177	276	IS1294 transposase	EZB24257.1	99%	transposase [Escherichia coli O169:H41 str. F9792]
146	-		119383	119601	72	Mutator family transposase	WP_032177298.1	100%	transposase [Escherichia coli]
147	-		119647	120516	289	Mutator family transposase	WP_021499168.1	99%	transposase, Mutator family protein [Escherichia coli]
148	-		120641	121483	280	IS66 family element, transposase	WP_032268780.1	100%	transposase [Escherichia coli]
149	-		121557	122219	220	Transposase/IS protein	EMW23878.1	100%	istB-like ATP binding family protein [Escherichia coli 2845650]
150	-		122336	122596	86	Transposase for insertion sequence	WP_000408657.1	100%	transposase IS100 [Escherichia coli]
151	-		122679	124292	537	IS66 family element, transposase	WP_013279331.1	99%	IS66 transposase [Escherichia coli]
152	-		124323	124673	116	ISCro1 transposase B	WP_000624720.1	100%	isocitrate lyase [Escherichia coli]
153	-		124670	125032	120	ISSfl4 ORF1	WP_000436083.1	100%	transposase [Escherichia coli]
154	-	*vir*K	125192	126142	316	Virulence factor VirK	WP_023486370.1	100%	Virulence factor VirK [Escherichia coli]
155	-		126147	127235	362	Glycosyl transferase family protein	EZB21298.1	100%	glycosyl transferase [Escherichia coli O169:H41 str. F9792]
155.1	-		127238	128029	263	Carbohydrate transporter	WP_032201412.1	100%	carbohydrate transporter [Escherichia coli]
156	-	*yde*A	128323	128823	166	Putative unknown function protein YdeA	EZB20256.1	100%	hypothetical protein BY55_23845 [Escherichia coli O169:H41 str. F9792]
157	-	*ydf*A	128865	129122	85	Putative unknown function protein YdfA	WP_001595062.1	100%	hypothetical protein [Escherichia coli]
158	+		129599	130012	137	Putative uncharacterized protein (hypothetical)	WP_001595064.1	100%	hypothetical protein [Escherichia coli]
159	+		130107	130316	69	Resolvase	ELG42020.1	100%	resolvase [Escherichia coli KTE101]
160	+		130362	130649	95	Transposase	ELG42021.1	100%	hypothetical protein A1WM_04608 [Escherichia coli KTE101]
161	+		130680	131135	151	Iso-IS1 ORF2	WP_001595070.1	100%	transposase, IS1 family [Escherichia coli]
162	-	*fae*G2	131427	132299	290	Putative fimbrial antigen, homologous to FaeG	WP_001595072.1	100%	hypothetical protein [Escherichia coli]
163	-	*fae*G1	132319	133149	276	Fimbrial antigen FaeG	WP_001595073.1	100%	hypothetical protein [Escherichia coli]
164	-	*fan*B	133298	133597	62	Regulatory protein FanB	WP_032201317.1	100%	hypothetical protein [Escherichia coli]
165	-	*fae*J	133735	134478	247	Fimbrial protein FaeJ	WP_001595074.1	100%	hypothetical protein [Escherichia coli]
166	-	*fae*I	134489	135253	254	Minor fimbrial subunit FaeI	ELG42026.1	100%	hypothetical protein A1WM_04613 [Escherichia coli KTE101]
167	-	*fae*H	135270	136106	278	Putative uncharacterized protein FaeH	ELG42027.1	100%	hypothetical protein A1WM_04614 [Escherichia coli KTE101]
168	-	*fae*F	136182	136685	167	Putative fimbrial protein FaeF	WP_001595078.1	100%	hypothetical protein [Escherichia coli]
169	-	*fae*E	136727	137461	244	Chaperone protein FaeE	ELG42029.1	99%	chaperone faeE [Escherichia coli KTE101]
170	-	*fae*D	137454	139853	799	Outer membrane usher protein FaeD			
171	-	*fae*C	139863	140495	210	Fimbrial protein FaeC	EZB23502.1	100%	fimbrial protein [Escherichia coli O169:H41 str. F9792]
172	-	*fan*A	140474	140749	91	Regulatory protein FanA	WP_001595082.1	100%	hypothetical protein [Escherichia coli]
173	+		141543	141683	46	NHL repeat protein	EMW26623.1	98%	hypothetical protein EC2845650_5263 [Escherichia coli 2845650]
174	-		141812	142027	71	Iso-IS1 ORF2	WP_024191423.1	100%	transposase [Escherichia coli]

175	+	143216	143482	88	Integrase	EQW42353.1	100%	transposase InsI for insertion sequence element IS30D [Escherichia coli UMEA 3065-1]
176	-	143514	143957	147	Integrase catalytic subunit	ELG41673.1	100%	hypothetical protein A1WM_04646 [Escherichia coli KTE101]
177	-	144538	144705	55	Transposase	WP_032189942.1	100%	transposase [Escherichia coli]
178	-	144754	145035	93	Putative uncharacterized protein	ELG41993.1	100%	hypothetical protein A1WM_04622 [Escherichia coli KTE101]

Table 2.　ETEC O169:H41 の病原プラスミド pEntYN10 と他の ETEC の RepFIIA プラスミドの特性比較

	Host strain									
	ETEC YN10	C921b-1	H10407			ETEC 1392/75	E24377A			ETEC 4266
Name	pEntYN10	pCoo*	pETEC948	pETEC666	pEntH10407	p1018	pETEC_80	pETEC_74	pETEC_35	pCss165Kan*
Accession no.		NC_007635*	FN649418	FN649417	NC_013507	FN822745	NC_009786	NC_009790	NC_009787	NC_022333*
Size (bp)	145,082	98,396*	94,797	66,681	67,094	101,857	79,237	74,244	34,367	165,311*
No. of predicted CDSs	182	94	113	84	99	133	68	69	29	222
Stability genes	psiAB, relE	stbAB, ccdAB, yacAB, mok/hok/soc	stbAB, psiAB, sopAB, yacAB, mok/hok/soc	stbAB, psiAB, relE, mok/hok/soc	stbAB, psiAB, relE, mok/hok/soc	stbAB, psiAB, ccdAB	stbAB, psiAB, ccdAB	psiAB, sopAB, ccdAB	stbAB, relE	stbAB, psiAB, ccdAB, relE, mok/hok/sok
No. of IS or transposase (%)	83 (45.6)	18 (19.1)	56 (49.6)	20 (23.8)	11 (11.1)	50 (37.6)	20 (29.4)	31 (44.9)	0 (0)	60 (27.0)
Reference	This study	Froehlich, et al.	Crossman, et al.	Crossman, et al.	Ochi, et al.	Crossman, et al.	Rasko, et al	Rasko, et al	Rasko, et al	Wajima, et al.

*Registered plasmid includes artificial kanamycin resistant gene *aphA*

Ⅲ．研究成果の刊行に関する一覧表

研究成果の刊行に関する一覧表

発表者氏名	論文タイトル	発表誌名	巻号	ページ	出版年
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